

Supplemental Table 3. Summary of data generated by liquid chromatography-t

number	filename	parent_cha	score	percent_sc	totalIntens	previous_a
2140	L5P_ZT.375	2	5.36	66.1	4.76E+05	(K)
1305	X1P_ZT.349	6	7.3	64.7	7.81E+04	(F)
1099	S2P_ZT_Ro	2	8.03	68	1.19E+05	(L)
2016	L1P_ZT.489	4	5.6	67.3	1.99E+06	(V)
19	S5P_ZT_Ro	2	19.52	88.2	1.88E+08	(K)
30	L3P_ZT.117	2	18.85	86.3	6.29E+07	(K)
37	S4P_ZT_Ro	2	18.03	88.2	1.54E+08	(K)
45	S2P_ZT_Ro	2	17.67	88.6	1.25E+08	(K)
46	S1P_ZT_Ro	2	17.67	88.5	1.46E+08	(K)
55	X4P_ZT.111	2	17.12	86.6	5.63E+07	(K)
56	S3P_ZT_Ro	2	17.07	86.5	1.01E+08	(K)
60	L3P_ZT.119	2	16.91	85.9	1.20E+08	(K)
74	X2P_ZT.118	2	16.25	80	3.09E+06	(K)
93	X3P_ZT.114	2	15.63	84.4	1.04E+08	(K)
96	S4P_ZT_Ro	2	15.58	81.3	8.01E+07	(K)
102	L3P_ZT.129	2	15.45	100	4.84E+07	(K)
106	L1P_ZT.112	2	15.39	82.2	4.33E+06	(K)
133	S5P_ZT_Ro	2	14.89	81.6	9.61E+07	(K)
151	S3P_ZT_Ro	2	14.62	79	2.05E+06	(K)
163	X2P_ZT.116	2	14.45	78.1	3.09E+06	(K)
199	X3P_ZT.113	2	13.94	78.8	5.43E+07	(K)
219	X4P_ZT.110	2	13.68	77.6	3.19E+07	(K)
225	X1P_ZT.121	2	13.6	91.1	2.56E+06	(K)
293	X5P_ZT.113	2	12.7	89	2.57E+06	(K)
331	S4P_ZT_Ro	2	12.42	67.2	2.27E+06	(K)
351	X4P_ZT.120	2	12.24	68	3.19E+07	(K)
379	S5P_ZT_Ro	2	11.89	75.8	9.61E+07	(K)
404	L4P_ZT.128	2	11.78	77.3	8.68E+05	(K)
644	L2P_ZT.111	2	10.02	84.8	5.49E+05	(K)
657	X1P_ZT.119	2	9.96	68.5	2.56E+06	(K)
865	L3P_ZT.128	2	8.93	63.7	6.14E+07	(K)
881	S5P_ZT_Ro	2	8.86	74	1.88E+08	(K)
1036	X1P_ZT.120	2	8.26	76.7	2.56E+06	(K)
699	L3P_ZT.334	3	9.75	68.4	2.79E+05	(K)
731	X2P_ZT.344	3	9.58	80.5	8.08E+04	(K)
1841	S5P_ZT_Ro	3	5.94	80.6	1.44E+05	(K)
1440	L4P_ZT.277	4	6.89	79.1	5.24E+05	(K)
2215	S4P_ZT_Ro	4	5.23	66.7	1.27E+06	(R)
1684	X1P_ZT.414	3	6.31	69.6	9.89E+05	(R)
2062	X2P_ZT.450	3	5.5	100	7.38E+05	(R)
2316	X2P_ZT.448	3	5.03	61	7.38E+05	(R)
2149	L3P_ZT.521	2	5.34	61.2	2.51E+04	(K)
1243	L2P_ZT.472	3	7.51	71.5	8.62E+04	(E)
1500	L1P_ZT.482	3	6.75	88.5	9.54E+04	(E)
1692	L5P_ZT.497	6	6.3	72.9	7.30E+04	(K)

1656 X3P_ZT.16:	2	6.39	62.2	1.03E+06 (R)
2031 S2P_ZT_Ro	2	5.56	66.2	3.97E+06 (R)
2181 S2P_ZT_Ro	3	5.28	60.8	3.35E+05 (K)
105 S4P_ZT_Ro	2	15.39	82.1	5.52E+06 (R)
158 S5P_ZT_Ro	3	14.56	83.8	7.52E+06 (R)
176 S5P_ZT_Ro	2	14.2	100	3.09E+06 (R)
247 S1P_ZT_Ro	3	13.32	77	1.65E+07 (R)
256 S2P_ZT_Ro	2	13.22	95	3.33E+06 (R)
266 S4P_ZT_Ro	3	13.09	81	1.26E+07 (R)
272 S3P_ZT_Ro	3	12.98	79.4	7.08E+06 (R)
330 S1P_ZT_Ro	2	12.43	85.6	6.36E+06 (R)
338 S3P_ZT_Ro	2	12.38	80.3	2.87E+06 (R)
391 X3P_ZT.47:	3	11.83	71.2	8.30E+05 (R)
539 S2P_ZT_Ro	3	10.8	78.6	8.13E+06 (R)
821 S1P_ZT_Ro	3	9.1	67.4	1.65E+07 (R)
914 X3P_ZT.47:	2	8.72	73	3.85E+05 (R)
999 S5P_ZT_Ro	3	8.37	61.6	7.52E+06 (R)
1205 L3P_ZT.54:	2	7.66	70.1	2.34E+06 (R)
270 S3P_ZT_Ro	2	13.02	85.5	2.67E+07 (R)
414 S5P_ZT_Ro	2	11.72	90.3	3.23E+07 (R)
421 S2P_ZT_Ro	2	11.66	88.8	3.79E+07 (R)
422 S1P_ZT_Ro	2	11.66	88.5	3.58E+07 (R)
431 X3P_ZT.66:	2	11.58	77.9	2.43E+07 (R)
447 S4P_ZT_Ro	2	11.49	85.8	2.91E+07 (R)
452 X4P_ZT.66:	2	11.44	84	1.83E+07 (R)
626 L3P_ZT.74:	2	10.16	88	1.69E+07 (R)
663 X2P_ZT.70:	2	9.94	71.7	1.49E+06 (R)
668 S2P_ZT_Ro	2	9.91	72.3	1.66E+07 (R)
790 S3P_ZT_Ro	2	9.26	82	1.11E+07 (R)
930 S5P_ZT_Ro	2	8.62	67.9	1.43E+07 (R)
943 X4P_ZT.71:	2	8.58	71.6	8.35E+06 (R)
960 S3P_ZT_Ro	2	8.51	63.7	1.11E+07 (R)
991 X3P_ZT.71:	2	8.41	72.9	1.10E+07 (R)
1090 L3P_ZT.78:	2	8.06	83	6.82E+06 (R)
1114 S5P_ZT_Ro	2	7.97	71.9	1.43E+07 (R)
1264 S5P_ZT_Ro	2	7.44	62.7	9.62E+05 (R)
1295 X3P_ZT.81:	2	7.32	69.8	1.69E+06 (R)
1311 L3P_ZT.88:	2	7.27	62.8	1.23E+06 (R)
1374 S2P_ZT_Ro	2	7.05	95.1	1.66E+07 (R)
1393 S4P_ZT_Ro	2	7	61.4	1.24E+07 (R)
1433 S4P_ZT_Ro	2	6.9	78.2	1.24E+07 (R)
1441 X4P_ZT.81:	2	6.88	74.6	1.57E+06 (R)
1466 S1P_ZT_Ro	2	6.82	62.2	1.60E+07 (R)
1747 S2P_ZT_Ro	2	6.2	100	2.04E+06 (R)
1754 S5P_ZT_Ro	2	6.18	69.9	9.62E+05 (R)
1940 S3P_ZT_Ro	2	5.73	86.3	1.11E+07 (R)
2003 S4P_ZT_Ro	2	5.62	68.4	2.91E+07 (R)

1629	S2P_ZT_Ro	3	6.46	62.6	2.21E+05 (R)
2265	S3P_ZT_Ro	2	5.15	78.9	4.69E+05 (R)
2184	S3P_ZT_Ro	4	5.27	80.6	8.44E+04 (R)
1118	S1P_ZT_Ro	4	7.96	65.5	1.02E+06 (R)
1681	S1P_ZT_Ro	5	6.32	79	1.85E+06 (R)
940	L4P_ZT.380	3	8.6	92.1	2.05E+07 (A)
2244	L4P_ZT.364	3	5.21	67.6	1.01E+06 (K)
2280	S4P_ZT_Ro	3	5.11	60.7	3.25E+04 (K)
1855	L2P_ZT.372	3	5.92	62.2	5.04E+05 (K)
1899	L2P_ZT.374	3	5.82	67.5	5.04E+05 (K)
2046	L5P_ZT.397	3	5.54	75.2	7.34E+05 (K)
1414	S1P_ZT_Ro	3	6.96	67.6	1.69E+06 (K)
1788	X4P_ZT.547	3	6.09	77.2	4.09E+04 (K)
1938	X1P_ZT.398	3	5.73	60.7	2.94E+04 (K)
1993	S1P_ZT_Ro	3	5.64	66.6	1.54E+05 (K)
1994	S1P_ZT_Ro	3	5.64	62.9	1.63E+06 (K)
2067	L2P_ZT.513	3	5.5	70.3	6.84E+04 (K)
2121	L5P_ZT.482	3	5.39	81.2	7.65E+04 (K)
2282	L5P_ZT.467	3	5.11	68.7	7.46E+04 (K)
2312	X2P_ZT.388	4	5.04	64.4	1.58E+05 (K)
2017	L5P_ZT.395	3	5.6	73.8	5.25E+05 (K)
2276	L4P_ZT.358	3	5.12	72.1	7.65E+04 (K)
1344	X2P_ZT.536	3	7.16	65.8	2.28E+04 (K)
1382	X3P_ZT.408	3	7.02	75.3	2.67E+05 (K)
1450	X2P_ZT.558	3	6.86	71.8	8.38E+04 (K)
1472	L2P_ZT.520	3	6.81	74.4	6.84E+04 (K)
1633	X4P_ZT.413	3	6.45	78.2	2.05E+05 (K)
1676	L2P_ZT.399	3	6.34	66.1	1.61E+05 (K)
1712	L5P_ZT.535	3	6.27	63.1	9.61E+04 (K)
1770	L2P_ZT.380	3	6.14	83.1	1.20E+05 (K)
1805	L2P_ZT.445	3	6.06	65.6	4.81E+04 (K)
1825	S1P_ZT_Ro	3	6	74.4	7.84E+04 (K)
1891	L2P_ZT.507	3	5.83	68.6	2.55E+04 (K)
1908	S5P_ZT_Ro	3	5.79	68.1	2.39E+05 (K)
1927	L5P_ZT.448	3	5.76	65.4	2.68E+06 (K)
1957	L1P_ZT.390	3	5.71	74.5	6.32E+04 (K)
2001	X2P_ZT.483	3	5.62	71.8	7.75E+04 (K)
2021	L2P_ZT.515	3	5.59	94.5	6.84E+04 (K)
2025	S1P_ZT_Ro	3	5.58	77.9	5.52E+05 (K)
2129	S1P_ZT_Ro	3	5.37	72.7	3.24E+06 (K)
2142	L5P_ZT.537	3	5.36	85.4	7.92E+04 (K)
2162	L5P_ZT.381	3	5.32	88	1.64E+08 (K)
2173	X4P_ZT.478	3	5.29	72.7	5.44E+04 (K)
2178	L5P_ZT.452	3	5.29	72.5	5.64E+05 (K)
2195	L5P_ZT.470	3	5.26	70	1.78E+05 (K)
2258	L5P_ZT.497	3	5.17	100	1.99E+05 (K)
2262	L5P_ZT.523	3	5.16	80.4	3.10E+05 (K)

2279 X3P_ZT.43:	3	5.11	69.9	3.81E+04 (K)
2321 L3P_ZT.39C	3	5.02	72.8	7.74E+06 (K)
2084 L3P_ZT.491	3	5.47	69.9	3.12E+05 (K)
1787 X4P_ZT.54:	4	6.09	81.3	1.94E+06 (K)
1451 L1P_ZT.437	6	6.86	75.5	1.02E+05 (Y)
2245 X3P_ZT.13:	2	5.2	67.8	1.36E+05 (K)
1845 X4P_ZT.34:	6	5.93	61.1	7.52E+04 (D)
1670 L5P_ZT.369	3	6.36	62.8	3.78E+05 (K)
1212 S5P_ZT_Ro	5	7.62	62.8	2.65E+04 (K)
2260 L3P_ZT.503	5	5.16	66.9	9.41E+04 (R)
1209 L2P_ZT.496	3	7.65	76.9	8.75E+05 (V)
1518 S4P_ZT_Ro	3	6.71	78	7.01E+05 (V)
1519 S4P_ZT_Ro	3	6.71	76.5	7.01E+05 (V)
1353 S2P_ZT_Ro	2	7.14	61.5	4.50E+06 (K)
1421 S1P_ZT_Ro	2	6.94	71.6	6.12E+06 (K)
1476 S4P_ZT_Ro	2	6.8	66	3.01E+06 (K)
1548 L4P_ZT.209	2	6.65	60.2	2.11E+06 (K)
1952 L4P_ZT.353	2	5.72	100	4.70E+05 (R)
967 S5P_ZT_Ro	3	8.49	81.9	4.68E+05 (R)
1079 S3P_ZT_Ro	3	8.08	65.6	5.53E+05 (R)
1139 X1P_ZT.368	3	7.87	64.8	3.73E+05 (R)
1790 X1P_ZT.367	3	6.09	77.7	3.73E+05 (R)
1999 X3P_ZT.19:	2	5.62	73.6	3.61E+05 (R)
2095 S5P_ZT_Ro	3	5.45	61.7	4.68E+05 (R)
2123 L2P_ZT.365	3	5.38	64.7	2.09E+05 (R)
2218 L2P_ZT.366	3	5.23	73.5	2.09E+05 (R)
806 L5P_ZT.145	2	9.18	80.5	4.92E+07 (K)
828 X1P_ZT.146	2	9.08	77.8	7.96E+07 (K)
896 X2P_ZT.145	2	8.78	77.1	3.35E+07 (K)
906 L3P_ZT.145	2	8.76	77.6	4.32E+07 (K)
912 S5P_ZT_Ro	2	8.73	82.4	7.12E+07 (K)
997 L2P_ZT.134	2	8.38	83.2	5.19E+07 (K)
1024 S1P_ZT_Ro	2	8.3	78.3	7.88E+07 (K)
1025 X5P_ZT.144	2	8.29	76.8	5.30E+07 (K)
1055 S4P_ZT_Ro	2	8.18	75.8	6.00E+07 (K)
1163 L4P_ZT.152	2	7.79	76	3.51E+07 (K)
1172 L4P_ZT.153	2	7.76	67.6	3.51E+07 (K)
1240 X3P_ZT.139	2	7.51	77.9	5.07E+07 (K)
1276 X4P_ZT.140	2	7.4	74.5	7.30E+07 (K)
1319 X5P_ZT.14:	2	7.24	65.9	5.30E+07 (K)
1361 L1P_ZT.138	2	7.11	81.4	3.11E+07 (K)
2311 L1P_ZT.392	2	5.05	64.2	3.58E+07 (K)
1261 X5P_ZT.37:	5	7.44	66.9	3.02E+05 (S)
1667 X2P_ZT.37:	5	6.36	65.3	6.26E+04 (S)
212 S3P_ZT_Ro	2	13.76	70.6	3.01E+06 (K)
518 S4P_ZT_Ro	2	10.93	63.8	3.27E+06 (K)
755 S5P_ZT_Ro	2	9.47	70.3	2.46E+06 (K)

763 S3P_ZT_Ro	3	9.43	60.2	2.55E+06 (K)
988 S3P_ZT_Ro	2	8.42	73.3	3.01E+06 (K)
1389 X4P_ZT.506	2	7	63.3	8.31E+05 (K)
1510 L3P_ZT.585	2	6.73	72.3	2.35E+06 (K)
1627 S5P_ZT_Ro	3	6.46	62.2	1.82E+06 (K)
302 S2P_ZT_Ro	2	12.63	79.6	5.11E+04 (K)
407 X4P_ZT.158	3	11.76	79.7	6.14E+05 (K)
501 S3P_ZT_Ro	3	11.06	67.8	2.28E+05 (K)
512 L3P_ZT.164	3	10.96	71.8	2.44E+06 (K)
529 L3P_ZT.162	3	10.86	77.7	2.44E+06 (K)
547 S4P_ZT_Ro	3	10.76	60.8	3.18E+04 (K)
880 X4P_ZT.159	3	8.86	74.9	6.14E+05 (K)
1092 S4P_ZT_Ro	4	8.05	80.2	3.23E+05 (K)
1096 S2P_ZT_Ro	4	8.04	63.2	4.29E+05 (K)
1302 L3P_ZT.163	2	7.31	64.2	3.07E+04 (K)
1332 L3P_ZT.161	3	7.21	85.6	2.44E+06 (K)
1376 L3P_ZT.162	2	7.05	70.3	3.07E+04 (K)
95 S4P_ZT_Ro	3	15.6	85.1	7.86E+06 (K)
148 S2P_ZT_Ro	3	14.64	82	6.64E+06 (K)
159 X4P_ZT.223	2	14.53	81.7	1.97E+06 (K)
177 S4P_ZT_Ro	4	14.2	85.4	2.58E+06 (K)
211 X4P_ZT.220	3	13.76	74.6	9.60E+06 (K)
223 S4P_ZT_Ro	2	13.65	89.5	2.22E+06 (K)
233 L3P_ZT.222	2	13.53	76.7	3.69E+06 (K)
238 S3P_ZT_Ro	3	13.44	78.2	7.13E+06 (K)
249 S2P_ZT_Ro	4	13.31	86	2.99E+06 (K)
322 S2P_ZT_Ro	2	12.5	72.8	1.96E+06 (K)
323 L3P_ZT.233	2	12.5	75.1	1.09E+05 (K)
377 S1P_ZT_Ro	4	11.94	75.1	2.96E+06 (K)
378 S3P_ZT_Ro	4	11.93	85	2.55E+06 (K)
399 S1P_ZT_Ro	3	11.81	73.5	6.70E+06 (K)
411 S1P_ZT_Ro	3	11.76	80.5	6.70E+06 (K)
420 S2P_ZT_Ro	2	11.66	76.5	1.96E+06 (K)
494 L3P_ZT.218	3	11.15	78.3	1.96E+07 (K)
555 X4P_ZT.236	3	10.68	65.6	3.24E+05 (K)
564 L3P_ZT.219	2	10.63	68.7	3.69E+06 (K)
576 S1P_ZT_Ro	2	10.47	72.2	2.06E+06 (K)
658 S4P_ZT_Ro	2	9.96	68.6	9.15E+04 (K)
722 L3P_ZT.221	2	9.64	65.3	3.69E+06 (K)
747 X4P_ZT.223	4	9.5	67.4	3.33E+05 (K)
777 X4P_ZT.223	2	9.35	63	1.97E+06 (K)
795 S1P_ZT_Ro	2	9.25	82.8	2.06E+06 (K)
1065 X4P_ZT.235	2	8.13	62.3	1.05E+05 (K)
1283 S3P_ZT_Ro	3	7.38	65	7.13E+06 (K)
1470 S1P_ZT_Ro	2	6.81	60.8	6.98E+04 (K)
1720 L1P_ZT.205	4	6.25	73.4	1.86E+04 (K)
2177 L3P_ZT.232	2	5.29	73	1.09E+05 (K)

2198 S4P_ZT_Ro	3	5.25	87.1	7.86E+06 (K)
41 S5P_ZT_Ro	2	17.92	84.8	4.46E+06 (K)
58 S3P_ZT_Ro	2	17.04	78.5	8.20E+06 (K)
75 S4P_ZT_Ro	2	16.19	86.2	5.68E+06 (K)
77 S3P_ZT_Ro	2	16.16	75.6	8.20E+06 (K)
108 S1P_ZT_Ro	2	15.33	74.9	7.57E+06 (K)
121 S3P_ZT_Ro	2	15.03	82.9	8.20E+06 (K)
139 S1P_ZT_Ro	3	14.83	74.6	5.38E+07 (K)
153 S2P_ZT_Ro	3	14.6	73.6	2.05E+07 (K)
173 S1P_ZT_Ro	2	14.27	70.1	7.57E+06 (K)
185 S3P_ZT_Ro	3	14.09	72.5	5.25E+07 (K)
200 S5P_ZT_Ro	3	13.92	68.8	3.31E+07 (K)
209 X4P_ZT.57	2	13.81	72.7	2.45E+06 (K)
213 S5P_ZT_Ro	2	13.74	95	4.46E+06 (K)
250 X3P_ZT.56	2	13.3	65	2.29E+06 (K)
295 S2P_ZT_Ro	2	12.7	66.3	2.69E+06 (K)
309 S4P_ZT_Ro	3	12.59	70.4	4.00E+07 (K)
346 S5P_ZT_Ro	2	12.29	66.3	4.46E+06 (K)
364 S2P_ZT_Ro	2	12.1	70.1	2.69E+06 (K)
409 X3P_ZT.56	3	11.76	62.3	1.26E+07 (K)
442 X5P_ZT.56	3	11.52	72.8	6.19E+05 (K)
473 S4P_ZT_Ro	2	11.3	84	5.68E+06 (K)
477 S2P_ZT_Ro	2	11.28	60.7	2.69E+06 (K)
524 S1P_ZT_Ro	2	10.89	77.2	7.57E+06 (K)
583 X2P_ZT.60	2	10.42	82.3	8.25E+04 (K)
621 S4P_ZT_Ro	2	10.21	89.7	1.27E+05 (K)
628 S5P_ZT_Ro	2	10.15	66.8	6.47E+04 (K)
640 L3P_ZT.65	2	10.06	63.3	3.08E+06 (K)
1016 S1P_ZT_Ro	3	8.33	72.1	5.38E+07 (K)
1503 X3P_ZT.50	2	6.74	70.9	2.29E+06 (K)
1718 S3P_ZT_Ro	2	6.25	71.5	2.52E+04 (K)
67 X3P_ZT.12	2	16.51	84.9	5.28E+05 (K)
88 S4P_ZT_Ro	3	15.72	80	2.65E+06 (K)
138 S1P_ZT_Ro	4	14.83	84	9.97E+06 (K)
183 S2P_ZT_Ro	3	14.1	84.4	2.79E+06 (K)
217 X4P_ZT.11	3	13.69	85	2.31E+06 (K)
248 L3P_ZT.12	3	13.32	89.6	2.34E+06 (K)
254 S1P_ZT_Ro	3	13.24	65.5	3.22E+06 (K)
345 X3P_ZT.12	3	12.3	84.8	3.18E+06 (K)
366 S3P_ZT_Ro	4	12.09	66	5.04E+05 (K)
373 S1P_ZT_Ro	3	11.98	72.3	3.22E+06 (K)
393 S4P_ZT_Ro	4	11.83	82.5	8.01E+06 (K)
417 S5P_ZT_Ro	3	11.67	68.3	2.61E+05 (K)
436 S5P_ZT_Ro	3	11.55	79.7	2.40E+06 (K)
462 X4P_ZT.11	2	11.37	64.2	4.26E+05 (K)
536 L3P_ZT.12	3	10.81	100	2.34E+06 (K)
538 S5P_ZT_Ro	4	10.8	88.9	7.89E+06 (K)

545 S1P_ZT_Ro	3	10.77	74.3	1.27E+05 (K)
617 S2P_ZT_Ro	3	10.22	65.4	2.42E+05 (K)
637 L3P_ZT.12	4	10.08	80.7	6.84E+06 (K)
677 S3P_ZT_Ro	4	9.85	77	9.72E+06 (K)
678 S4P_ZT_Ro	3	9.84	72.7	2.65E+06 (K)
694 L3P_ZT.12	3	9.77	68.1	2.34E+06 (K)
740 S5P_ZT_Ro	4	9.56	64	5.86E+05 (K)
771 S3P_ZT_Ro	3	9.4	69.2	3.09E+06 (K)
861 S2P_ZT_Ro	4	8.95	68.9	9.15E+06 (K)
905 S5P_ZT_Ro	3	8.76	63.1	2.40E+06 (K)
963 S3P_ZT_Ro	3	8.5	66.1	3.09E+06 (K)
996 S5P_ZT_Ro	2	8.38	65.3	9.58E+04 (K)
1095 S4P_ZT_Ro	4	8.04	60.4	8.01E+06 (K)
1211 S2P_ZT_Ro	4	7.63	64.1	5.89E+05 (K)
2039 X4P_ZT.13	4	5.54	70.7	1.47E+05 (K)
2087 S4P_ZT_Ro	4	5.46	64.3	6.93E+05 (K)
22 S2P_ZT_Ro	2	19.43	96.2	5.04E+06 (K)
48 S4P_ZT_Ro	2	17.62	87.6	9.25E+06 (K)
63 S1P_ZT_Ro	2	16.83	84.9	5.93E+06 (K)
83 S3P_ZT_Ro	2	15.88	83.9	4.46E+06 (K)
90 S5P_ZT_Ro	3	15.69	78.7	2.21E+06 (K)
91 S1P_ZT_Ro	4	15.66	95	5.85E+07 (K)
122 S1P_ZT_Ro	2	15.01	90.2	5.93E+06 (K)
123 S5P_ZT_Ro	3	14.97	82.9	3.76E+07 (K)
124 S2P_ZT_Ro	3	14.97	80.9	2.24E+07 (K)
140 S3P_ZT_Ro	2	14.81	87.6	4.46E+06 (K)
149 S4P_ZT_Ro	4	14.62	85.2	1.09E+08 (K)
161 X4P_ZT.17	4	14.45	94.5	3.55E+07 (K)
168 S2P_ZT_Ro	2	14.34	85.7	5.04E+06 (K)
175 L3P_ZT.17	3	14.21	82.5	5.19E+07 (K)
179 X4P_ZT.17	3	14.18	89.1	1.47E+07 (K)
184 S2P_ZT_Ro	4	14.1	84.5	6.16E+07 (K)
205 S1P_ZT_Ro	3	13.88	77.9	2.18E+07 (K)
206 S5P_ZT_Ro	4	13.87	83.8	1.11E+08 (K)
216 S3P_ZT_Ro	3	13.7	81.4	2.23E+06 (K)
234 S3P_ZT_Ro	3	13.49	78.3	2.23E+06 (K)
242 X3P_ZT.17	4	13.39	78.9	4.34E+07 (K)
259 X3P_ZT.17	2	13.2	81.8	4.70E+06 (K)
277 X4P_ZT.19	3	12.87	70.9	2.48E+06 (K)
279 S1P_ZT_Ro	3	12.85	87.8	2.30E+06 (K)
280 X4P_ZT.17	2	12.84	85.6	3.29E+06 (K)
291 S3P_ZT_Ro	4	12.71	73.3	5.49E+06 (K)
298 S4P_ZT_Ro	3	12.64	70.6	2.10E+06 (K)
319 S4P_ZT_Ro	3	12.53	81.1	3.98E+07 (K)
326 S3P_ZT_Ro	4	12.48	83.9	4.51E+07 (K)
340 S2P_ZT_Ro	2	12.37	74	7.02E+05 (K)
353 L3P_ZT.19	2	12.22	81.1	2.52E+05 (K)

357 S4P_ZT_Ro	3	12.18	70.8	2.10E+06 (K)
358 L1P_ZT.165	3	12.18	76.1	1.01E+06 (K)
359 L3P_ZT.193	4	12.17	68.8	4.92E+06 (K)
381 X4P_ZT.190	2	11.88	78.5	4.81E+05 (K)
394 S3P_ZT_Ro	2	11.83	76.2	4.46E+06 (K)
396 S5P_ZT_Ro	4	11.82	70	5.08E+06 (K)
402 X3P_ZT.190	2	11.79	71.9	1.77E+05 (K)
403 S5P_ZT_Ro	2	11.79	69.3	7.21E+06 (K)
408 X4P_ZT.176	2	11.76	80.1	3.29E+06 (K)
418 S5P_ZT_Ro	2	11.67	72.9	7.21E+06 (K)
430 S3P_ZT_Ro	2	11.59	80.1	4.46E+06 (K)
441 S1P_ZT_Ro	4	11.53	65.3	5.85E+07 (K)
455 S1P_ZT_Ro	2	11.42	81.5	7.94E+05 (K)
458 S4P_ZT_Ro	2	11.4	72	5.85E+05 (K)
464 S4P_ZT_Ro	3	11.37	67.2	2.10E+06 (K)
465 S3P_ZT_Ro	3	11.37	69.6	1.69E+07 (K)
470 S4P_ZT_Ro	3	11.33	70.4	3.98E+07 (K)
478 S5P_ZT_Ro	2	11.26	83.4	7.21E+06 (K)
479 S2P_ZT_Ro	2	11.25	72.9	7.02E+05 (K)
481 S3P_ZT_Ro	2	11.23	83.7	4.22E+05 (K)
483 S2P_ZT_Ro	3	11.22	70	2.12E+06 (K)
490 L3P_ZT.179	4	11.18	71.3	1.42E+08 (K)
495 S5P_ZT_Ro	2	11.14	77	5.27E+05 (K)
508 S4P_ZT_Ro	2	10.98	78.1	9.25E+06 (K)
510 S5P_ZT_Ro	4	10.96	66.1	1.11E+08 (K)
511 S5P_ZT_Ro	3	10.96	62.9	3.76E+07 (K)
521 S5P_ZT_Ro	2	10.9	74.8	7.21E+06 (K)
546 L3P_ZT.179	3	10.77	79.9	5.19E+07 (K)
554 L3P_ZT.181	2	10.7	61	1.03E+07 (K)
567 S5P_ZT_Ro	3	10.59	66	2.21E+06 (K)
577 X4P_ZT.174	3	10.46	69.2	1.47E+07 (K)
582 S1P_ZT_Ro	2	10.43	75.4	5.93E+06 (K)
584 L3P_ZT.180	2	10.42	73.2	1.03E+07 (K)
589 S1P_ZT_Ro	3	10.4	79.7	2.18E+07 (K)
594 S3P_ZT_Ro	3	10.38	68.9	2.23E+06 (K)
599 L3P_ZT.183	3	10.35	88.4	5.19E+07 (K)
602 L3P_ZT.182	2	10.32	66.1	1.03E+07 (K)
619 X3P_ZT.174	3	10.21	73.3	1.81E+07 (K)
636 S2P_ZT_Ro	2	10.08	71.5	5.04E+06 (K)
643 L3P_ZT.179	2	10.03	62.2	1.03E+07 (K)
650 S5P_ZT_Ro	2	9.99	73.3	5.27E+05 (K)
653 S4P_ZT_Ro	4	9.98	84.1	5.04E+06 (K)
670 X3P_ZT.174	2	9.89	73.4	4.70E+06 (K)
693 S1P_ZT_Ro	4	9.77	68.2	6.83E+06 (K)
707 S5P_ZT_Ro	2	9.7	67	7.21E+06 (K)
724 S1P_ZT_Ro	2	9.63	64.8	5.93E+06 (K)
727 X4P_ZT.174	3	9.6	68.5	1.47E+07 (K)

733 S4P_ZT_Ro	2	9.58	63.6	5.85E+05 (K)
743 S4P_ZT_Ro	2	9.55	69.7	9.25E+06 (K)
757 S4P_ZT_Ro	2	9.44	70.9	5.85E+05 (K)
784 S2P_ZT_Ro	2	9.3	76.3	7.02E+05 (K)
796 S5P_ZT_Ro	2	9.24	70.3	7.21E+06 (K)
844 L3P_ZT.195	2	9.01	72	2.52E+05 (K)
845 X4P_ZT.190	3	9	61.4	2.48E+06 (K)
895 L3P_ZT.194	3	8.8	66.6	2.43E+06 (K)
922 L3P_ZT.177	2	8.69	69.9	1.03E+07 (K)
1011 S2P_ZT_Ro	4	8.34	69.7	6.10E+06 (K)
1023 S5P_ZT_Ro	3	8.3	70.7	2.21E+06 (K)
1027 S1P_ZT_Ro	3	8.28	74.3	2.18E+07 (K)
1049 S3P_ZT_Ro	2	8.21	68.7	4.22E+05 (K)
1220 S4P_ZT_Ro	2	7.58	61.2	9.25E+06 (K)
1234 X3P_ZT.191	2	7.54	66.6	1.77E+05 (K)
1267 S1P_ZT_Ro	3	7.44	60.1	2.18E+07 (K)
1300 S2P_ZT_Ro	4	7.31	70.5	6.16E+07 (K)
1307 S2P_ZT_Ro	4	7.3	66.3	6.16E+07 (K)
1422 L1P_ZT.166	3	6.93	88	1.00E+06 (K)
1445 L3P_ZT.191	3	6.88	61.8	2.43E+06 (K)
1535 S2P_ZT_Ro	3	6.68	64.6	2.12E+06 (K)
1613 X4P_ZT.191	3	6.48	62.3	2.48E+06 (K)
2010 L1P_ZT.178	2	5.61	61.2	1.02E+05 (K)
2210 S1P_ZT_Ro	2	5.24	72	2.86E+05 (K)
1810 X3P_ZT.186	4	6.04	70	6.51E+05 (K)
1762 L5P_ZT.542	4	6.17	75.4	5.52E+04 (D)
857 L1P_ZT.319	3	8.96	65.3	2.79E+05 (Q)
276 S3P_ZT_Ro	2	12.91	85.7	1.23E+05 (G)
544 S2P_ZT_Ro	2	10.77	67.4	3.03E+05 (G)
679 S4P_ZT_Ro	2	9.84	65.3	4.44E+05 (G)
2277 L5P_ZT.123	3	5.12	62.9	1.09E+05 (K)
2310 S5P_ZT_Ro	6	5.05	70.4	3.78E+04 (K)
1924 L2P_ZT.354	5	5.76	64.1	1.74E+06 (K)
1983 X2P_ZT.383	5	5.65	84.7	1.17E+06 (K)
2037 L3P_ZT.378	5	5.55	65.9	5.80E+05 (K)
2253 X4P_ZT.376	5	5.17	74	7.77E+04 (K)
923 L2P_ZT.261	5	8.66	66.4	5.37E+06 (R)
1052 X5P_ZT.271	5	8.19	69.4	2.90E+06 (R)
1137 L3P_ZT.269	5	7.88	64	9.93E+05 (R)
1149 S3P_ZT_Ro	5	7.85	62.1	2.77E+06 (R)
1150 S2P_ZT_Ro	5	7.85	65.3	2.07E+06 (R)
1333 L5P_ZT.278	5	7.21	64.4	7.91E+05 (R)
1554 X1P_ZT.269	5	6.63	63.9	2.62E+05 (R)
1632 X4P_ZT.274	5	6.45	82	2.11E+06 (R)
1833 S2P_ZT_Ro	5	5.97	71.8	2.07E+06 (R)
1844 X4P_ZT.271	5	5.93	89.4	2.11E+06 (R)
1904 S1P_ZT_Ro	5	5.8	73.8	2.23E+06 (R)

1963 S4P_ZT_Ro	5	5.69	69.7	2.45E+06 (R)
2285 S5P_ZT_Ro	5	5.1	73.4	6.33E+05 (R)
1038 L3P_ZT.363	3	8.26	68.2	6.83E+05 (-)
1371 L3P_ZT.353	3	7.07	63.3	1.64E+06 (G)
1250 X5P_ZT.649	3	7.48	83.9	1.33E+05 (K)
2148 L3P_ZT.519	6	5.34	61.1	6.08E+04 (K)
1256 S1P_ZT_Ro	3	7.47	63.4	8.48E+04 (R)
2130 S1P_ZT_Ro	3	5.37	67.7	8.48E+04 (R)
1245 S5P_ZT_Ro	2	7.5	100	5.87E+06 (K)
1317 X5P_ZT.466	2	7.25	100	4.93E+06 (K)
2042 S2P_ZT_Ro	2	5.54	93.2	5.37E+07 (K)
76 S3P_ZT_Ro	2	16.16	86.6	9.93E+07 (K)
78 L3P_ZT.105	2	16.14	85.4	2.70E+08 (K)
99 S4P_ZT_Ro	2	15.54	83.4	1.93E+08 (K)
126 X4P_ZT.873	2	14.96	81.3	2.09E+08 (K)
131 X3P_ZT.986	2	14.91	82.2	1.65E+08 (K)
155 S1P_ZT_Ro	2	14.57	80.4	1.97E+08 (K)
164 S4P_ZT_Ro	2	14.42	69.8	9.11E+07 (K)
170 S2P_ZT_Ro	2	14.29	82.9	1.15E+08 (K)
171 S5P_ZT_Ro	2	14.27	82.4	1.68E+08 (K)
182 S2P_ZT_Ro	2	14.13	85.7	5.72E+07 (K)
239 S2P_ZT_Ro	2	13.42	75.4	5.72E+07 (K)
241 S1P_ZT_Ro	2	13.41	68.9	9.18E+07 (K)
271 L3P_ZT.113	2	13	67.3	1.21E+08 (K)
297 S5P_ZT_Ro	2	12.67	71	7.88E+07 (K)
310 S3P_ZT_Ro	2	12.59	72.3	4.67E+07 (K)
450 S3P_ZT_Ro	2	11.46	69.3	4.67E+07 (K)
497 X5P_ZT.106	2	11.13	68.6	3.11E+06 (K)
552 S5P_ZT_Ro	2	10.71	63.2	7.88E+07 (K)
738 X4P_ZT.976	2	9.56	62.9	2.09E+08 (K)
1320 X5P_ZT.993	2	7.24	62.8	3.11E+06 (K)
288 S4P_ZT_Ro	2	12.75	82.7	1.70E+06 (K)
300 S1P_ZT_Ro	2	12.64	82.9	2.14E+06 (K)
463 X4P_ZT.183	2	11.37	78.9	1.45E+06 (K)
515 S5P_ZT_Ro	2	10.93	81.1	1.55E+06 (K)
588 S3P_ZT_Ro	2	10.4	78.9	2.39E+06 (K)
688 S2P_ZT_Ro	2	9.79	76	2.62E+06 (K)
929 X3P_ZT.183	2	8.62	74.1	1.78E+06 (K)
939 L3P_ZT.187	2	8.6	64.5	1.09E+06 (K)
246 S2P_ZT_Ro	2	13.35	85.9	2.59E+07 (K)
336 X4P_ZT.307	2	12.39	80	1.78E+07 (K)
416 X4P_ZT.306	2	11.68	70.8	1.78E+07 (K)
486 S1P_ZT_Ro	2	11.2	73.4	3.03E+07 (K)
890 L3P_ZT.303	2	8.83	74	1.61E+07 (K)
114 X4P_ZT.219	4	15.21	74.8	2.40E+04 (K)
1606 S4P_ZT_Ro	7	6.5	60.3	1.30E+06 (R)
1973 S1P_ZT_Ro	4	5.67	100	6.30E+05 (R)

128	S3P_ZT_Ro	4	14.93	65.8	1.42E+06 (R)
197	S2P_ZT_Ro	4	13.98	68.6	1.55E+06 (R)
230	S2P_ZT_Ro	4	13.56	61.1	1.55E+06 (R)
278	X3P_ZT.21	3	12.85	68.6	1.57E+06 (R)
443	X4P_ZT.21	4	11.52	66.7	1.03E+06 (R)
563	S3P_ZT_Ro	3	10.63	62.5	5.76E+05 (R)
711	S3P_ZT_Ro	4	9.69	63.2	1.42E+06 (R)
1019	X3P_ZT.21	3	8.31	63.4	1.57E+06 (R)
1887	L3P_ZT.21	4	5.84	65.8	1.45E+06 (R)
1540	L5P_ZT.44	5	6.66	69.2	1.44E+06 (R)
2229	S3P_ZT_Ro	6	5.22	100	7.34E+04 (K)
934	S5P_ZT_Ro	7	8.61	60.9	1.64E+04 (R)
1523	S5P_ZT_Ro	7	6.7	61.6	2.24E+04 (R)
1123	S4P_ZT_Ro	4	7.94	61	2.07E+05 (K)
1565	S5P_ZT_Ro	6	6.6	61.3	1.30E+05 (K)
2309	X5P_ZT.50	7	5.05	65.6	7.52E+06 (K)
1736	S2P_ZT_Ro	3	6.22	100	1.16E+06 (R)
1874	X4P_ZT.30	3	5.88	64.8	9.62E+04 (R)
1979	L5P_ZT.21	2	5.66	83.7	1.22E+06 (R)
2283	L5P_ZT.49	4	5.11	63.2	7.42E+04 (R)
2238	X1P_ZT.14	2	5.21	90.6	9.25E+06 (K)
1077	L3P_ZT.33	4	8.09	67.4	8.89E+04 (K)
2024	X1P_ZT.49	3	5.58	87.9	1.03E+05 (K)
1975	X1P_ZT.21	2	5.66	75.6	2.44E+06 (R)
1474	X3P_ZT.50	3	6.8	63.9	2.23E+06 (R)
1784	S2P_ZT_Ro	3	6.1	63.5	1.31E+06 (R)
1851	X3P_ZT.50	3	5.92	100	2.23E+06 (R)
1853	S5P_ZT_Ro	3	5.92	100	1.60E+06 (R)
2106	L5P_ZT.49	3	5.42	100	9.92E+05 (R)
2249	L4P_ZT.11	4	5.2	100	5.08E+04 (K)
1941	L2P_ZT.32	3	5.73	67.7	5.09E+04 (R)
2317	X1P_ZT.27	2	5.03	61.4	3.51E+05 (K)
1654	S3P_ZT_Ro	4	6.4	65.1	1.92E+06 (R)
2251	X2P_ZT.24	3	5.18	78.8	1.77E+04 (R)
1424	L4P_ZT.27	3	6.93	86.6	2.09E+06 (R)
1567	S2P_ZT_Ro	4	6.6	76.4	5.49E+04 (R)
1202	S4P_ZT_Ro	3	7.66	62.5	2.65E+06 (R)
1303	L5P_ZT.47	3	7.31	62.3	1.66E+05 (R)
1469	S5P_ZT_Ro	3	6.81	64.9	2.14E+06 (R)
2102	X4P_ZT.52	4	5.42	100	5.85E+04 (R)
1780	X5P_ZT.17	4	6.11	67.7	1.38E+05 (K)
1974	L1P_ZT.15	4	5.67	66.4	5.89E+04 (K)
1221	L2P_ZT.22	3	7.58	84.6	5.75E+05 (R)
1313	X4P_ZT.24	3	7.26	74.5	7.73E+05 (R)
1323	S3P_ZT_Ro	3	7.23	75.7	9.65E+05 (R)
1592	S4P_ZT_Ro	3	6.54	68.2	1.62E+06 (R)
1860	S2P_ZT_Ro	3	5.91	79.2	8.77E+05 (R)

1894 X3P_ZT.248	3	5.82	69.9	1.34E+06 (R)
2011 L1P_ZT.228	3	5.61	67.8	7.09E+05 (R)
2072 X4P_ZT.528	7	5.48	68.2	2.72E+05 (S)
917 L1P_ZT.458	3	8.72	73.9	4.26E+04 (V)
1419 X3P_ZT.468	3	6.94	66.7	6.06E+04 (V)
1499 S4P_ZT_Ro	3	6.75	100	7.69E+04 (V)
2235 X3P_ZT.258	2	5.21	65.7	2.82E+06 (R)
938 S2P_ZT_Ro	3	8.6	61.7	4.62E+07 (R)
956 S4P_ZT_Ro	3	8.54	61	3.82E+07 (R)
1053 S3P_ZT_Ro	3	8.19	62.6	3.40E+07 (R)
1057 L5P_ZT.328	3	8.16	62.7	1.59E+07 (R)
1461 S5P_ZT_Ro	3	6.83	66.2	4.51E+07 (R)
1494 X3P_ZT.314	3	6.76	67	2.92E+07 (R)
1506 L4P_ZT.318	3	6.74	67.8	5.93E+06 (R)
1174 L2P_ZT.518	5	7.75	66.7	8.76E+04 (K)
1789 X2P_ZT.528	7	6.09	78.1	5.71E+04 (K)
2213 X4P_ZT.378	2	5.23	62.6	8.53E+04 (K)
1151 S5P_ZT_Ro	3	7.84	72.9	9.70E+06 (H)
1508 L4P_ZT.488	3	6.74	64.5	8.86E+05 (H)
1645 X1P_ZT.488	3	6.42	100	1.18E+06 (H)
1783 S4P_ZT_Ro	3	6.1	91.6	1.23E+07 (H)
1498 S4P_ZT_Ro	3	6.75	61.5	8.57E+04 (H)
1933 S2P_ZT_Ro	2	5.74	79.2	4.99E+05 (R)
2183 X3P_ZT.374	4	5.27	64.3	2.55E+04 (R)
1596 S3P_ZT_Ro	4	6.52	60.8	2.35E+05 (K)
1 S3P_ZT_Ro	2	25.6	97.1	7.39E+06 (K)
2 S1P_ZT_Ro	2	25.22	92.8	1.00E+07 (K)
3 S2P_ZT_Ro	2	23.15	96.2	1.50E+07 (K)
4 X3P_ZT.558	2	22.01	91.6	4.43E+06 (K)
5 S5P_ZT_Ro	2	21.12	88.6	6.80E+06 (K)
25 L3P_ZT.614	3	19.26	89.7	3.57E+07 (K)
32 S4P_ZT_Ro	2	18.73	80.3	2.38E+07 (K)
35 L3P_ZT.638	2	18.4	87.8	1.31E+07 (K)
47 S1P_ZT_Ro	3	17.64	83.6	2.72E+07 (K)
54 X4P_ZT.558	2	17.24	85.6	7.45E+06 (K)
62 S2P_ZT_Ro	3	16.83	80.7	4.48E+07 (K)
68 S3P_ZT_Ro	3	16.51	85.3	1.81E+07 (K)
69 X5P_ZT.548	2	16.48	88.8	4.44E+05 (K)
70 L3P_ZT.680	2	16.45	70.7	1.31E+07 (K)
87 L5P_ZT.634	2	15.81	80.6	6.66E+04 (K)
100 S4P_ZT_Ro	2	15.48	86.2	2.38E+07 (K)
144 S1P_ZT_Ro	2	14.77	66.3	1.00E+07 (K)
154 S3P_ZT_Ro	3	14.58	71.6	1.81E+07 (K)
235 X4P_ZT.558	3	13.48	64	1.66E+07 (K)
273 X4P_ZT.618	2	12.97	61.4	7.45E+06 (K)
292 L4P_ZT.712	2	12.71	70	3.55E+05 (K)
360 X4P_ZT.574	2	12.16	68.7	7.45E+06 (K)

472 X5P_ZT.54	3	11.32	66	1.51E+06 (K)
735 S1P_ZT_Ro	2	9.58	69.7	1.00E+07 (K)
770 X1P_ZT.71	3	9.4	84.1	8.33E+06 (K)
1196 L3P_ZT.66	3	7.68	69	3.57E+07 (K)
1233 S1P_ZT_Ro	3	7.55	62.1	2.72E+07 (K)
1178 S4P_ZT_Ro	3	7.74	67.2	9.09E+04 (K)
15 X2P_ZT.59	2	19.85	75.7	5.18E+05 (K)
31 S2P_ZT_Ro	2	18.74	78.8	1.50E+07 (K)
33 S4P_ZT_Ro	2	18.53	84	2.38E+07 (K)
53 X3P_ZT.54	3	17.36	78	8.40E+06 (K)
65 S5P_ZT_Ro	3	16.55	81	2.37E+07 (K)
84 S4P_ZT_Ro	3	15.86	79.3	6.78E+07 (K)
1155 S2P_ZT_Ro	3	7.82	64.4	4.48E+07 (K)
959 X3P_ZT.23	2	8.51	68.9	9.02E+05 (S)
1418 L5P_ZT.43	3	6.95	71.2	8.01E+04 (K)
824 S1P_ZT_Ro	2	9.09	63.7	1.25E+06 (S)
2176 S1P_ZT_Ro	2	5.29	85.4	5.25E+05 (R)
119 S2P_ZT_Ro	2	15.05	85.4	1.31E+08 (R)
134 S3P_ZT_Ro	2	14.88	83.3	9.36E+07 (R)
135 S5P_ZT_Ro	2	14.86	83.7	2.72E+08 (R)
143 S1P_ZT_Ro	2	14.77	82.2	1.48E+08 (R)
172 S4P_ZT_Ro	2	14.27	80.7	2.95E+08 (R)
178 L3P_ZT.16	2	14.19	80.6	1.69E+08 (R)
228 X4P_ZT.15	2	13.57	78.9	2.84E+08 (R)
296 X3P_ZT.15	2	12.69	79.2	1.35E+08 (R)
387 S2P_ZT_Ro	2	11.86	76.1	1.24E+06 (R)
500 X3P_ZT.12	2	11.07	68.3	5.82E+05 (R)
550 X2P_ZT.16	2	10.74	75	7.46E+06 (R)
634 S5P_ZT_Ro	2	10.08	65.7	9.07E+05 (R)
645 S4P_ZT_Ro	2	10.01	62.4	1.57E+06 (R)
661 S1P_ZT_Ro	2	9.95	73.6	1.34E+06 (R)
830 X4P_ZT.12	2	9.06	66.6	1.02E+06 (R)
846 L3P_ZT.12	2	9	62	9.07E+05 (R)
1514 S3P_ZT_Ro	2	6.72	77.4	4.76E+05 (R)
1832 L1P_ZT.15	2	5.98	75.9	5.67E+06 (R)
1634 X3P_ZT.23	3	6.45	100	6.29E+05 (K)
1969 X2P_ZT.47	4	5.67	100	4.98E+04 (I)
1878 S2P_ZT_Ro	5	5.87	67.8	6.11E+04 (K)
1144 S1P_ZT_Ro	2	7.86	71.6	4.59E+04 (R)
2154 L5P_ZT.82	3	5.33	83.8	4.16E+04 (R)
2168 X3P_ZT.78	3	5.3	83.9	8.07E+04 (R)
1746 S4P_ZT_Ro	3	6.2	63.3	8.01E+04 (R)
1034 L1P_ZT.48	3	8.27	79.8	5.07E+05 (R)
1142 X4P_ZT.49	3	7.86	77.4	2.50E+05 (R)
1454 L2P_ZT.47	3	6.85	66.4	2.88E+05 (R)
1925 L3P_ZT.49	3	5.76	61.8	4.93E+05 (R)
978 X5P_ZT.25	5	8.44	64.1	2.34E+05 (R)

71 X4P_ZT.560	2	16.42	72.9	1.03E+08 (F)
79 S3P_ZT_Ro	2	16.13	81.3	1.64E+07 (F)
97 S4P_ZT_Ro	2	15.55	81.6	3.23E+06 (F)
98 L3P_ZT.637	2	15.55	80	1.41E+06 (F)
261 S4P_ZT_Ro	2	13.13	72.5	8.44E+06 (F)
263 S2P_ZT_Ro	2	13.11	79.7	1.26E+07 (F)
275 S1P_ZT_Ro	2	12.92	76	2.60E+07 (F)
312 S5P_ZT_Ro	2	12.58	80.9	8.66E+06 (F)
318 X3P_ZT.560	2	12.54	71.9	4.16E+07 (F)
485 L3P_ZT.650	2	11.21	68.5	1.41E+06 (F)
813 S2P_ZT_Ro	2	9.13	62.3	3.10E+07 (F)
157 L3P_ZT.805	2	14.57	88.4	4.40E+06 (P)
307 X4P_ZT.705	2	12.59	85	3.95E+06 (P)
532 S3P_ZT_Ro	2	10.84	71.2	3.91E+06 (P)
654 S2P_ZT_Ro	2	9.98	66.3	4.97E+06 (P)
687 S4P_ZT_Ro	2	9.79	62.2	4.56E+06 (P)
868 S2P_ZT_Ro	2	8.92	61.3	7.53E+06 (S)
1058 L1P_ZT.417	2	8.15	66.1	5.06E+06 (K)
1438 X1P_ZT.395	2	6.89	62.9	2.81E+07 (K)
1484 L3P_ZT.415	2	6.78	86.7	1.64E+06 (K)
1600 L5P_ZT.445	2	6.52	75.5	5.39E+05 (K)
1753 L4P_ZT.428	2	6.19	76.2	3.52E+04 (K)
1767 X1P_ZT.416	2	6.14	61.2	5.92E+05 (K)
1850 X3P_ZT.434	2	5.92	76.1	2.55E+06 (K)
1857 L3P_ZT.460	2	5.92	100	1.84E+06 (K)
1911 L3P_ZT.425	2	5.79	63.2	1.14E+07 (K)
2020 L1P_ZT.415	2	5.59	64.3	8.65E+06 (K)
2075 X3P_ZT.437	2	5.47	100	2.74E+05 (K)
2138 L2P_ZT.395	2	5.36	92.6	2.28E+07 (K)
2163 L5P_ZT.440	2	5.32	78.3	1.07E+06 (K)
2179 X2P_ZT.420	2	5.28	70	7.95E+06 (K)
2189 X1P_ZT.410	2	5.26	88.7	8.38E+05 (K)
2194 L5P_ZT.437	2	5.26	90.6	2.06E+06 (K)
2222 X5P_ZT.445	2	5.22	88.9	4.35E+05 (K)
2226 X3P_ZT.454	2	5.22	100	2.98E+05 (K)
2232 L2P_ZT.430	2	5.22	100	3.69E+04 (K)
2233 L3P_ZT.465	2	5.22	100	5.69E+04 (K)
2248 L1P_ZT.418	2	5.2	80.3	3.84E+06 (K)
2255 X1P_ZT.415	2	5.17	78	8.36E+04 (K)
2296 L4P_ZT.427	2	5.09	85.6	3.52E+04 (K)
109 S5P_ZT_Ro	2	15.32	87.9	5.92E+06 (S)
118 X3P_ZT.359	2	15.07	88.4	3.03E+06 (S)
141 X4P_ZT.360	2	14.8	91.6	7.84E+06 (S)
150 S4P_ZT_Ro	2	14.62	87	8.26E+06 (S)
186 L3P_ZT.532	2	14.09	68.4	6.43E+04 (S)
257 L3P_ZT.360	2	13.21	86.9	4.39E+06 (S)
328 S4P_ZT_Ro	2	12.45	86.4	1.01E+05 (S)

339	S5P_ZT_Ro	2	12.37	80.7	8.26E+04 (S)
342	S1P_ZT_Ro	2	12.36	91.3	6.70E+06 (S)
356	S1P_ZT_Ro	2	12.2	79.9	6.70E+06 (S)
468	S4P_ZT_Ro	2	11.34	74.6	8.26E+06 (S)
525	S3P_ZT_Ro	2	10.88	72.6	2.57E+06 (S)
553	S3P_ZT_Ro	2	10.71	63.7	6.56E+04 (S)
569	S1P_ZT_Ro	2	10.56	90.6	3.32E+04 (S)
648	L3P_ZT.359	2	10.01	68.9	4.36E+06 (S)
651	S2P_ZT_Ro	2	9.99	92.2	5.22E+04 (S)
681	S2P_ZT_Ro	2	9.82	62.1	2.38E+06 (S)
1237	L1P_ZT.386	2	7.53	60.9	4.94E+07 (S)
385	X3P_ZT.128	2	11.86	88.6	2.20E+07 (R)
386	S5P_ZT_Ro	2	11.86	89	2.03E+07 (R)
400	S2P_ZT_Ro	2	11.8	86	1.99E+07 (R)
401	S1P_ZT_Ro	2	11.8	86.6	2.17E+07 (R)
406	X4P_ZT.129	2	11.76	84.9	1.98E+07 (R)
475	L3P_ZT.134	2	11.29	85.6	2.03E+07 (R)
476	S4P_ZT_Ro	2	11.28	84.8	1.84E+07 (R)
503	S3P_ZT_Ro	2	11.02	94.9	2.09E+07 (R)
507	S5P_ZT_Ro	2	11	77.2	2.03E+07 (R)
520	X1P_ZT.137	2	10.91	83.5	9.12E+05 (R)
526	S4P_ZT_Ro	2	10.87	77.4	1.84E+07 (R)
528	S3P_ZT_Ro	2	10.86	88	2.14E+07 (R)
665	X2P_ZT.139	2	9.93	78	1.23E+06 (R)
973	S2P_ZT_Ro	2	8.47	64	1.99E+07 (R)
989	S1P_ZT_Ro	2	8.42	73.8	2.17E+07 (R)
1087	X4P_ZT.127	2	8.06	70.9	1.98E+07 (R)
1138	X5P_ZT.130	2	7.87	66.1	5.83E+05 (R)
1156	L3P_ZT.139	2	7.82	63.4	2.03E+07 (R)
1958	L2P_ZT.328	2	5.71	86	3.56E+05 (R)
1955	X3P_ZT.478	3	5.71	61.7	1.73E+06 (K)
362	S4P_ZT_Ro	2	12.14	73.2	4.96E+07 (R)
451	X4P_ZT.527	2	11.44	68.2	1.32E+08 (R)
461	X3P_ZT.549	2	11.38	72.2	3.94E+07 (R)
499	S1P_ZT_Ro	2	11.08	69.7	2.82E+07 (R)
596	L3P_ZT.607	2	10.37	67.5	7.74E+07 (R)
611	S2P_ZT_Ro	2	10.25	66.5	2.55E+07 (R)
630	S3P_ZT_Ro	2	10.15	70.7	4.40E+07 (R)
751	S5P_ZT_Ro	2	9.48	63.9	5.11E+07 (R)
756	L3P_ZT.718	2	9.46	74.9	6.99E+05 (R)
1185	X5P_ZT.530	2	7.72	68.4	1.25E+06 (R)
1954	X4P_ZT.639	2	5.71	80.7	1.83E+07 (R)
517	S4P_ZT_Ro	2	10.93	62.3	2.79E+06 (R)
659	S3P_ZT_Ro	2	9.96	67.5	3.15E+06 (R)
750	S1P_ZT_Ro	2	9.49	62.5	3.71E+06 (R)
850	S2P_ZT_Ro	2	8.99	62.3	4.89E+06 (R)
1104	S2P_ZT_Ro	2	8.02	85.6	4.89E+06 (R)

1116	S1P_ZT_Ro	2	7.97	62.6	3.71E+06 (R)
1678	X4P_ZT.48:	2	6.33	64.9	1.96E+05 (R)
847	X4P_ZT.32(6	8.99	68.2	2.10E+06 (R)
1559	L4P_ZT.32:	5	6.63	78.3	3.78E+05 (R)
2257	L4P_ZT.317	5	5.17	100	3.78E+05 (R)
1146	S1P_ZT_Ro	3	7.86	65	3.00E+04 (R)
6	S3P_ZT_Ro	2	21.11	97.3	1.12E+08 (R)
20	L3P_ZT.104	2	19.52	95.6	3.51E+08 (R)
21	X4P_ZT.97:	2	19.45	92.7	2.37E+08 (R)
24	S1P_ZT_Ro	2	19.28	96.7	2.12E+08 (R)
26	S5P_ZT_Ro	2	19.23	95.2	1.90E+08 (R)
27	S4P_ZT_Ro	2	19.19	93.5	2.24E+08 (R)
36	X3P_ZT.98:	2	18.36	90.4	1.90E+08 (R)
42	S2P_ZT_Ro	2	17.91	92.9	1.28E+08 (R)
313	L5P_ZT.11(2	12.58	83.7	3.71E+06 (R)
337	X2P_ZT.10:	2	12.39	72.4	7.06E+06 (R)
365	S1P_ZT_Ro	2	12.1	64.7	2.12E+08 (R)
471	L4P_ZT.12(2	11.33	79.9	4.44E+06 (R)
587	S5P_ZT_Ro	2	10.4	60.7	1.90E+08 (R)
603	S4P_ZT_Ro	2	10.31	71.4	2.24E+08 (R)
728	S2P_ZT_Ro	2	9.59	86.6	1.28E+08 (R)
767	X1P_ZT.11:	2	9.41	73.1	5.72E+06 (R)
833	L1P_ZT.104	2	9.06	72.2	9.06E+06 (R)
855	S2P_ZT_Ro	2	8.97	60.2	1.28E+08 (R)
1056	L1P_ZT.105	2	8.17	68.8	9.06E+06 (R)
116	S2P_ZT_Ro	3	15.17	100	6.52E+04 (R)
180	S3P_ZT_Ro	3	14.14	61.4	2.80E+06 (R)
202	S4P_ZT_Ro	3	13.89	63.6	3.69E+06 (R)
203	S2P_ZT_Ro	3	13.89	63.8	3.80E+06 (R)
264	S5P_ZT_Ro	3	13.1	60.7	3.35E+06 (R)
274	L3P_ZT.248	3	12.95	67.1	1.80E+06 (R)
695	X4P_ZT.25:	3	9.76	63.5	1.60E+06 (R)
1028	S1P_ZT_Ro	2	8.28	68.8	9.26E+05 (R)
1260	L3P_ZT.247	2	7.45	60.5	3.96E+05 (R)
1984	X2P_ZT.47:	3	5.65	61.7	3.10E+05 (R)
1816	X5P_ZT.354	5	6.02	64.4	1.27E+05 (R)
1341	X5P_ZT.21:	4	7.16	63.2	3.03E+06 (R)
1646	S2P_ZT_Ro	4	6.42	62.6	5.93E+05 (R)
2023	L5P_ZT.219	4	5.59	64.8	2.18E+06 (R)
2153	S1P_ZT_Ro	4	5.33	63.7	1.37E+06 (R)
2029	L1P_ZT.485	5	5.57	72.3	1.97E+04 (R)
2098	S2P_ZT_Ro	6	5.44	71.8	2.86E+05 (R)
1316	S1P_ZT_Ro	3	7.26	66.1	4.54E+06 (R)
1576	L4P_ZT.116	3	6.58	100	8.47E+06 (R)
1616	L3P_ZT.114	3	6.48	73.5	3.26E+05 (R)
1705	X2P_ZT.10:	3	6.28	100	1.33E+06 (R)
1758	X2P_ZT.10(3	6.17	100	1.33E+06 (R)

1995 L1P_ZT.101	3	5.64	87.3	1.07E+07 (R)
1452 X3P_ZT.249	3	6.85	61.9	2.32E+06 (R)
974 S2P_ZT_Ro	6	8.47	73.2	4.82E+04 (R)
1966 S2P_ZT_Ro	6	5.68	72.3	3.16E+04 (R)
1141 S1P_ZT_Ro	6	7.87	66.5	5.04E+04 (R)
1189 L1P_ZT.220	2	7.71	65.3	1.05E+06 (G)
1551 X3P_ZT.368	6	6.64	71.3	2.26E+04 (R)
1659 X2P_ZT.376	6	6.37	67.3	1.08E+06 (R)
2043 S1P_ZT_Ro	6	5.54	77.4	1.27E+06 (R)
2040 X2P_ZT.514	2	5.54	71.7	3.30E+04 (R)
558 L3P_ZT.269	2	10.66	60.9	1.44E+08 (R)
578 S4P_ZT_Ro	2	10.46	62.2	1.75E+08 (R)
624 L1P_ZT.236	2	10.17	63	3.73E+06 (R)
625 X2P_ZT.289	2	10.16	62.9	7.57E+06 (R)
680 S5P_ZT_Ro	2	9.83	62.7	3.21E+07 (R)
684 S3P_ZT_Ro	2	9.8	61.9	4.39E+07 (R)
696 X4P_ZT.253	2	9.76	61.1	1.37E+08 (R)
715 S2P_ZT_Ro	2	9.67	66.7	4.99E+07 (R)
720 L1P_ZT.258	2	9.65	65.2	4.45E+06 (R)
762 S4P_ZT_Ro	2	9.43	61.4	5.20E+07 (R)
775 S1P_ZT_Ro	2	9.37	60.9	6.26E+07 (R)
803 X2P_ZT.264	2	9.18	68.3	3.99E+06 (R)
811 L3P_ZT.249	2	9.15	61.3	6.07E+07 (R)
887 X4P_ZT.271	2	8.84	62	1.37E+08 (R)
915 S5P_ZT_Ro	2	8.72	100	3.21E+07 (R)
1046 S2P_ZT_Ro	2	8.22	87.6	3.28E+05 (R)
1072 L1P_ZT.258	2	8.11	86.8	4.45E+06 (R)
1119 L1P_ZT.255	2	7.96	70	4.45E+06 (R)
1175 L3P_ZT.268	2	7.75	61.5	1.44E+08 (R)
1197 X1P_ZT.260	2	7.67	82.9	2.87E+06 (R)
1268 L2P_ZT.237	2	7.44	68.6	5.54E+05 (R)
1360 X3P_ZT.271	2	7.11	85.6	1.24E+08 (R)
1388 L1P_ZT.256	2	7.01	66.3	4.45E+06 (R)
1394 S3P_ZT_Ro	2	7	100	1.28E+08 (R)
1521 L4P_ZT.263	2	6.71	85.1	7.27E+05 (R)
1639 S3P_ZT_Ro	2	6.43	64.3	4.39E+07 (R)
1800 X4P_ZT.184	2	6.06	78.3	3.78E+06 (R)
1823 S1P_ZT_Ro	2	6	75.7	6.26E+07 (R)
1935 L2P_ZT.253	2	5.74	68.6	1.76E+06 (R)
1949 L2P_ZT.238	2	5.72	100	5.54E+05 (R)
1951 L3P_ZT.287	2	5.72	100	1.51E+05 (R)
1978 L4P_ZT.282	2	5.66	81.2	1.50E+06 (R)
2033 L1P_ZT.292	4	5.56	67	4.02E+05 (K)
1364 X3P_ZT.364	7	7.09	60.6	4.99E+04 (K)
371 S4P_ZT_Ro	3	11.99	81.2	4.46E+06 (N)
664 X4P_ZT.174	2	9.93	76.2	3.51E+05 (N)
675 S1P_ZT_Ro	3	9.88	89.2	1.81E+06 (N)

783 S2P_ZT_Ro	3	9.31	79.4	2.48E+06 (N)
822 L3P_ZT.177	3	9.1	76.4	1.00E+07 (N)
921 L3P_ZT.179	2	8.7	75.2	2.06E+06 (N)
1183 S3P_ZT_Ro	3	7.73	62	1.71E+06 (N)
1198 S3P_ZT_Ro	3	7.67	65.2	1.71E+06 (N)
1478 X4P_ZT.177	3	6.78	67.3	2.03E+06 (N)
1530 L3P_ZT.182	3	6.69	87.2	1.03E+07 (N)
1643 X3P_ZT.786	4	6.42	100	3.90E+05 (N)
367 L3P_ZT.138	4	12.08	81	2.01E+06 (N)
484 S4P_ZT_Ro	4	11.21	76	2.11E+06 (N)
600 S4P_ZT_Ro	2	10.33	83.1	2.42E+05 (N)
633 S2P_ZT_Ro	4	10.09	82.3	2.50E+06 (N)
700 S5P_ZT_Ro	2	9.74	78.7	2.64E+05 (N)
706 S1P_ZT_Ro	2	9.71	81.4	2.62E+05 (N)
718 X4P_ZT.137	2	9.65	69	3.95E+05 (N)
764 S2P_ZT_Ro	3	9.43	69	1.74E+06 (N)
842 S1P_ZT_Ro	4	9.02	69.8	2.12E+06 (N)
843 S2P_ZT_Ro	2	9.01	91.7	2.80E+05 (N)
948 L3P_ZT.136	4	8.58	62.8	2.01E+06 (N)
957 S1P_ZT_Ro	2	8.53	73.3	2.62E+05 (N)
981 S5P_ZT_Ro	4	8.44	63.3	2.57E+06 (N)
1018 S3P_ZT_Ro	4	8.32	66.9	1.64E+06 (N)
1121 S5P_ZT_Ro	3	7.95	66.8	1.82E+06 (N)
1186 X3P_ZT.128	4	7.72	60.1	3.69E+06 (N)
1218 X3P_ZT.137	2	7.58	70.9	4.63E+05 (N)
1266 S2P_ZT_Ro	4	7.44	60.3	2.50E+06 (N)
1273 S4P_ZT_Ro	3	7.42	100	1.57E+06 (N)
1357 S1P_ZT_Ro	4	7.12	100	2.12E+06 (N)
1358 L3P_ZT.138	3	7.12	100	1.47E+06 (N)
691 S4P_ZT_Ro	4	9.77	62.8	1.18E+06 (E)
953 L5P_ZT.482	4	8.55	68.3	1.23E+06 (E)
1397 X4P_ZT.479	4	6.99	82.8	1.23E+06 (E)
1672 X2P_ZT.487	4	6.34	89	1.51E+06 (E)
1703 X4P_ZT.507	4	6.28	83.6	1.19E+05 (K)
2048 X2P_ZT.269	2	5.53	76.5	1.05E+05 (R)
1996 S2P_ZT_Ro	4	5.63	75.3	1.46E+06 (R)
1806 X3P_ZT.363	7	6.05	68.6	1.80E+05 (N)
2034 L3P_ZT.359	7	5.56	75	1.93E+05 (N)
1583 X4P_ZT.150	3	6.56	74.3	1.12E+05 (T)
1618 L5P_ZT.463	5	6.48	64.7	7.96E+04 (L)
752 L4P_ZT.250	2	9.48	68.3	4.83E+06 (K)
776 X1P_ZT.229	2	9.36	74.8	2.69E+07 (K)
815 X2P_ZT.247	2	9.12	70.7	1.02E+07 (K)
874 S2P_ZT_Ro	2	8.89	69.4	9.94E+06 (K)
910 S1P_ZT_Ro	2	8.74	77.9	1.59E+07 (K)
949 L5P_ZT.244	2	8.58	73.5	1.00E+07 (K)
969 S5P_ZT_Ro	2	8.48	74.3	1.47E+07 (K)

976 S4P_ZT_Ro	2	8.45	69.8	1.05E+07 (K)
1098 X3P_ZT.236	2	8.03	80.3	2.43E+07 (K)
1152 X2P_ZT.246	2	7.83	72.8	1.02E+07 (K)
1169 L1P_ZT.220	2	7.77	69.9	1.01E+07 (K)
1173 S3P_ZT_Ro	2	7.75	71.7	9.02E+06 (K)
1369 X4P_ZT.239	2	7.07	72.3	5.05E+06 (K)
1464 L2P_ZT.221	2	6.83	66.9	8.79E+06 (K)
1737 L3P_ZT.236	2	6.22	71	1.23E+07 (K)
1815 X5P_ZT.241	2	6.02	70.3	1.06E+07 (K)
1837 L4P_ZT.248	2	5.96	64.7	8.62E+06 (K)
2197 X1P_ZT.239	2	5.25	62.1	1.31E+07 (K)
2185 L4P_ZT.264	2	5.27	68.7	1.02E+06 (K)
1113 S1P_ZT_Ro	2	7.98	77.6	1.01E+06 (K)
1279 X3P_ZT.291	3	7.39	82.4	9.13E+05 (K)
1346 S4P_ZT_Ro	2	7.15	60.7	7.64E+05 (K)
1653 S4P_ZT_Ro	2	6.4	60.3	7.64E+05 (K)
1749 L5P_ZT.300	3	6.2	100	1.25E+06 (K)
1774 X1P_ZT.280	3	6.13	78.1	4.76E+05 (K)
1897 S1P_ZT_Ro	2	5.82	80.2	9.54E+05 (K)
2054 L5P_ZT.309	3	5.53	65.4	1.51E+06 (K)
2104 L5P_ZT.298	3	5.42	63.1	1.25E+06 (K)
2186 L5P_ZT.304	3	5.27	65.4	1.25E+06 (K)
2302 X3P_ZT.321	2	5.06	92.3	3.19E+05 (K)
1593 S3P_ZT_Ro	2	6.54	67.9	3.12E+06 (K)
2322 L4P_ZT.264	2	5.02	75.6	1.13E+06 (K)
2047 X3P_ZT.179	2	5.53	62.3	2.24E+05 (K)
1495 X4P_ZT.508	3	6.75	100	6.41E+04 (L)
858 L3P_ZT.174	2	8.96	77.3	1.21E+06 (N)
1097 X5P_ZT.173	2	8.03	64.5	3.41E+05 (N)
902 L1P_ZT.799	2	8.77	77.4	1.01E+05 (K)
1404 L1P_ZT.797	3	6.98	70.8	1.69E+05 (K)
2058 X1P_ZT.869	3	5.51	70.1	5.91E+05 (K)
1826 L3P_ZT.511	3	6	62	7.17E+06 (K)
1906 X4P_ZT.263	4	5.79	63.5	4.12E+04 (K)
1368 S2P_ZT_Ro	5	7.08	64.7	4.81E+04 (Y)
798 S1P_ZT_Ro	3	9.22	70.5	1.54E+05 (Y)
1931 S1P_ZT_Ro	3	5.75	68	3.82E+04 (K)
2147 S1P_ZT_Ro	3	5.34	69.1	5.02E+05 (K)
1238 X4P_ZT.291	3	7.52	69.5	2.68E+04 (G)
1453 X3P_ZT.289	3	6.85	62.5	2.17E+05 (G)
1765 S4P_ZT_Ro	3	6.15	61.8	4.27E+05 (G)
1081 X5P_ZT.826	3	8.07	68.2	3.16E+04 (R)
1247 X4P_ZT.161	3	7.49	67.8	3.72E+04 (R)
1824 S1P_ZT_Ro	3	6	74.9	2.06E+06 (K)
1876 X5P_ZT.359	4	5.87	64.4	4.51E+05 (F)
1242 L2P_ZT.269	3	7.51	75	1.40E+06 (C)
1512 X3P_ZT.270	3	6.72	74.8	1.08E+06 (C)

1588	L3P_ZT.269	3	6.55	68.3	1.45E+06 (C)
1724	S4P_ZT_Ro	3	6.24	74.4	2.00E+06 (C)
1527	L2P_ZT.477	3	6.7	60.6	3.33E+05 (L)
1686	S4P_ZT_Ro	3	6.31	75.2	2.61E+05 (L)
1182	S5P_ZT_Ro	4	7.73	72.1	3.29E+06 (K)
1324	L1P_ZT.205	2	7.23	62.8	5.84E+05 (K)
1960	L5P_ZT.228	3	5.71	68	1.28E+05 (K)
1200	L5P_ZT.533	4	7.67	80.2	7.48E+05 (K)
1642	X3P_ZT.557	4	6.42	62	9.73E+05 (K)
1791	L1P_ZT.417	4	6.09	72.3	1.94E+06 (K)
1862	L3P_ZT.537	4	5.91	70	1.16E+06 (K)
2208	X1P_ZT.266	5	5.24	61.2	5.62E+05 (K)
1093	S2P_ZT_Ro	3	8.05	61.2	3.11E+05 (K)
1716	X1P_ZT.280	3	6.25	60.1	2.70E+05 (K)
1944	X1P_ZT.283	3	5.72	78.4	2.70E+05 (K)
1102	S5P_ZT_Ro	3	8.02	72.2	1.62E+05 (K)
1700	S1P_ZT_Ro	3	6.29	77	2.87E+05 (K)
1896	S2P_ZT_Ro	3	5.82	75.7	2.09E+05 (K)
2221	L5P_ZT.488	3	5.23	71.4	2.61E+05 (K)
2250	L5P_ZT.489	3	5.2	69.6	2.61E+05 (K)
2171	L1P_ZT.494	3	5.3	61.6	1.91E+05 (K)
1132	S3P_ZT_Ro	3	7.9	61.3	1.27E+06 (K)
1509	X1P_ZT.293	3	6.73	68.5	1.00E+06 (K)
1689	S4P_ZT_Ro	3	6.3	60.1	1.51E+06 (K)
1846	S5P_ZT_Ro	3	5.93	75.9	1.14E+06 (K)
1100	X5P_ZT.320	5	8.02	62.6	9.31E+05 (K)
1623	S1P_ZT_Ro	3	6.47	66.3	1.52E+04 (K)
1722	L5P_ZT.320	5	6.25	73.9	2.46E+06 (K)
1868	S2P_ZT_Ro	4	5.9	65.2	2.62E+06 (K)
1895	X2P_ZT.323	5	5.82	77.8	1.53E+06 (K)
1932	S3P_ZT_Ro	3	5.74	62.2	2.01E+05 (K)
2079	S5P_ZT_Ro	3	5.47	63.4	7.86E+04 (K)
2234	L4P_ZT.282	5	5.22	60.8	5.34E+04 (K)
1337	L3P_ZT.299	6	7.19	61	5.76E+04 (K)
2318	L5P_ZT.377	4	5.03	61.7	9.18E+04 (K)
1577	L4P_ZT.189	3	6.58	69.3	5.37E+04 (C)
1339	X4P_ZT.464	4	7.17	88.5	4.29E+06 (L)
2315	X3P_ZT.317	2	5.03	61.4	4.36E+05 (K)
2105	L5P_ZT.445	3	5.42	75.5	2.83E+05 (K)
1507	L4P_ZT.380	4	6.74	63.9	1.83E+04 (K)
1872	S4P_ZT_Ro	4	5.89	79	1.81E+05 (K)
2101	S1P_ZT_Ro	4	5.43	73.1	3.94E+05 (K)
2243	L3P_ZT.525	4	5.21	62.2	8.30E+04 (K)
1885	X3P_ZT.467	5	5.84	62	1.28E+05 (K)
1680	S2P_ZT_Ro	3	6.32	76.5	1.27E+04 (K)
871	X3P_ZT.344	5	8.89	66.2	5.94E+05 (K)
1039	L3P_ZT.535	4	8.26	63.2	7.11E+05 (K)

1180	L4P_ZT.497	4	7.74	62.2	5.55E+05 (K)
1943	L4P_ZT.408	5	5.73	67.5	3.21E+04 (K)
1017	L5P_ZT.465	5	8.33	61.3	6.99E+04 (K)
1793	X5P_ZT.291	5	6.08	70.5	4.05E+05 (K)
1907	X4P_ZT.293	5	5.79	74.6	1.51E+06 (K)
2160	S1P_ZT_Ro	3	5.32	62.1	2.50E+05 (K)
1934	S1P_ZT_Ro	6	5.74	69.3	3.45E+04 (K)
1078	L4P_ZT.998	2	8.09	63.1	5.90E+05 (I)
2151	X4P_ZT.141	2	5.33	63.5	9.98E+04 (K)
2112	L2P_ZT.218	2	5.41	80.3	1.19E+06 (K)
2300	L3P_ZT.229	2	5.07	70.6	2.63E+06 (K)
1601	X3P_ZT.248	3	6.51	73.8	1.88E+05 (K)
1050	X4P_ZT.219	3	8.2	63.2	5.17E+04 (N)
1345	X3P_ZT.217	3	7.15	63.7	4.98E+04 (N)
1297	S3P_ZT_Ro	6	7.32	64.3	1.34E+05 (R)
1776	S2P_ZT_Ro	5	6.13	69.8	3.53E+04 (R)
1948	S1P_ZT_Ro	3	5.72	77.2	9.69E+04 (R)
2268	L3P_ZT.248	2	5.15	89.1	6.21E+05 (R)
1367	S3P_ZT_Ro	2	7.08	61.4	1.92E+06 (R)
1752	L1P_ZT.457	2	6.19	66.6	2.57E+06 (R)
1852	S5P_ZT_Ro	2	5.92	61.5	2.29E+06 (R)
1103	S3P_ZT_Ro	2	8.02	76.1	3.13E+06 (R)
1425	X5P_ZT.527	2	6.92	83.7	2.45E+06 (R)
1561	X1P_ZT.476	2	6.62	84.6	1.69E+06 (R)
2220	L5P_ZT.432	3	5.23	66	4.46E+05 (R)
1775	S3P_ZT_Ro	7	6.13	64.4	2.39E+05 (R)
2013	X3P_ZT.221	4	5.6	88.4	7.80E+05 (R)
1071	S3P_ZT_Ro	3	8.11	67.7	2.75E+06 (D)
1277	X3P_ZT.320	3	7.4	66.5	2.80E+06 (D)
1282	X1P_ZT.311	3	7.38	65.2	3.63E+06 (D)
1405	L2P_ZT.304	3	6.98	61.2	3.78E+06 (D)
1446	L4P_ZT.326	3	6.88	72.9	2.40E+06 (D)
1449	L1P_ZT.306	3	6.87	63.4	5.43E+06 (D)
1556	S4P_ZT_Ro	3	6.63	61.4	3.10E+06 (D)
1638	X3P_ZT.321	3	6.43	64	2.80E+06 (D)
1595	S5P_ZT_Ro	5	6.52	83.2	1.84E+05 (V)
879	L5P_ZT.526	3	8.87	68.7	1.24E+07 (V)
908	X1P_ZT.490	3	8.75	71.3	8.04E+06 (V)
992	S5P_ZT_Ro	3	8.41	69.4	2.58E+07 (V)
1048	X3P_ZT.530	3	8.21	67.9	1.56E+07 (V)
1076	X4P_ZT.527	3	8.09	67.5	1.13E+07 (V)
1115	S3P_ZT_Ro	3	7.97	71.7	2.31E+07 (V)
1158	S5P_ZT_Ro	3	7.8	65.3	2.58E+07 (V)
1391	S5P_ZT_Ro	3	7	68.2	2.58E+07 (V)
1444	L2P_ZT.498	3	6.88	67.1	1.43E+07 (V)
1534	X4P_ZT.511	3	6.68	60.2	4.49E+04 (V)
1630	L1P_ZT.509	3	6.46	62.1	2.47E+07 (V)

1235 X3P_ZT.470	4	7.54	64.4	9.39E+04 (V)
862 S1P_ZT_Ro	3	8.94	60.2	5.78E+06 (K)
2133 X2P_ZT.130	2	5.36	68.7	8.35E+05 (R)
875 X5P_ZT.250	3	8.88	64.7	1.12E+05 (R)
952 L3P_ZT.240	3	8.56	67.3	2.41E+05 (R)
1080 L1P_ZT.230	3	8.08	83.7	2.54E+05 (R)
1094 X3P_ZT.240	3	8.04	67.4	1.80E+05 (R)
1120 X3P_ZT.240	3	7.95	66.7	1.80E+05 (R)
1536 L5P_ZT.250	3	6.68	71.4	4.20E+05 (R)
1811 X2P_ZT.250	3	6.04	70	2.64E+05 (R)
1928 X4P_ZT.250	3	5.75	100	2.52E+05 (R)
826 L4P_ZT.230	2	9.09	68.7	1.45E+06 (R)
1035 X2P_ZT.220	2	8.26	77.7	1.66E+06 (R)
1191 L3P_ZT.210	2	7.7	73.5	5.20E+06 (R)
1223 L1P_ZT.200	2	7.57	63.6	1.25E+06 (R)
1522 X5P_ZT.220	2	6.7	66.3	1.63E+06 (R)
1673 X1P_ZT.210	2	6.34	67.5	1.53E+06 (R)
1723 S4P_ZT_Ro	2	6.24	84	5.58E+06 (R)
1743 S1P_ZT_Ro	2	6.21	82.8	4.66E+06 (R)
1766 L5P_ZT.220	2	6.15	70.7	3.08E+06 (R)
1777 X3P_ZT.210	2	6.12	78.7	2.20E+06 (R)
1820 S3P_ZT_Ro	2	6.01	68.5	4.87E+06 (R)
1915 S5P_ZT_Ro	2	5.78	76.8	8.15E+06 (R)
2073 S2P_ZT_Ro	2	5.48	65.4	4.11E+06 (R)
2150 X5P_ZT.220	2	5.33	67.6	1.63E+06 (R)
2158 S3P_ZT_Ro	2	5.32	65.9	4.87E+06 (R)
2284 X3P_ZT.210	2	5.1	61.5	2.20E+06 (R)
2308 L4P_ZT.180	2	5.06	64.2	1.87E+05 (R)
2207 X2P_ZT.100	2	5.24	61	1.13E+06 (R)
2298 L3P_ZT.190	2	5.08	64.5	8.89E+05 (R)
2044 L4P_ZT.120	2	5.54	81	2.67E+05 (R)
2002 S5P_ZT_Ro	2	5.62	67.5	3.07E+05 (R)
713 S4P_ZT_Ro	2	9.68	61.9	1.53E+06 (F)
1003 X5P_ZT.190	3	8.36	63	3.75E+06 (F)
1582 L3P_ZT.360	3	6.57	65.3	3.89E+04 (E)
1310 L5P_ZT.450	3	7.28	62.6	6.67E+04 (G)
1399 L3P_ZT.240	3	6.99	70.1	8.80E+05 (V)
1798 S2P_ZT_Ro	7	6.07	60.2	2.90E+05 (R)
1386 S2P_ZT_Ro	6	7.02	65.5	1.65E+05 (R)
1336 X5P_ZT.820	3	7.19	67.7	2.31E+06 (E)
1589 L4P_ZT.990	3	6.55	60.3	2.28E+06 (E)
1603 X3P_ZT.820	3	6.51	62.6	3.52E+06 (E)
1965 X5P_ZT.820	2	5.68	77.5	5.65E+05 (K)
2175 S2P_ZT_Ro	2	5.29	71.4	4.86E+05 (K)
1515 S2P_ZT_Ro	4	6.72	72.4	5.98E+04 (K)
1348 S4P_ZT_Ro	5	7.15	62.7	3.98E+05 (R)
1416 S4P_ZT_Ro	5	6.95	67.4	3.98E+05 (R)

1575 L3P_ZT.528	5	6.58	69.2	2.03E+05 (R)
1594 L3P_ZT.531	5	6.53	80.5	2.05E+05 (R)
1719 S2P_ZT_Ro	5	6.25	65.4	3.95E+05 (R)
1735 S5P_ZT_Ro	5	6.22	72.2	3.14E+05 (R)
1828 S1P_ZT_Ro	4	5.99	61.2	1.32E+05 (R)
1893 L5P_ZT.530	5	5.83	67.5	3.93E+04 (R)
1919 S3P_ZT_Ro	5	5.77	68.4	2.98E+05 (R)
1971 S2P_ZT_Ro	5	5.67	72.4	3.95E+05 (R)
2049 S1P_ZT_Ro	5	5.53	69.6	3.98E+05 (R)
2036 X3P_ZT.159	2	5.55	77.1	5.75E+06 (R)
2056 S4P_ZT_Ro	3	5.52	62.5	1.20E+06 (-)
2080 L2P_ZT.171	2	5.47	92.6	2.61E+05 (-)
1314 S5P_ZT_Ro	5	7.26	73.2	1.29E+05 (K)
1489 S3P_ZT_Ro	5	6.77	61.4	1.76E+06 (K)
2301 L5P_ZT.404	3	5.07	91.6	6.85E+05 (K)
1734 X1P_ZT.407	4	6.22	61.1	3.38E+05 (K)
2266 S1P_ZT_Ro	2	5.15	69.4	1.11E+06 (K)
1819 S4P_ZT_Ro	3	6.01	73	1.64E+06 (K)
2094 S5P_ZT_Ro	2	5.45	65.8	3.25E+05 (K)
2254 X2P_ZT.369	7	5.17	84.8	6.20E+04 (R)
1125 X2P_ZT.130	3	7.93	91.8	2.80E+06 (K)
1228 S2P_ZT_Ro	3	7.56	66.1	1.17E+06 (K)
1409 S5P_ZT_Ro	3	6.97	100	1.03E+06 (K)
1443 S4P_ZT_Ro	3	6.88	77.9	6.34E+05 (K)
1625 L5P_ZT.131	3	6.47	100	2.79E+06 (K)
2240 S5P_ZT_Ro	3	5.21	82.1	1.03E+06 (K)
1335 S3P_ZT_Ro	4	7.2	75.1	1.45E+05 (F)
954 X2P_ZT.547	4	8.54	79.4	4.52E+05 (L)
1214 L5P_ZT.537	4	7.62	72.1	2.46E+05 (L)
1270 X3P_ZT.547	4	7.43	86.8	1.84E+05 (L)
1586 X5P_ZT.559	4	6.55	79.9	3.22E+05 (L)
1649 S2P_ZT_Ro	7	6.41	60.9	8.60E+05 (W)
1768 S4P_ZT_Ro	6	6.14	60.8	3.48E+04 (K)
2174 X1P_ZT.217	6	5.29	67.7	7.11E+03 (A)
742 L5P_ZT.197	3	9.56	61.5	5.91E+05 (R)
1799 L4P_ZT.204	3	6.07	70	1.74E+05 (R)
1585 X2P_ZT.553	5	6.56	63.4	3.76E+05 (E)
971 X4P_ZT.483	7	8.47	65	4.23E+05 (D)
647 L3P_ZT.250	2	10.01	77.4	2.36E+05 (N)
810 S4P_ZT_Ro	2	9.15	70.1	2.87E+05 (N)
913 X4P_ZT.250	2	8.72	67.8	1.50E+05 (N)
955 S5P_ZT_Ro	2	8.54	70.2	3.16E+05 (N)
1321 X4P_ZT.470	5	7.23	63.5	1.07E+05 (G)
726 L4P_ZT.320	2	9.61	73.5	1.49E+06 (D)
1015 S1P_ZT_Ro	2	8.33	65.4	3.25E+06 (D)
1021 S4P_ZT_Ro	2	8.31	68.9	2.45E+06 (D)
1377 X1P_ZT.300	2	7.04	69.6	8.72E+05 (D)

1005 S5P_ZT_Ro	3	8.36	62	6.90E+06 (V)
1154 S3P_ZT_Ro	3	7.82	62.3	1.77E+07 (V)
942 L4P_ZT.267	2	8.59	62.9	2.98E+05 (G)
1181 S5P_ZT_Ro	2	7.73	63.8	5.34E+05 (G)
1248 L3P_ZT.501	5	7.49	70.3	7.84E+04 (K)
1289 X5P_ZT.593	5	7.36	69.3	6.88E+04 (K)
1557 L3P_ZT.526	5	6.63	78.9	4.19E+04 (K)
2006 L1P_ZT.464	4	5.62	67.3	1.56E+06 (K)
1578 X5P_ZT.383	3	6.57	62.6	6.55E+06 (K)
2199 S4P_ZT_Ro	5	5.25	100	1.88E+04 (K)
2061 X5P_ZT.237	2	5.5	100	8.19E+05 (K)
2064 S4P_ZT_Ro	2	5.5	100	6.16E+05 (K)
2231 L2P_ZT.216	2	5.22	90.8	1.34E+06 (K)
2247 S1P_ZT_Ro	6	5.2	75	3.67E+04 (K)
2293 S1P_ZT_Ro	2	5.09	67	8.22E+05 (R)
1560 X2P_ZT.470	7	6.62	67	2.73E+05 (R)
1581 L2P_ZT.485	3	6.57	67.5	1.51E+05 (R)
2069 S5P_ZT_Ro	3	5.49	71.5	1.09E+05 (R)
2100 X3P_ZT.514	3	5.43	88.4	7.83E+04 (R)
1807 S5P_ZT_Ro	5	6.05	61.9	3.08E+06 (R)
1552 S3P_ZT_Ro	4	6.64	77.3	2.81E+04 (K)
1176 L5P_ZT.429	6	7.75	100	1.42E+05 (K)
1407 X3P_ZT.497	5	6.97	71.4	7.55E+04 (K)
1620 X3P_ZT.498	5	6.47	72.5	3.66E+04 (K)
1725 S2P_ZT_Ro	7	6.24	64	2.87E+05 (K)
2242 S2P_ZT_Ro	4	5.21	82.5	1.38E+04 (K)
419 S5P_ZT_Ro	2	11.67	88.8	2.30E+06 (F)
794 S4P_ZT_Ro	2	9.25	73.2	2.94E+06 (F)
841 S3P_ZT_Ro	2	9.02	85.4	2.25E+06 (F)
983 S2P_ZT_Ro	2	8.44	72.1	3.60E+06 (F)
1037 S1P_ZT_Ro	2	8.26	69.8	1.42E+06 (F)
1107 S4P_ZT_Ro	2	8.01	66.4	2.94E+06 (F)
1225 X3P_ZT.465	2	7.56	60.2	1.04E+05 (F)
559 X4P_ZT.473	2	10.65	82.2	2.91E+05 (K)
568 X2P_ZT.480	2	10.58	79.5	3.43E+05 (K)
646 L2P_ZT.452	2	10.01	70.9	8.63E+05 (K)
655 X3P_ZT.476	2	9.97	85.5	2.76E+05 (K)
702 L5P_ZT.475	2	9.74	77.4	1.21E+06 (K)
820 S4P_ZT_Ro	2	9.1	80.4	4.40E+05 (K)
965 L3P_ZT.473	2	8.5	70.8	1.23E+06 (K)
995 L1P_ZT.464	2	8.39	70.4	1.46E+06 (K)
1263 X1P_ZT.446	2	7.44	71.3	2.74E+06 (K)
1293 X2P_ZT.483	2	7.34	80.6	9.30E+05 (K)
1342 X5P_ZT.486	2	7.16	67.2	1.01E+06 (K)
1362 L1P_ZT.462	2	7.11	74.4	1.35E+06 (K)
1631 L2P_ZT.453	2	6.46	74.9	9.68E+05 (K)
1708 X1P_ZT.449	2	6.27	70.3	2.73E+06 (K)

2307	L3P_ZT.474	2	5.06	70.4	5.27E+05 (K)
1423	L2P_ZT.516	4	6.93	71	1.16E+07 (K)
1674	S5P_ZT_Ro	4	6.34	78.9	8.33E+06 (K)
1829	X4P_ZT.551	4	5.98	62.5	1.64E+07 (K)
2108	L5P_ZT.554	4	5.42	62.9	8.86E+06 (K)
1487	S4P_ZT_Ro	4	6.77	74	6.92E+05 (K)
1614	S5P_ZT_Ro	4	6.48	68.9	7.01E+05 (K)
2122	S2P_ZT_Ro	3	5.38	61.6	1.18E+06 (K)
1400	L3P_ZT.543	5	6.99	78.2	4.48E+04 (V)
1590	X3P_ZT.544	3	6.54	60.7	6.96E+04 (I)
2211	L3P_ZT.460	6	5.24	60.5	3.13E+05 (V)
1378	X1P_ZT.484	3	7.04	61.8	1.47E+05 (I)
1545	S5P_ZT_Ro	3	6.65	60.6	8.81E+05 (I)
1740	L4P_ZT.485	3	6.22	64.6	1.06E+05 (I)
1031	X2P_ZT.524	3	8.27	60.1	2.25E+05 (R)
1124	L1P_ZT.502	3	7.94	72.2	6.99E+05 (R)
1546	S4P_ZT_Ro	3	6.65	86.7	1.00E+06 (R)
1707	S4P_ZT_Ro	3	6.28	86.3	1.00E+06 (R)
1717	S3P_ZT_Ro	3	6.25	81.5	1.88E+05 (R)
1748	S1P_ZT_Ro	3	6.2	100	2.35E+05 (R)
1886	S5P_ZT_Ro	3	5.84	74.9	6.92E+05 (R)
2191	S2P_ZT_Ro	3	5.26	63.4	5.26E+05 (R)
1626	L5P_ZT.351	3	6.47	68.7	3.77E+04 (R)
1067	L4P_ZT.833	2	8.13	73.7	3.21E+06 (R)
1428	S4P_ZT_Ro	2	6.92	69.9	3.55E+06 (R)
1505	L3P_ZT.745	2	6.74	79.1	3.60E+06 (R)
1526	S2P_ZT_Ro	2	6.7	73.5	4.85E+06 (R)
1529	S1P_ZT_Ro	2	6.69	74.3	7.65E+06 (R)
1544	X2P_ZT.691	2	6.65	83	3.51E+06 (R)
1972	S2P_ZT_Ro	2	5.67	68.8	4.85E+06 (R)
1161	X3P_ZT.391	6	7.79	61.5	4.36E+04 (R)
1492	L3P_ZT.389	5	6.77	63.7	2.53E+04 (R)
1696	X3P_ZT.391	6	6.29	65.8	3.44E+04 (R)
1989	L3P_ZT.389	6	5.65	61.3	2.61E+04 (R)
1779	S4P_ZT_Ro	2	6.12	60.8	1.05E+07 (K)
2052	L5P_ZT.128	2	5.53	76.6	1.09E+07 (K)
2267	L2P_ZT.289	2	5.15	64.7	1.28E+05 (K)
2214	X3P_ZT.391	3	5.23	73.1	5.92E+04 (K)
1165	S1P_ZT_Ro	3	7.78	66.2	6.08E+04 (F)
1647	L1P_ZT.359	3	6.42	61.9	1.67E+05 (F)
919	L4P_ZT.179	2	8.71	69.6	9.35E+05 (K)
946	S2P_ZT_Ro	2	8.58	74.4	6.14E+05 (K)
1216	S3P_ZT_Ro	2	7.61	62.9	5.85E+05 (K)
1296	S4P_ZT_Ro	2	7.32	70.8	5.94E+05 (K)
1334	S5P_ZT_Ro	2	7.2	69.2	8.18E+05 (K)
1338	S1P_ZT_Ro	2	7.18	64	6.89E+05 (K)
1465	S2P_ZT_Ro	2	6.82	63.1	3.12E+06 (K)

1877 S3P_ZT_Ro	2	5.87	65.1	1.13E+07 (K)
1898 L2P_ZT.280	2	5.82	63.3	1.14E+07 (K)
1287 X1P_ZT.274	6	7.37	69.5	2.16E+05 (T)
1290 S4P_ZT_Ro	6	7.35	68.8	2.60E+05 (T)
1458 S3P_ZT_Ro	6	6.84	65	2.01E+06 (T)
1549 L5P_ZT.289	6	6.65	68.4	2.09E+05 (T)
1682 L3P_ZT.279	6	6.32	65.1	2.04E+05 (T)
2005 S3P_ZT_Ro	6	5.62	65	1.17E+05 (T)
2246 S3P_ZT_Ro	6	5.2	65.7	1.78E+06 (T)
2291 X1P_ZT.274	6	5.09	60.1	1.33E+05 (T)
778 L5P_ZT.295	2	9.35	72.2	3.52E+05 (C)
2206 X4P_ZT.547	5	5.24	63.5	1.52E+05 (N)
2241 S4P_ZT_Ro	2	5.21	74	7.04E+04 (K)
1064 X4P_ZT.204	3	8.13	66.5	4.79E+05 (K)
1370 X3P_ZT.204	3	7.07	66.1	4.66E+05 (K)
1385 S2P_ZT_Ro	3	7.02	60.3	9.02E+05 (K)
1432 S4P_ZT_Ro	2	6.9	60.3	8.08E+04 (K)
1713 S4P_ZT_Ro	3	6.26	67.8	4.91E+05 (K)
1922 X5P_ZT.204	2	5.76	60.9	1.52E+05 (K)
2111 S2P_ZT_Ro	2	5.41	76.5	4.44E+05 (K)
1434 L2P_ZT.410	3	6.9	66.4	3.54E+05 (L)
1555 S5P_ZT_Ro	3	6.63	60.2	9.26E+05 (L)
1602 X3P_ZT.434	3	6.51	65.5	4.96E+05 (L)
1950 L2P_ZT.411	3	5.72	78.9	3.54E+05 (L)
1343 X3P_ZT.304	2	7.16	62.3	2.61E+05 (K)
1913 X3P_ZT.306	2	5.78	81.6	3.36E+05 (K)
1204 L2P_ZT.495	3	7.66	68.6	6.72E+05 (K)
2077 X2P_ZT.526	3	5.47	78.2	5.24E+05 (K)
1883 S1P_ZT_Ro	2	5.86	76.8	2.14E+06 (R)
1947 S1P_ZT_Ro	2	5.72	88	5.36E+06 (R)
2137 S1P_ZT_Ro	2	5.36	71.9	2.70E+07 (R)
2305 S1P_ZT_Ro	2	5.06	61.9	2.14E+06 (R)
1665 L5P_ZT.217	3	6.37	70	1.04E+05 (R)
1640 S1P_ZT_Ro	3	6.43	67.9	6.59E+04 (R)
1663 L1P_ZT.454	3	6.37	72.9	5.13E+05 (R)
1892 L5P_ZT.467	3	5.83	69.1	4.25E+05 (R)
1964 S1P_ZT_Ro	3	5.69	67.8	6.59E+04 (R)
2144 X2P_ZT.474	3	5.34	84.5	2.85E+05 (R)
2159 S3P_ZT_Ro	3	5.32	61.4	3.68E+05 (R)
2180 S2P_ZT_Ro	3	5.28	68	7.56E+05 (R)
2263 X5P_ZT.554	3	5.15	61.7	2.05E+04 (R)
958 X2P_ZT.314	2	8.52	67.1	7.50E+06 (R)
1171 L3P_ZT.329	2	7.76	66.7	4.96E+06 (R)
1187 X1P_ZT.364	2	7.72	63.1	6.61E+04 (R)
1217 S1P_ZT_Ro	2	7.6	70.9	6.81E+06 (R)
1231 L3P_ZT.291	2	7.56	70	1.32E+07 (R)
1249 L5P_ZT.371	2	7.49	64.7	1.84E+05 (R)

1257	L3P_ZT.366	2	7.47	61.3	3.63E+04 (R)
1274	L3P_ZT.396	2	7.41	61	1.90E+05 (R)
1298	L3P_ZT.267	2	7.32	70.9	2.00E+07 (R)
1304	X2P_ZT.286	2	7.3	71.2	1.57E+07 (R)
1467	S1P_ZT_Ro	2	6.82	69.1	3.38E+07 (R)
1471	L1P_ZT.294	2	6.81	68.1	1.11E+06 (R)
1486	X3P_ZT.276	2	6.77	68.1	1.64E+07 (R)
1488	S4P_ZT_Ro	2	6.77	68.4	3.64E+07 (R)
1493	X5P_ZT.326	2	6.76	67.7	7.80E+04 (R)
1513	S5P_ZT_Ro	2	6.72	65.8	3.99E+07 (R)
1516	L5P_ZT.383	2	6.72	61.1	1.33E+05 (R)
1525	S3P_ZT_Ro	2	6.7	66.8	4.54E+07 (R)
1537	X4P_ZT.316	2	6.67	64.9	3.95E+06 (R)
1538	S3P_ZT_Ro	2	6.67	63.8	1.33E+06 (R)
1591	X2P_ZT.306	2	6.54	63.1	1.00E+07 (R)
1610	L3P_ZT.348	2	6.5	69.2	2.01E+06 (R)
1644	X1P_ZT.284	2	6.42	65.4	9.70E+06 (R)
1651	L4P_ZT.334	2	6.41	63	3.43E+06 (R)
1688	X1P_ZT.266	2	6.3	69.5	1.66E+07 (R)
1693	X4P_ZT.336	2	6.29	70.1	1.39E+06 (R)
1730	L5P_ZT.300	2	6.23	67.2	2.08E+07 (R)
1732	X1P_ZT.286	2	6.22	67.3	9.24E+06 (R)
1733	X1P_ZT.366	2	6.22	64.8	2.82E+04 (R)
1742	S2P_ZT_Ro	2	6.21	66.1	1.95E+07 (R)
1778	X1P_ZT.304	2	6.12	63.6	4.51E+06 (R)
1781	L1P_ZT.300	2	6.11	63.9	3.40E+06 (R)
1785	L2P_ZT.272	2	6.1	65.5	5.42E+06 (R)
1856	L3P_ZT.325	2	5.92	61.1	5.42E+06 (R)
1871	X3P_ZT.310	2	5.89	63.8	6.46E+06 (R)
2000	X3P_ZT.294	2	5.62	69.9	1.41E+07 (R)
2007	L3P_ZT.310	2	5.62	64.4	6.55E+06 (R)
2071	L4P_ZT.375	2	5.49	64.8	1.66E+04 (R)
2118	X2P_ZT.316	2	5.39	60.5	5.09E+04 (R)
2134	S3P_ZT_Ro	2	5.36	70.4	3.72E+06 (R)
2139	L3P_ZT.296	2	5.36	69.4	9.38E+06 (R)
2141	L5P_ZT.400	2	5.36	69.7	2.54E+05 (R)
2237	X2P_ZT.404	2	5.21	84.8	6.74E+04 (R)
2264	X3P_ZT.386	2	5.15	65.5	1.60E+04 (R)
2270	L5P_ZT.280	2	5.14	65	1.48E+07 (R)
2271	L2P_ZT.286	2	5.13	70	5.43E+06 (R)
2272	L2P_ZT.385	2	5.13	83.4	6.52E+04 (R)
2306	L2P_ZT.410	2	5.06	89.2	2.65E+05 (R)
2325	L1P_ZT.317	2	5.01	69.7	1.78E+06 (R)
1847	L1P_ZT.377	4	5.93	65.6	4.18E+04 (R)
2196	X4P_ZT.444	5	5.25	100	3.30E+04 (R)
1396	X5P_ZT.386	2	6.99	65.1	1.13E+05 (R)
1429	S1P_ZT_Ro	3	6.92	71.9	9.25E+05 (R)

1636 S4P_ZT_Ro	3	6.45	75.7	1.70E+06 (R)
1706 S5P_ZT_Ro	3	6.28	67.9	1.50E+06 (R)
716 L3P_ZT.504	6	9.67	78.4	1.06E+05 (R)
1288 S1P_ZT_Ro	4	7.37	74.6	3.53E+06 (R)
1387 S3P_ZT_Ro	4	7.01	72.5	2.12E+06 (R)
1533 L5P_ZT.371	4	6.69	66.1	1.80E+06 (R)
1584 X3P_ZT.367	4	6.56	62	3.37E+06 (R)
1608 S2P_ZT_Ro	4	6.5	66.7	3.15E+06 (R)
1812 L2P_ZT.351	4	6.04	60.1	2.06E+06 (R)
2074 X4P_ZT.367	4	5.47	64.4	2.22E+06 (R)
2287 S5P_ZT_Ro	7	5.1	61.6	5.31E+04 (R)
698 L2P_ZT.482	6	9.75	74.5	1.55E+05 (R)
1224 L1P_ZT.420	2	7.57	60.4	1.21E+07 (R)
1109 X4P_ZT.243	3	8	70.9	1.93E+05 (N)
7 S5P_ZT_Ro	2	20.66	97.6	8.82E+07 (-)
8 S4P_ZT_Ro	2	20.62	96.8	1.16E+08 (-)
9 S4P_ZT_Ro	2	20.62	97.7	1.16E+08 (-)
10 S3P_ZT_Ro	2	20.42	97.8	9.75E+07 (-)
11 L3P_ZT.325	2	20.41	97.5	1.59E+08 (-)
12 S2P_ZT_Ro	2	20.39	97.5	9.98E+07 (-)
13 S1P_ZT_Ro	2	20.12	97.2	9.67E+07 (-)
16 X3P_ZT.343	2	19.77	92.7	6.73E+07 (-)
17 X3P_ZT.329	2	19.62	97.6	1.19E+08 (-)
18 L1P_ZT.313	2	19.55	95.3	2.17E+07 (-)
23 S2P_ZT_Ro	2	19.34	96.8	9.98E+07 (-)
28 S3P_ZT_Ro	2	18.9	98.5	9.75E+07 (-)
29 X4P_ZT.329	2	18.87	97.6	1.23E+08 (-)
34 S5P_ZT_Ro	2	18.5	94.4	8.82E+07 (-)
38 L4P_ZT.338	2	18	92.2	4.71E+06 (-)
40 L3P_ZT.389	2	17.96	91.7	1.83E+05 (-)
43 L2P_ZT.317	2	17.73	93.2	4.41E+06 (-)
44 S4P_ZT_Ro	2	17.67	91.6	2.87E+06 (-)
49 X4P_ZT.347	2	17.61	96	3.71E+07 (-)
50 S3P_ZT_Ro	2	17.61	90.2	2.22E+06 (-)
51 X2P_ZT.344	2	17.59	94.6	2.26E+07 (-)
52 L3P_ZT.359	2	17.44	91	3.35E+06 (-)
59 L3P_ZT.342	2	17.02	94.5	4.15E+07 (-)
61 X4P_ZT.403	2	16.83	88.3	1.03E+06 (-)
64 S2P_ZT_Ro	2	16.72	85.5	4.16E+06 (-)
66 S4P_ZT_Ro	2	16.54	87.3	1.90E+06 (-)
72 X5P_ZT.347	2	16.35	94.7	1.57E+07 (-)
81 X3P_ZT.360	2	15.98	91.8	1.87E+06 (-)
89 S1P_ZT_Ro	2	15.71	92.9	1.09E+08 (-)
111 S5P_ZT_Ro	2	15.25	85.1	1.48E+06 (-)
113 S4P_ZT_Ro	2	15.22	85.5	1.45E+06 (-)
115 X3P_ZT.367	2	15.17	76.1	1.82E+06 (-)
125 S1P_ZT_Ro	2	14.97	91.4	3.22E+06 (-)

129	L3P_ZT.371	2	14.93	85.5	6.00E+05 (-)
142	X4P_ZT.360	2	14.77	85.6	7.55E+05 (-)
145	X4P_ZT.384	2	14.7	77.7	1.00E+06 (-)
147	X4P_ZT.373	2	14.68	70.7	7.39E+05 (-)
162	X4P_ZT.370	2	14.45	84	1.14E+06 (-)
167	L3P_ZT.390	2	14.37	82.2	1.83E+05 (-)
181	L3P_ZT.368	2	14.14	88.9	1.27E+06 (-)
187	S1P_ZT_Ro	2	14.08	82.4	3.01E+05 (-)
188	L3P_ZT.433	2	14.08	77.1	7.96E+05 (-)
192	S1P_ZT_Ro	2	14.04	86.6	1.61E+06 (-)
196	S3P_ZT_Ro	2	13.99	86.8	8.02E+05 (-)
198	L3P_ZT.386	2	13.96	69.7	1.83E+05 (-)
224	S1P_ZT_Ro	2	13.64	82.9	4.58E+05 (-)
226	S5P_ZT_Ro	2	13.6	82.1	3.60E+05 (-)
227	S2P_ZT_Ro	2	13.59	82.2	4.46E+05 (-)
232	L3P_ZT.378	2	13.56	77.4	1.77E+06 (-)
240	S1P_ZT_Ro	2	13.42	77.8	1.38E+06 (-)
255	X3P_ZT.363	2	13.22	85	1.24E+06 (-)
262	S2P_ZT_Ro	2	13.11	75.1	9.05E+05 (-)
269	S2P_ZT_Ro	2	13.03	79.8	1.24E+06 (-)
283	X3P_ZT.356	2	12.78	80	4.63E+06 (-)
285	S4P_ZT_Ro	2	12.78	86.6	1.28E+06 (-)
286	S2P_ZT_Ro	2	12.77	79.2	6.20E+06 (-)
287	L3P_ZT.365	2	12.76	66.7	1.87E+06 (-)
290	S2P_ZT_Ro	2	12.72	73.3	1.33E+06 (-)
303	S1P_ZT_Ro	2	12.63	75.1	1.29E+06 (-)
335	L3P_ZT.323	2	12.4	79.7	1.05E+07 (-)
343	S2P_ZT_Ro	2	12.35	75.5	1.89E+06 (-)
349	S1P_ZT_Ro	2	12.27	63.9	8.39E+05 (-)
350	S4P_ZT_Ro	2	12.26	75.2	8.35E+05 (-)
352	S5P_ZT_Ro	2	12.24	83.8	1.64E+06 (-)
354	S3P_ZT_Ro	2	12.21	68.8	1.48E+06 (-)
368	S2P_ZT_Ro	2	12.05	79.8	9.33E+05 (-)
370	X4P_ZT.363	2	12.04	75.3	2.11E+06 (-)
374	X3P_ZT.383	2	11.97	76.3	1.50E+06 (-)
380	S2P_ZT_Ro	2	11.89	73.3	5.53E+05 (-)
389	X4P_ZT.396	2	11.84	74.5	1.30E+06 (-)
410	S2P_ZT_Ro	2	11.76	64.5	1.08E+06 (-)
412	S1P_ZT_Ro	2	11.73	69.1	1.32E+05 (-)
425	L3P_ZT.393	2	11.64	80.5	1.75E+05 (-)
427	L3P_ZT.409	2	11.6	81.9	2.83E+05 (-)
428	L3P_ZT.414	2	11.6	72.2	2.83E+05 (-)
432	S2P_ZT_Ro	2	11.58	76.1	1.37E+06 (-)
435	L1P_ZT.318	2	11.56	88.4	2.17E+07 (-)
445	S3P_ZT_Ro	2	11.5	77.3	5.51E+05 (-)
449	L3P_ZT.392	2	11.48	79.1	3.00E+05 (-)
460	S2P_ZT_Ro	2	11.39	80.5	1.64E+06 (-)

469	X4P_ZT.396	2	11.33	70	8.60E+05 (-)
474	X3P_ZT.388	2	11.29	61.8	9.11E+05 (-)
487	X4P_ZT.386	2	11.18	63.7	9.21E+05 (-)
492	X3P_ZT.391	2	11.16	67.7	7.02E+05 (-)
493	S1P_ZT_Ro	2	11.15	71.4	2.06E+06 (-)
496	S1P_ZT_Ro	2	11.14	76.5	1.28E+06 (-)
505	L3P_ZT.385	2	11.01	78.1	1.83E+05 (-)
506	X3P_ZT.408	2	11	82.4	7.89E+05 (-)
513	S4P_ZT_Ro	2	10.94	65.8	3.68E+06 (-)
530	X3P_ZT.411	2	10.85	66.3	6.28E+05 (-)
533	S2P_ZT_Ro	2	10.84	60.9	9.78E+05 (-)
534	L1P_ZT.324	2	10.82	71.2	2.17E+07 (-)
540	S5P_ZT_Ro	2	10.79	72.8	1.42E+06 (-)
542	X3P_ZT.399	2	10.78	61.4	8.73E+05 (-)
543	S3P_ZT_Ro	2	10.78	71	1.73E+05 (-)
565	S3P_ZT_Ro	2	10.61	71.2	6.75E+05 (-)
566	S5P_ZT_Ro	2	10.6	72	5.46E+04 (-)
570	S4P_ZT_Ro	2	10.55	75.8	8.25E+05 (-)
572	S1P_ZT_Ro	2	10.52	63.9	1.49E+06 (-)
573	X3P_ZT.366	2	10.51	69.5	9.00E+04 (-)
580	X4P_ZT.327	2	10.44	64.8	9.61E+06 (-)
590	X3P_ZT.373	2	10.39	67.8	1.49E+06 (-)
597	X3P_ZT.398	2	10.35	70.7	8.04E+05 (-)
601	X3P_ZT.378	2	10.32	71.8	1.27E+06 (-)
605	S2P_ZT_Ro	2	10.3	73.5	2.08E+06 (-)
609	S1P_ZT_Ro	2	10.28	76.5	6.58E+05 (-)
612	S2P_ZT_Ro	2	10.24	77.1	2.75E+05 (-)
614	L3P_ZT.426	2	10.23	70.2	6.50E+05 (-)
629	S4P_ZT_Ro	2	10.15	73.6	3.19E+06 (-)
635	S5P_ZT_Ro	2	10.08	63.2	3.60E+05 (-)
638	S4P_ZT_Ro	2	10.07	72.6	5.75E+05 (-)
674	S3P_ZT_Ro	2	9.88	79.6	3.59E+05 (-)
682	L3P_ZT.449	2	9.81	64.5	1.18E+04 (-)
686	S1P_ZT_Ro	2	9.8	72.2	1.30E+06 (-)
689	S2P_ZT_Ro	2	9.79	75.4	5.06E+05 (-)
701	S5P_ZT_Ro	2	9.74	63.2	1.18E+06 (-)
710	X4P_ZT.407	2	9.69	76.3	7.69E+05 (-)
712	S1P_ZT_Ro	2	9.69	78.9	5.02E+05 (-)
721	X5P_ZT.346	2	9.64	70.2	1.57E+07 (-)
732	S5P_ZT_Ro	2	9.58	73.4	3.39E+05 (-)
734	S2P_ZT_Ro	2	9.58	71.3	1.29E+06 (-)
765	L3P_ZT.377	2	9.43	72	1.76E+06 (-)
772	L3P_ZT.418	2	9.38	63.7	3.07E+05 (-)
782	L3P_ZT.427	2	9.33	73.3	7.00E+05 (-)
785	X4P_ZT.388	2	9.29	94.5	3.30E+04 (-)
799	S5P_ZT_Ro	2	9.21	68.3	1.13E+06 (-)
808	S1P_ZT_Ro	2	9.17	60.9	4.06E+06 (-)

809	L1P_ZT.31E	2	9.17	60.5	1.21E+07 (-)
817	S2P_ZT_Ro	2	9.12	66.9	1.04E+06 (-)
818	L3P_ZT.367	2	9.12	71.7	1.52E+06 (-)
823	X4P_ZT.42E	2	9.09	61.9	5.59E+05 (-)
866	X4P_ZT.39E	2	8.92	85.7	2.48E+05 (-)
870	X3P_ZT.39E	2	8.9	63.5	5.39E+05 (-)
872	X3P_ZT.40E	2	8.89	71	8.82E+05 (-)
878	X4P_ZT.38E	2	8.87	63.3	8.27E+05 (-)
885	L3P_ZT.41C	2	8.86	68	3.58E+05 (-)
888	X4P_ZT.36E	2	8.84	64.3	1.33E+06 (-)
900	L3P_ZT.37C	2	8.78	64.1	8.78E+05 (-)
901	S1P_ZT_Ro	2	8.77	61.5	7.27E+05 (-)
903	L3P_ZT.44E	2	8.77	60.6	8.06E+05 (-)
907	L3P_ZT.43E	2	8.76	65.7	7.37E+05 (-)
916	S2P_ZT_Ro	2	8.72	72.5	1.36E+06 (-)
935	X4P_ZT.39E	2	8.6	70.5	3.33E+05 (-)
936	X4P_ZT.42C	2	8.6	72	3.03E+04 (-)
947	S2P_ZT_Ro	2	8.58	64.2	1.35E+06 (-)
962	S4P_ZT_Ro	2	8.5	68.4	8.42E+05 (-)
980	X4P_ZT.39E	2	8.44	77.9	9.72E+05 (-)
984	X4P_ZT.36E	2	8.43	81.8	2.02E+06 (-)
1012	S2P_ZT_Ro	2	8.34	60.9	7.76E+05 (-)
1029	S1P_ZT_Ro	2	8.28	92	4.30E+05 (-)
1044	X3P_ZT.40E	2	8.22	68.8	8.30E+05 (-)
1047	S1P_ZT_Ro	2	8.22	68.2	7.50E+05 (-)
1054	X4P_ZT.42E	2	8.18	62	5.85E+05 (-)
1062	S1P_ZT_Ro	2	8.14	63.4	3.33E+06 (-)
1069	X3P_ZT.39E	2	8.11	60.8	3.32E+05 (-)
1070	S4P_ZT_Ro	2	8.11	64	2.14E+06 (-)
1074	S2P_ZT_Ro	2	8.1	78.3	6.17E+07 (-)
1084	X3P_ZT.35E	2	8.07	64.4	3.35E+06 (-)
1101	X4P_ZT.38E	2	8.02	70.5	1.12E+06 (-)
1106	L3P_ZT.42E	2	8.02	68.8	7.26E+05 (-)
1111	X3P_ZT.36E	2	7.98	78.6	1.86E+06 (-)
1147	L3P_ZT.38E	2	7.86	63.2	1.36E+06 (-)
1162	L3P_ZT.40E	2	7.79	85.2	5.50E+05 (-)
1184	S3P_ZT_Ro	2	7.73	73.1	9.06E+05 (-)
1190	X4P_ZT.37E	2	7.7	72	3.57E+05 (-)
1201	S4P_ZT_Ro	2	7.66	63.9	1.98E+06 (-)
1210	X3P_ZT.38E	2	7.64	68.5	1.12E+06 (-)
1229	S2P_ZT_Ro	2	7.56	79.2	8.44E+05 (-)
1254	X3P_ZT.40E	2	7.47	88.2	9.32E+05 (-)
1285	L3P_ZT.43E	2	7.38	94.8	7.85E+05 (-)
1350	X3P_ZT.37E	2	7.14	67.5	1.28E+06 (-)
1398	X3P_ZT.44E	2	6.99	69.1	5.75E+05 (-)
1401	X4P_ZT.43E	2	6.98	68.2	5.09E+05 (-)
1455	X3P_ZT.38E	2	6.84	82	9.96E+05 (-)

1468 X3P_ZT.410	2	6.81	69.5	6.93E+05 (-)
1570 X4P_ZT.360	2	6.58	75.7	1.69E+06 (-)
1635 X3P_ZT.420	2	6.45	74.2	5.73E+04 (-)
1641 L3P_ZT.461	2	6.43	65.2	4.42E+04 (-)
1652 X4P_ZT.420	2	6.4	85.1	3.03E+04 (-)
1677 X4P_ZT.430	2	6.33	66.4	3.43E+05 (-)
1691 L3P_ZT.441	2	6.3	80.1	7.96E+05 (-)
1772 X3P_ZT.400	2	6.13	65	9.11E+05 (-)
1794 X5P_ZT.340	2	6.08	86.8	1.57E+07 (-)
1817 S3P_ZT_Ro	2	6.02	62.9	5.69E+05 (-)
1839 S3P_ZT_Ro	2	5.95	76.6	7.39E+06 (-)
1900 X4P_ZT.410	2	5.81	76.9	3.03E+04 (-)
1920 L2P_ZT.390	2	5.77	76	2.55E+05 (-)
2035 L3P_ZT.447	2	5.56	70.7	1.18E+04 (-)
2096 S2P_ZT_Ro	2	5.45	65.7	1.53E+07 (-)
2128 S2P_ZT_Ro	2	5.37	67.2	6.50E+05 (-)
384 L3P_ZT.330	2	11.88	82.2	4.11E+04 (-)
527 S4P_ZT_Ro	2	10.86	73.3	1.69E+05 (-)
877 X4P_ZT.330	2	8.87	68.8	5.20E+04 (-)
928 X4P_ZT.340	2	8.62	63.6	4.32E+04 (-)
1032 S3P_ZT_Ro	2	8.27	66.5	6.38E+03 (-)
1195 S5P_ZT_Ro	2	7.68	62.5	2.50E+04 (-)
1406 X5P_ZT.300	2	6.97	65.2	3.20E+05 (-)
1504 S3P_ZT_Ro	2	6.74	93.4	1.26E+05 (-)
1751 S5P_ZT_Ro	2	6.19	91.5	7.54E+04 (-)
2085 S5P_ZT_Ro	2	5.46	71	7.54E+04 (-)
166 L3P_ZT.491	3	14.4	86.3	9.63E+04 (-)
931 S2P_ZT_Ro	3	8.62	71.2	1.95E+05 (-)
2018 X3P_ZT.300	3	5.59	76.5	2.90E+05 (R)
1490 S1P_ZT_Ro	2	6.77	61.6	7.19E+05 (K)
1599 L5P_ZT.200	2	6.52	61.7	1.59E+06 (K)
2114 X2P_ZT.200	2	5.4	65	2.03E+06 (K)
2274 X4P_ZT.530	3	5.12	64.1	1.04E+05 (K)
961 S1P_ZT_Ro	4	8.51	65.7	2.37E+05 (K)
1148 S5P_ZT_Ro	4	7.85	69.2	5.85E+04 (K)
1604 S3P_ZT_Ro	4	6.51	61.2	1.41E+05 (K)
1773 X2P_ZT.520	4	6.13	70.1	2.79E+05 (K)
2288 S1P_ZT_Ro	3	5.1	85.8	1.56E+05 (K)
1835 L5P_ZT.490	2	5.97	63.6	3.44E+06 (K)
1262 X4P_ZT.480	7	7.44	71.8	8.70E+05 (K)
2278 X4P_ZT.400	3	5.11	72.9	1.25E+06 (K)
2319 X4P_ZT.400	3	5.02	74.3	1.25E+06 (K)
1843 L3P_ZT.510	4	5.94	69.2	6.65E+04 (K)
1573 L2P_ZT.410	6	6.58	71.4	7.96E+04 (D)
2089 L2P_ZT.140	2	5.46	63.4	1.33E+06 (K)
2055 X5P_ZT.490	6	5.52	61.4	3.04E+04 (R)
1711 S2P_ZT_Ro	5	6.27	64	1.53E+06 (R)

1246 S2P_ZT_Ro	5	7.5	62.4	9.92E+05 (K)
736 X5P_ZT.539	5	9.56	77.4	6.71E+05 (K)
851 L2P_ZT.497	5	8.99	63.2	5.32E+05 (K)
937 S5P_ZT_Ro	5	8.6	64.4	8.44E+05 (K)
1091 X5P_ZT.539	5	8.05	69.6	2.04E+05 (K)
1157 S2P_ZT_Ro	4	7.81	72.4	2.28E+04 (K)
1241 L1P_ZT.508	5	7.51	65.9	5.36E+05 (K)
1381 X2P_ZT.529	5	7.03	79	5.20E+05 (K)
1655 L5P_ZT.522	5	6.4	66.2	7.09E+05 (K)
1831 S3P_ZT_Ro	5	5.98	65.1	3.06E+05 (K)
829 S2P_ZT_Ro	4	9.08	63.7	1.05E+05 (K)
1687 L2P_ZT.444	4	6.31	74.1	4.82E+05 (K)
1569 S3P_ZT_Ro	4	6.59	60.1	1.95E+04 (K)
1704 X3P_ZT.351	6	6.28	66.5	3.70E+04 (K)
1873 L3P_ZT.503	4	5.89	77.5	1.31E+04 (K)
1133 L2P_ZT.298	4	7.9	67.2	1.10E+06 (D)
1936 L2P_ZT.354	3	5.74	60.4	8.98E+05 (E)
2068 X5P_ZT.504	5	5.49	78.2	5.15E+04 (I)
1219 X3P_ZT.382	6	7.58	84.7	2.47E+05 (F)
1624 L1P_ZT.364	6	6.47	75.5	3.81E+04 (F)
1930 S4P_ZT_Ro	2	5.75	65.7	3.69E+06 (R)
2124 L3P_ZT.524	2	5.38	65.6	8.74E+04 (R)
2143 S3P_ZT_Ro	3	5.35	64.4	4.95E+04 (R)
2209 S2P_ZT_Ro	3	5.24	81.4	8.11E+04 (R)
2273 L3P_ZT.524	3	5.13	65.4	8.05E+04 (R)
2294 S1P_ZT_Ro	3	5.09	66.3	9.19E+04 (R)
749 S4P_ZT_Ro	6	9.49	63.4	1.02E+05 (S)
1756 L5P_ZT.505	4	6.18	65.3	9.44E+05 (F)
1890 S1P_ZT_Ro	7	5.83	84	4.45E+04 (R)
1483 L2P_ZT.469	3	6.78	61.8	1.59E+05 (R)
1568 L5P_ZT.494	3	6.6	79.8	1.46E+05 (R)
1675 S4P_ZT_Ro	3	6.34	67.5	2.99E+04 (R)
1814 L3P_ZT.491	3	6.03	67.2	2.31E+05 (R)
2093 X2P_ZT.501	3	5.45	66.3	9.99E+04 (R)
1215 X4P_ZT.539	7	7.61	64.6	1.27E+06 (R)
1402 X2P_ZT.494	7	6.98	69.1	2.98E+06 (R)
1473 X5P_ZT.501	7	6.8	83.2	4.79E+06 (R)
1714 S3P_ZT_Ro	7	6.26	60.6	3.13E+05 (R)
1942 L2P_ZT.516	7	5.73	62.7	3.33E+06 (R)
1988 L1P_ZT.475	7	5.65	64.9	2.05E+06 (R)
1977 L4P_ZT.277	5	5.66	64.2	7.85E+05 (K)
1771 L2P_ZT.438	3	6.14	60.9	7.32E+04 (A)
627 X1P_ZT.248	3	10.15	71.9	6.66E+05 (V)
1269 X5P_ZT.256	3	7.43	64.8	1.12E+06 (V)
130 S4P_ZT_Ro	2	14.92	81.1	6.22E+05 (L)
222 S4P_ZT_Ro	2	13.66	83.9	6.79E+04 (L)
383 S3P_ZT_Ro	2	11.88	69.6	5.26E+04 (L)

434 S3P_ZT_Ro	2	11.56	68.1	5.26E+04 (L)
466 S4P_ZT_Ro	2	11.36	68.8	7.05E+05 (L)
672 X4P_ZT.334	2	9.88	65.3	2.54E+05 (L)
773 X4P_ZT.261	2	9.37	84	4.78E+05 (L)
898 S3P_ZT_Ro	2	8.78	61.3	8.07E+05 (L)
2165 X2P_ZT.471	5	5.31	68.8	3.91E+05 (K)
2323 L5P_ZT.465	5	5.02	80.5	7.68E+05 (K)
1130 L1P_ZT.358	5	7.91	62.3	5.40E+04 (K)
1792 L5P_ZT.388	2	6.09	66.5	4.38E+07 (K)
1797 X2P_ZT.390	2	6.07	66.7	4.75E+07 (K)
1981 X5P_ZT.381	2	5.65	66.6	6.24E+07 (K)
1990 X1P_ZT.361	2	5.64	66.4	9.33E+07 (K)
1480 S2P_ZT_Ro	7	6.78	78.6	6.96E+04 (Q)
2066 L1P_ZT.528	5	5.5	64.5	3.89E+04 (C)
1457 S5P_ZT_Ro	3	6.84	64.7	1.40E+05 (C)
1801 X3P_ZT.386	3	6.06	60.4	2.72E+05 (C)
2164 X5P_ZT.478	3	5.31	64.2	3.75E+04 (K)
1252 S4P_ZT_Ro	6	7.48	63	1.73E+04 (K)
1255 S4P_ZT_Ro	7	7.47	70.6	1.54E+06 (L)
1694 X4P_ZT.361	5	6.29	76.6	4.91E+05 (L)
1808 S4P_ZT_Ro	7	6.05	60.8	1.54E+06 (L)
1976 L1P_ZT.351	6	5.66	73.2	7.79E+05 (L)
2156 X2P_ZT.376	5	5.32	74.9	8.46E+05 (L)
1410 S5P_ZT_Ro	2	6.97	64.8	9.60E+05 (R)
1821 S5P_ZT_Ro	2	6	67.3	9.60E+05 (R)
1901 X1P_ZT.291	2	5.81	71.6	4.93E+05 (R)
1945 X1P_ZT.300	2	5.72	75.5	4.93E+05 (R)
2161 L4P_ZT.313	2	5.32	61.3	5.24E+05 (R)
1580 X2P_ZT.534	7	6.57	70.3	4.47E+04 (R)
2051 L2P_ZT.487	4	5.53	63.7	1.48E+05 (R)
2107 L5P_ZT.546	7	5.42	61.3	4.89E+04 (R)
237 S4P_ZT_Ro	2	13.44	76.9	2.82E+06 (V)
392 X2P_ZT.291	2	11.83	70.1	2.05E+06 (V)
488 X2P_ZT.294	2	11.18	72.2	2.05E+06 (V)
498 L3P_ZT.282	2	11.09	72.5	1.69E+06 (V)
683 S5P_ZT_Ro	2	9.8	80.4	3.35E+06 (V)
723 S2P_ZT_Ro	2	9.63	74.5	3.54E+06 (V)
746 L5P_ZT.292	2	9.52	63.6	2.30E+06 (V)
802 X1P_ZT.274	2	9.2	66.6	1.88E+06 (V)
825 L1P_ZT.266	2	9.09	61.1	3.01E+06 (V)
889 S1P_ZT_Ro	2	8.84	65.1	3.88E+06 (V)
1083 X3P_ZT.281	2	8.07	84.3	1.94E+06 (V)
1482 L1P_ZT.252	4	6.78	70.6	6.99E+05 (L)
1669 L5P_ZT.277	4	6.36	66.3	4.25E+05 (L)
1671 X5P_ZT.271	4	6.34	68.3	5.53E+05 (L)
2014 X2P_ZT.278	5	5.6	73.7	1.21E+06 (L)
2057 S1P_ZT_Ro	5	5.52	61	9.30E+05 (L)

2236 X2P_ZT.278	4	5.21	66.3	8.35E+05 (L)
1363 L4P_ZT.205	3	7.11	71.8	4.51E+04 (D)
834 X3P_ZT.888	2	9.05	80.3	2.42E+05 (A)
1135 X2P_ZT.326	3	7.88	88.1	3.12E+04 (F)
692 S2P_ZT_Ro	3	9.77	63.9	6.76E+06 (S)
827 X3P_ZT.461	3	9.08	72.7	2.11E+06 (S)
839 S4P_ZT_Ro	3	9.02	74	2.98E+06 (S)
904 X4P_ZT.454	3	8.76	82.3	4.95E+06 (S)
925 L1P_ZT.445	3	8.64	76.5	6.94E+06 (S)
933 X2P_ZT.459	3	8.61	77.7	2.46E+06 (S)
972 S5P_ZT_Ro	3	8.47	86	2.52E+06 (S)
993 S3P_ZT_Ro	3	8.4	79.9	2.49E+06 (S)
994 X3P_ZT.461	3	8.39	74.6	1.43E+06 (S)
1170 L2P_ZT.433	3	7.77	89.6	1.72E+06 (S)
1308 L4P_ZT.437	3	7.3	78.4	4.61E+06 (S)
1372 X3P_ZT.451	3	7.05	94.2	2.18E+06 (S)
1496 S5P_ZT_Ro	3	6.75	75.3	2.52E+06 (S)
1553 L3P_ZT.461	3	6.64	68.8	1.31E+06 (S)
1564 L3P_ZT.460	3	6.61	68.6	3.34E+06 (S)
1660 X1P_ZT.430	3	6.37	77.7	7.22E+06 (S)
1796 X3P_ZT.457	3	6.07	95.2	2.18E+06 (S)
1657 X3P_ZT.211	3	6.39	67.4	2.16E+05 (S)
1666 X3P_ZT.214	3	6.36	74.2	2.16E+05 (S)
2135 S2P_ZT_Ro	4	5.36	62.4	2.54E+04 (R)
1485 X5P_ZT.381	6	6.77	70	1.07E+05 (P)
2152 X3P_ZT.501	3	5.33	73.6	7.77E+05 (K)
1760 S5P_ZT_Ro	7	6.17	79.6	7.79E+04 (-)
1757 X4P_ZT.211	4	6.17	73.2	1.91E+04 (-)
1870 L5P_ZT.222	4	5.9	76.5	4.37E+04 (-)
1962 S5P_ZT_Ro	4	5.69	76.6	3.18E+04 (-)
1937 X3P_ZT.291	3	5.73	85.3	2.59E+06 (K)
1355 X2P_ZT.354	7	7.13	67.6	1.21E+06 (-)
2015 L1P_ZT.137	3	5.6	61.2	7.89E+04 (K)
2050 L2P_ZT.133	3	5.53	72.9	1.75E+05 (K)
835 X5P_ZT.543	4	9.03	63.2	2.21E+05 (K)
1435 L2P_ZT.481	4	6.9	62.9	9.55E+04 (-)
1946 S4P_ZT_Ro	5	5.72	100	4.42E+04 (-)
2227 X2P_ZT.271	5	5.22	74.6	3.89E+06 (-)
1621 S5P_ZT_Ro	7	6.47	100	6.78E+05 (-)
1764 S3P_ZT_Ro	7	6.16	82.8	4.10E+05 (-)
1956 S4P_ZT_Ro	7	5.71	62	1.06E+06 (-)
1075 X4P_ZT.509	3	8.09	61.1	3.78E+06 (-)
2217 S3P_ZT_Ro	6	5.23	73.6	1.38E+05 (-)
1763 X5P_ZT.441	5	6.16	65.1	6.46E+04 (-)
2269 L3P_ZT.345	7	5.14	74.9	7.10E+04 (-)
1662 S4P_ZT_Ro	5	6.37	63.7	2.11E+06 (-)
1715 S1P_ZT_Ro	5	6.26	66.6	1.61E+06 (-)

1741 X3P_ZT.260	5	6.21	64	2.97E+06 (-)
1761 L1P_ZT.242	5	6.17	66.3	1.01E+06 (-)
2053 L5P_ZT.269	5	5.53	66.7	1.49E+06 (-)
1809 S2P_ZT_Ro	5	6.05	66.3	2.47E+04 (R)
1373 S2P_ZT_Ro	5	7.05	63.8	3.67E+04 (-)
1615 S3P_ZT_Ro	3	6.48	64.8	6.93E+05 (R)
2167 X4P_ZT.500	3	5.3	70	4.71E+04 (-)
1980 L5P_ZT.375	3	5.66	63.3	3.25E+06 (-)
2109 X5P_ZT.379	2	5.41	84.4	1.30E+06 (-)
1818 S5P_ZT_Ro	3	6.01	67.3	6.47E+05 (-)
2224 X4P_ZT.314	3	5.22	84.1	2.85E+04 (-)
2203 L2P_ZT.435	2	5.25	100	1.95E+05 (-)
1882 S2P_ZT_Ro	2	5.86	78.2	4.77E+05 (K)
1275 L4P_ZT.177	2	7.41	83.4	3.33E+05 (K)
1517 S4P_ZT_Ro	2	6.71	85.6	3.00E+05 (K)
2192 S1P_ZT_Ro	2	5.26	63.2	2.06E+06 (R)
1437 X2P_ZT.559	4	6.89	91.4	4.30E+04 (R)
2081 L2P_ZT.482	6	5.47	100	2.25E+05 (R)
779 X2P_ZT.170	2	9.34	64.3	3.81E+06 (K)
2328 L4P_ZT.440	2	5.01	64.5	1.03E+05 (K)
1729 L4P_ZT.384	2	6.23	71.3	1.69E+04 (K)
2032 S1P_ZT_Ro	2	5.56	74.4	6.62E+05 (K)
2219 L2P_ZT.372	2	5.23	61.9	4.47E+05 (K)
1617 L3P_ZT.536	4	6.48	77.8	1.09E+05 (K)
2187 L5P_ZT.541	4	5.27	70.2	7.73E+04 (K)
986 X3P_ZT.500	2	8.42	62.8	1.67E+06 (K)
1637 L2P_ZT.479	2	6.44	68.3	1.72E+06 (K)
1759 X1P_ZT.469	2	6.17	60.5	1.14E+06 (K)
1863 L5P_ZT.504	2	5.91	74.1	1.45E+06 (K)
2041 S3P_ZT_Ro	2	5.54	62.3	2.10E+06 (K)
2060 L4P_ZT.371	3	5.51	74.5	3.58E+06 (K)
2099 X4P_ZT.500	2	5.43	62.3	1.49E+06 (K)
2126 X2P_ZT.380	3	5.37	100	3.72E+06 (K)
1803 S4P_ZT_Ro	2	6.06	67.6	2.27E+05 (K)
2303 X2P_ZT.510	2	5.06	79.3	5.22E+04 (K)
1244 X2P_ZT.310	2	7.5	85.9	5.80E+04 (K)
1738 L3P_ZT.417	3	6.22	100	4.69E+06 (K)
758 S1P_ZT_Ro	3	9.44	69.9	6.06E+06 (K)
805 L2P_ZT.449	3	9.18	72.3	8.96E+05 (K)
1253 S1P_ZT_Ro	3	7.48	69.1	6.06E+06 (K)
1331 L1P_ZT.459	3	7.21	68.7	2.20E+06 (K)
1356 S2P_ZT_Ro	3	7.13	60.4	7.84E+05 (K)
1475 X1P_ZT.444	3	6.8	70.5	1.05E+07 (K)
1511 L4P_ZT.450	3	6.73	63.1	3.14E+06 (K)
1542 X4P_ZT.470	3	6.65	67	4.99E+05 (K)
1875 S5P_ZT_Ro	3	5.88	63.1	1.40E+06 (K)
1888 X1P_ZT.440	3	5.83	70.5	1.05E+07 (K)

1918 S5P_ZT_Ro	3	5.77	65	1.40E+06 (K)
2065 S3P_ZT_Ro	5	5.5	100	5.88E+04 (R)
2201 S1P_ZT_Ro	5	5.25	100	5.99E+04 (R)
2120 L2P_ZT.368	3	5.39	78.6	8.22E+06 (R)
1462 S5P_ZT_Ro	4	6.83	61.4	1.59E+05 (K)
1739 L4P_ZT.481	4	6.22	100	4.54E+04 (K)
2182 L3P_ZT.399	5	5.28	62	5.15E+05 (K)
1327 L4P_ZT.492	7	7.22	76	5.02E+04 (N)
1840 X4P_ZT.550	7	5.94	60.9	2.83E+06 (N)
294 S4P_ZT_Ro	2	12.7	89.7	7.18E+05 (R)
317 S2P_ZT_Ro	2	12.55	85.9	1.08E+06 (R)
424 S3P_ZT_Ro	2	11.64	86.4	1.21E+06 (R)
592 L3P_ZT.910	2	10.39	64	1.01E+06 (R)
717 L3P_ZT.893	2	9.67	67.7	1.01E+06 (R)
1066 X4P_ZT.833	2	8.13	80	9.29E+05 (R)
1384 S3P_ZT_Ro	2	7.02	75.7	1.21E+06 (R)
1607 S3P_ZT_Ro	2	6.5	65.1	1.21E+06 (R)
80 S1P_ZT_Ro	2	16.09	96.7	1.56E+07 (R)
86 S2P_ZT_Ro	2	15.84	96.7	1.76E+07 (R)
137 S3P_ZT_Ro	2	14.83	95.9	2.24E+07 (R)
165 S4P_ZT_Ro	2	14.42	100	2.67E+07 (R)
169 L3P_ZT.176	2	14.3	94.7	4.07E+07 (R)
282 X4P_ZT.170	2	12.79	94.3	1.41E+07 (R)
551 L1P_ZT.164	2	10.72	77.8	1.73E+06 (R)
586 X2P_ZT.175	2	10.4	90.9	2.22E+06 (R)
1045 X1P_ZT.174	2	8.22	71.9	7.19E+06 (R)
1294 X5P_ZT.175	2	7.33	64.2	1.91E+06 (R)
1598 L4P_ZT.186	2	6.52	80.8	9.98E+05 (R)
941 L2P_ZT.313	3	8.59	62.6	1.52E+06 (G)
156 L3P_ZT.108	2	14.57	82.6	1.38E+07 (G)
236 S1P_ZT_Ro	2	13.45	86.2	1.42E+07 (G)
344 S3P_ZT_Ro	2	12.34	80.6	6.88E+06 (G)
347 S4P_ZT_Ro	2	12.29	76.6	1.08E+07 (G)
523 S4P_ZT_Ro	2	10.89	73.5	1.08E+07 (G)
623 S5P_ZT_Ro	2	10.2	76.3	1.59E+07 (G)
1009 S4P_ZT_Ro	2	8.34	62.3	9.36E+06 (G)
932 X3P_ZT.563	3	8.61	67.1	3.22E+05 (R)
1004 X4P_ZT.573	2	8.36	70.2	2.95E+05 (R)
1041 X4P_ZT.570	3	8.23	67.5	2.83E+05 (R)
1086 S2P_ZT_Ro	3	8.07	63.8	5.52E+05 (R)
1207 X4P_ZT.120	2	7.65	72.7	7.90E+05 (R)
1354 L3P_ZT.649	2	7.14	77.4	3.62E+05 (R)
146 S4P_ZT_Ro	2	14.69	81.6	2.79E+06 (R)
208 S2P_ZT_Ro	2	13.82	74.2	2.79E+06 (R)
268 L3P_ZT.128	2	13.04	83.1	6.88E+05 (R)
305 S5P_ZT_Ro	2	12.6	84.1	2.59E+06 (R)
429 S3P_ZT_Ro	2	11.59	77.8	4.75E+06 (R)

437	S5P_ZT_Ro	3	11.54	78.7	7.14E+06 (R)
440	S3P_ZT_Ro	3	11.53	82.2	8.06E+06 (R)
459	S1P_ZT_Ro	2	11.4	76.8	2.93E+06 (R)
480	X3P_ZT.12	3	11.24	77	4.57E+06 (R)
509	X4P_ZT.11	2	10.96	73.2	1.71E+06 (R)
575	S1P_ZT_Ro	2	10.47	73.6	2.93E+06 (R)
660	S4P_ZT_Ro	3	9.95	74.7	7.10E+06 (R)
704	L3P_ZT.12	3	9.72	72.7	5.49E+06 (R)
708	S3P_ZT_Ro	2	9.7	76.3	4.75E+06 (R)
730	X3P_ZT.12	2	9.58	70.7	2.56E+06 (R)
739	S5P_ZT_Ro	2	9.56	65.6	2.59E+06 (R)
745	S2P_ZT_Ro	3	9.52	72.1	7.59E+06 (R)
886	X3P_ZT.11	3	8.85	65.9	4.57E+06 (R)
1203	S1P_ZT_Ro	3	7.66	61.8	7.82E+06 (R)
1265	S2P_ZT_Ro	2	7.44	61.2	2.79E+06 (R)
1351	X2P_ZT.12	3	7.14	69.2	1.98E+05 (R)
1502	X4P_ZT.12	3	6.74	67.1	5.43E+06 (R)
1112	S4P_ZT_Ro	4	7.98	62.2	2.18E+05 (D)
1239	S5P_ZT_Ro	3	7.52	73.5	2.07E+05 (D)
1609	L3P_ZT.21	5	6.5	63.2	2.56E+07 (V)
2205	X5P_ZT.21	5	5.24	68.1	2.56E+07 (V)
1232	L3P_ZT.43	3	7.56	79	8.52E+04 (P)
1281	L1P_ZT.411	3	7.39	64.7	1.42E+06 (P)
1456	X1P_ZT.41	3	6.84	63.6	2.87E+05 (P)
1709	S4P_ZT_Ro	3	6.27	76.8	7.42E+05 (P)
1699	S3P_ZT_Ro	2	6.29	91.4	3.90E+05 (K)
1813	S5P_ZT_Ro	2	6.03	62.9	7.07E+05 (K)
2146	S2P_ZT_Ro	3	5.34	61.5	3.14E+04 (K)
1366	X4P_ZT.23	3	7.08	77.6	3.24E+05 (K)
945	S5P_ZT_Ro	4	8.58	70.7	3.66E+05 (K)
1916	S2P_ZT_Ro	3	5.78	66.8	6.61E+04 (K)
1412	X2P_ZT.42	4	6.96	81	4.08E+04 (K)
1848	L4P_ZT.44	4	5.93	73	6.12E+04 (K)
2116	L3P_ZT.39	4	5.4	67.7	1.69E+05 (K)
863	L1P_ZT.38	3	8.94	75.1	2.82E+05 (K)
893	S2P_ZT_Ro	3	8.81	71.4	3.15E+05 (K)
1299	X1P_ZT.50	4	7.31	64.7	4.91E+05 (K)
1903	X3P_ZT.42	3	5.8	62	2.94E+05 (K)
1664	L3P_ZT.50	5	6.37	100	1.47E+05 (R)
1430	L2P_ZT.51	4	6.92	75	3.63E+04 (K)
2022	L4P_ZT.49	4	5.59	69.2	1.45E+04 (K)
2216	S4P_ZT_Ro	4	5.23	67.8	1.27E+05 (K)
2259	X2P_ZT.54	4	5.16	64.6	6.74E+04 (K)
491	L5P_ZT.36	4	11.18	64	3.60E+07 (M)
502	X1P_ZT.33	4	11.03	65.7	4.13E+07 (M)
519	X3P_ZT.35	4	10.92	61.9	3.67E+07 (M)
574	S5P_ZT_Ro	4	10.49	62.9	4.24E+07 (M)

768 S2P_ZT_Ro	4	9.41	61.4	3.15E+07 (M)
780 L1P_ZT.339	4	9.34	66.4	5.70E+07 (M)
789 L3P_ZT.355	4	9.27	65.6	4.55E+07 (M)
793 S1P_ZT_Ro	4	9.26	64.5	3.15E+07 (M)
800 S3P_ZT_Ro	4	9.21	62.2	3.15E+07 (M)
854 X5P_ZT.364	4	8.97	64	3.02E+07 (M)
911 L4P_ZT.354	4	8.74	60.3	3.66E+07 (M)
1126 X4P_ZT.357	4	7.92	60.6	3.09E+07 (M)
1259 S4P_ZT_Ro	4	7.45	61.1	3.38E+07 (M)
1528 X1P_ZT.344	4	6.69	63.3	4.13E+07 (M)
2082 L2P_ZT.484	3	5.47	100	3.29E+06 (A)
190 L3P_ZT.846	3	14.06	81.4	3.75E+07 (R)
221 S3P_ZT_Ro	3	13.67	83.5	3.05E+07 (R)
245 S2P_ZT_Ro	3	13.36	83.2	4.28E+07 (R)
265 S4P_ZT_Ro	3	13.1	84.6	2.51E+07 (R)
301 S5P_ZT_Ro	3	12.63	85.4	3.75E+07 (R)
306 S3P_ZT_Ro	2	12.6	90.3	3.83E+07 (R)
314 S1P_ZT_Ro	2	12.57	90.4	5.52E+07 (R)
324 L3P_ZT.831	3	12.49	60.3	3.75E+07 (R)
329 L3P_ZT.830	2	12.44	93.3	4.89E+07 (R)
333 X4P_ZT.743	3	12.41	80.9	3.21E+07 (R)
363 S2P_ZT_Ro	2	12.13	92.5	5.75E+07 (R)
395 X4P_ZT.753	2	11.82	91	3.97E+07 (R)
415 X3P_ZT.748	3	11.7	100	2.71E+07 (R)
433 S5P_ZT_Ro	2	11.56	91.7	9.32E+07 (R)
439 X4P_ZT.773	3	11.53	70.9	3.21E+07 (R)
446 S1P_ZT_Ro	3	11.5	83.1	5.80E+07 (R)
467 X5P_ZT.748	2	11.35	86.9	3.09E+07 (R)
522 S4P_ZT_Ro	2	10.89	92.6	1.16E+08 (R)
607 L4P_ZT.960	2	10.29	77.4	7.80E+06 (R)
615 X2P_ZT.783	2	10.22	81.6	1.61E+07 (R)
816 X2P_ZT.803	3	9.12	65.4	1.81E+07 (R)
1460 X4P_ZT.743	2	6.83	68.3	8.02E+07 (R)
1721 L2P_ZT.793	2	6.25	73.3	2.03E+07 (R)
1914 S5P_ZT_Ro	2	5.78	65	9.32E+07 (R)
2170 L1P_ZT.255	3	5.3	63.6	1.66E+07 (R)
1222 S5P_ZT_Ro	3	7.57	66.6	9.43E+04 (I)
1312 X5P_ZT.113	2	7.26	72.6	1.42E+05 (K)
2155 X3P_ZT.113	2	5.32	66.2	2.99E+04 (K)
1917 L2P_ZT.518	3	5.78	65.4	1.07E+05 (A)
1834 L3P_ZT.488	6	5.97	66.1	4.53E+04 (I)
2012 L3P_ZT.363	6	5.61	60.3	1.54E+05 (K)
869 L4P_ZT.308	3	8.91	60.8	1.37E+05 (Y)
1413 S4P_ZT_Ro	7	6.96	78.8	1.42E+05 (R)
1648 S4P_ZT_Ro	4	6.41	63.8	5.01E+06 (R)
2063 S5P_ZT_Ro	4	5.5	65.3	4.25E+06 (R)
1550 L5P_ZT.510	6	6.65	60.3	1.95E+05 (R)

1619 X5P_ZT.524	6	6.47	100	1.54E+05 (R)
1953 X5P_ZT.524	6	5.71	77.7	1.72E+05 (R)
2078 X1P_ZT.474	6	5.47	73.1	1.61E+05 (R)
579 X2P_ZT.383	5	10.45	74	2.81E+05 (K)
448 S1P_ZT_Ro	2	11.48	82.3	9.74E+04 (L)
548 S4P_ZT_Ro	2	10.76	74	6.35E+05 (L)
585 X3P_ZT.165	2	10.41	66.7	8.71E+05 (L)
685 S2P_ZT_Ro	2	9.8	71.2	5.22E+04 (L)
748 S4P_ZT_Ro	2	9.5	71.9	6.35E+05 (L)
814 S1P_ZT_Ro	2	9.13	66.2	1.25E+06 (L)
951 L3P_ZT.328	2	8.57	71	5.99E+04 (L)
1013 S2P_ZT_Ro	2	8.33	74.5	7.35E+05 (L)
1068 X3P_ZT.330	2	8.11	67.9	1.64E+05 (L)
1532 L5P_ZT.233	2	6.69	73.5	5.23E+06 (K)
1563 L4P_ZT.265	3	6.62	100	1.10E+06 (L)
210 S4P_ZT_Ro	3	13.8	67.9	5.85E+06 (R)
289 S2P_ZT_Ro	4	12.75	86.5	2.81E+06 (R)
369 S2P_ZT_Ro	3	12.05	70.9	6.37E+06 (R)
382 S4P_ZT_Ro	4	11.88	68.7	1.93E+06 (R)
549 S3P_ZT_Ro	4	10.76	61.7	1.97E+06 (R)
606 S3P_ZT_Ro	4	10.29	65.2	1.97E+06 (R)
964 S3P_ZT_Ro	3	8.5	76.4	4.85E+06 (R)
1230 S2P_ZT_Ro	2	7.56	88	8.77E+05 (R)
1272 S5P_ZT_Ro	2	7.42	65.4	3.84E+05 (R)
1923 S5P_ZT_Ro	3	5.76	61.9	3.04E+06 (R)
1961 S4P_ZT_Ro	2	5.7	61.1	1.69E+07 (R)
1986 S4P_ZT_Ro	4	5.65	87.4	1.93E+06 (R)
92 X4P_ZT.125	3	15.63	90.2	5.88E+05 (R)
218 L3P_ZT.131	3	13.69	80	5.57E+05 (R)
251 S4P_ZT_Ro	3	13.29	81.4	4.42E+05 (R)
315 L3P_ZT.143	4	12.56	76.2	6.19E+04 (R)
321 S1P_ZT_Ro	4	12.51	94.9	9.23E+05 (R)
398 S1P_ZT_Ro	3	11.81	79.3	1.86E+05 (R)
593 S4P_ZT_Ro	3	10.38	77.7	4.42E+05 (R)
669 S1P_ZT_Ro	3	9.91	87.8	1.86E+05 (R)
840 S3P_ZT_Ro	3	9.02	64.5	1.99E+05 (R)
849 S3P_ZT_Ro	4	8.99	70.7	1.00E+06 (R)
950 S3P_ZT_Ro	4	8.57	72.9	3.51E+05 (R)
1008 X4P_ZT.125	2	8.34	61.5	1.59E+05 (R)
1159 S4P_ZT_Ro	4	7.8	82.4	5.55E+05 (R)
1271 S2P_ZT_Ro	4	7.43	90.3	2.01E+06 (R)
1415 X4P_ZT.125	5	6.95	73.1	1.37E+05 (R)
1459 S2P_ZT_Ro	5	6.84	60.2	2.20E+05 (R)
1520 L3P_ZT.132	2	6.71	71	5.21E+04 (R)
1539 S2P_ZT_Ro	4	6.66	73.6	5.95E+05 (R)
1562 S4P_ZT_Ro	4	6.62	62	1.24E+06 (R)
2070 L3P_ZT.140	4	5.49	65.7	1.48E+05 (R)

57 S4P_ZT_Ro	3	17.05	89.6	6.14E+06 (R)
73 L3P_ZT.187	4	16.26	94.5	4.03E+07 (R)
107 S2P_ZT_Ro	4	15.34	90.8	7.79E+06 (R)
160 X4P_ZT.18:	3	14.48	94.8	6.24E+06 (R)
191 X4P_ZT.19:	4	14.04	78.1	3.55E+06 (R)
193 S4P_ZT_Ro	5	14.02	95.9	2.08E+06 (R)
204 S2P_ZT_Ro	5	13.88	86.5	2.51E+06 (R)
215 L3P_ZT.194	3	13.71	80.7	1.49E+06 (R)
220 S4P_ZT_Ro	2	13.67	80	1.39E+06 (R)
231 S1P_ZT_Ro	3	13.56	82.5	2.92E+06 (R)
267 S3P_ZT_Ro	3	13.08	95.3	1.41E+06 (R)
299 S3P_ZT_Ro	3	12.64	87	1.41E+06 (R)
457 S4P_ZT_Ro	4	11.41	76.5	1.51E+07 (R)
489 S3P_ZT_Ro	4	11.18	94	6.50E+05 (R)
556 S2P_ZT_Ro	3	10.67	76.3	4.40E+06 (R)
571 S3P_ZT_Ro	5	10.53	72.9	9.31E+05 (R)
591 L3P_ZT.192	4	10.39	77.3	3.32E+06 (R)
598 S4P_ZT_Ro	2	10.35	60.6	3.41E+04 (R)
639 L3P_ZT.186	3	10.07	75.5	1.22E+07 (R)
662 X4P_ZT.18:	4	9.94	71.3	1.91E+07 (R)
838 S4P_ZT_Ro	2	9.02	70.6	1.39E+06 (R)
852 S4P_ZT_Ro	2	8.98	69.4	1.39E+06 (R)
894 S1P_ZT_Ro	2	8.8	70.5	2.65E+05 (R)
927 S1P_ZT_Ro	2	8.63	75.8	2.65E+05 (R)
968 S1P_ZT_Ro	5	8.49	76.7	1.87E+06 (R)
970 X4P_ZT.19:	3	8.47	60.9	1.40E+06 (R)
975 X4P_ZT.18:	2	8.46	64.2	9.90E+05 (R)
1002 L3P_ZT.186	4	8.37	66.5	4.03E+07 (R)
1010 S3P_ZT_Ro	2	8.34	63.2	7.02E+04 (R)
1073 S2P_ZT_Ro	2	8.1	64.6	5.94E+05 (R)
1088 S2P_ZT_Ro	2	8.06	71	5.94E+05 (R)
1168 S4P_ZT_Ro	2	7.77	65.4	1.39E+06 (R)
1213 S2P_ZT_Ro	5	7.62	69	2.51E+06 (R)
1280 X2P_ZT.190	4	7.39	61.7	6.86E+05 (R)
1329 S3P_ZT_Ro	5	7.21	77.2	9.31E+05 (R)
1541 X4P_ZT.19:	2	6.65	62.5	2.43E+05 (R)
2004 S3P_ZT_Ro	3	5.62	65.1	1.41E+06 (R)
2145 S3P_ZT_Ro	4	5.34	78.3	6.50E+05 (R)
2289 L3P_ZT.194	2	5.1	84.9	1.48E+05 (R)
14 S4P_ZT_Ro	3	19.96	93.5	1.32E+07 (R)
39 S3P_ZT_Ro	3	17.97	88.7	6.04E+06 (R)
94 S5P_ZT_Ro	3	15.6	86.2	8.08E+06 (R)
101 X3P_ZT.504	3	15.47	85.6	1.71E+07 (R)
110 S2P_ZT_Ro	3	15.32	85.9	1.50E+07 (R)
252 S1P_ZT_Ro	3	13.26	86.2	3.66E+07 (R)
397 S1P_ZT_Ro	3	11.82	69.2	3.66E+07 (R)
413 X4P_ZT.51:	3	11.72	70	1.11E+07 (R)

423 S2P_ZT_Ro	3	11.65	78.6	1.50E+07 (R)
562 L3P_ZT.598	3	10.64	75.1	2.50E+07 (R)
642 S5P_ZT_Ro	3	10.03	66.6	8.08E+06 (R)
652 L3P_ZT.597	4	9.99	73.6	2.80E+07 (R)
909 S3P_ZT_Ro	4	8.74	60.3	1.30E+07 (R)
1042 S4P_ZT_Ro	3	8.23	66.5	1.32E+07 (R)
1291 S1P_ZT_Ro	4	7.35	61	2.92E+06 (R)
82 X4P_ZT.104	4	15.94	91.6	1.73E+06 (R)
112 L3P_ZT.111	4	15.23	83.8	3.85E+06 (R)
281 S5P_ZT_Ro	3	12.8	70.2	1.01E+06 (R)
304 S5P_ZT_Ro	3	12.61	79.8	1.01E+06 (R)
308 S5P_ZT_Ro	4	12.59	78.1	4.94E+06 (R)
332 L3P_ZT.110	5	12.42	100	1.99E+06 (R)
375 S5P_ZT_Ro	4	11.96	72.9	4.94E+06 (R)
537 X3P_ZT.104	4	10.8	75.8	4.51E+06 (R)
613 S5P_ZT_Ro	4	10.23	80.1	1.06E+05 (R)
760 S4P_ZT_Ro	4	9.43	91.6	3.96E+04 (R)
856 X3P_ZT.103	2	8.96	67.5	6.17E+04 (R)
860 S4P_ZT_Ro	3	8.95	67.5	5.42E+05 (R)
897 S5P_ZT_Ro	5	8.78	69.5	4.12E+06 (R)
926 X3P_ZT.103	5	8.63	71.9	2.76E+06 (R)
966 S5P_ZT_Ro	4	8.49	66.2	4.94E+06 (R)
1000 L3P_ZT.110	3	8.37	70.7	7.11E+05 (R)
1061 S4P_ZT_Ro	3	8.14	63.7	5.42E+05 (R)
1352 S4P_ZT_Ro	3	7.14	65.2	5.42E+05 (R)
1726 X3P_ZT.103	4	6.23	77.2	1.42E+05 (R)
2314 X3P_ZT.103	5	5.03	67.6	2.47E+05 (R)
85 X3P_ZT.139	3	15.84	92.8	8.99E+06 (R)
103 S5P_ZT_Ro	3	15.44	88.6	8.71E+05 (R)
117 S2P_ZT_Ro	3	15.16	93.4	4.77E+06 (R)
120 X4P_ZT.144	3	15.04	88.5	5.85E+06 (R)
127 X3P_ZT.158	3	14.95	100	1.64E+06 (R)
132 S1P_ZT_Ro	3	14.91	92.4	2.96E+06 (R)
136 S4P_ZT_Ro	3	14.84	90.4	4.46E+06 (R)
152 S2P_ZT_Ro	5	14.6	87	1.35E+07 (R)
174 L3P_ZT.149	3	14.24	83.9	6.56E+06 (R)
189 S5P_ZT_Ro	3	14.07	90.4	7.27E+06 (R)
194 S5P_ZT_Ro	2	13.99	72.9	1.57E+05 (R)
201 S2P_ZT_Ro	4	13.9	83.6	2.69E+06 (R)
207 S3P_ZT_Ro	3	13.85	92.6	1.54E+06 (R)
214 S2P_ZT_Ro	3	13.74	81.6	7.60E+05 (R)
243 X3P_ZT.143	3	13.37	93.8	8.96E+06 (R)
244 S4P_ZT_Ro	3	13.37	80.5	8.28E+05 (R)
258 X4P_ZT.140	3	13.2	87.7	5.85E+06 (R)
260 L3P_ZT.163	3	13.19	74.4	1.02E+06 (R)
284 S4P_ZT_Ro	4	12.78	78.8	1.46E+07 (R)
316 S5P_ZT_Ro	4	12.55	87.5	2.48E+07 (R)

320	L3P_ZT.149	4	12.52	79.8	2.95E+07 (R)
325	X3P_ZT.146	3	12.48	86.3	8.99E+06 (R)
327	S2P_ZT_Ro	4	12.47	86.3	1.59E+07 (R)
334	S5P_ZT_Ro	5	12.4	86.2	2.10E+07 (R)
341	S3P_ZT_Ro	3	12.36	81.1	4.29E+05 (R)
348	L3P_ZT.163	2	12.29	81.5	2.25E+05 (R)
355	S1P_ZT_Ro	4	12.2	82.4	2.05E+06 (R)
361	X4P_ZT.144	4	12.15	77	2.08E+07 (R)
372	S1P_ZT_Ro	2	11.99	76.5	6.11E+05 (R)
376	S4P_ZT_Ro	5	11.94	81.8	9.82E+06 (R)
388	X3P_ZT.160	3	11.85	78.1	1.64E+06 (R)
405	X4P_ZT.141	5	11.77	86.7	1.02E+07 (R)
444	S1P_ZT_Ro	4	11.51	84.4	1.01E+07 (R)
453	S4P_ZT_Ro	2	11.44	75	8.31E+05 (R)
454	S4P_ZT_Ro	3	11.42	88	4.46E+06 (R)
456	S5P_ZT_Ro	2	11.41	65.9	1.57E+05 (R)
482	S3P_ZT_Ro	4	11.22	76.1	6.13E+06 (R)
531	S4P_ZT_Ro	4	10.84	73.4	2.83E+06 (R)
535	X3P_ZT.158	2	10.81	82	3.62E+05 (R)
560	S3P_ZT_Ro	5	10.65	80	5.03E+06 (R)
561	S5P_ZT_Ro	4	10.64	83	3.06E+06 (R)
581	L3P_ZT.149	5	10.44	66.5	1.49E+07 (R)
595	X3P_ZT.143	4	10.37	76.1	1.90E+07 (R)
604	S4P_ZT_Ro	2	10.3	70	8.31E+05 (R)
608	S1P_ZT_Ro	5	10.28	67.1	9.12E+06 (R)
618	S2P_ZT_Ro	4	10.22	70.8	1.59E+07 (R)
620	S4P_ZT_Ro	4	10.21	69.7	1.46E+07 (R)
622	S3P_ZT_Ro	4	10.21	67.8	1.22E+06 (R)
632	X3P_ZT.156	4	10.12	74.7	4.83E+06 (R)
641	X3P_ZT.145	3	10.04	77.2	8.99E+06 (R)
656	L3P_ZT.155	2	9.97	60.5	8.49E+05 (R)
667	S2P_ZT_Ro	3	9.93	80.4	7.60E+05 (R)
673	X3P_ZT.139	5	9.88	67.8	8.23E+06 (R)
676	X4P_ZT.157	4	9.86	75.3	4.39E+06 (R)
690	L3P_ZT.162	4	9.79	72.6	3.75E+06 (R)
697	L3P_ZT.155	5	9.76	63.2	1.49E+07 (R)
703	S5P_ZT_Ro	3	9.72	81.1	7.27E+06 (R)
709	X4P_ZT.143	3	9.69	69.2	5.85E+06 (R)
725	X3P_ZT.142	4	9.61	71.4	1.90E+07 (R)
753	X3P_ZT.141	4	9.47	72.2	1.43E+07 (R)
754	S5P_ZT_Ro	4	9.47	66	2.48E+07 (R)
759	L3P_ZT.153	4	9.44	65.3	2.95E+07 (R)
761	S4P_ZT_Ro	3	9.43	67	4.46E+06 (R)
766	S3P_ZT_Ro	3	9.42	72.4	4.29E+05 (R)
769	X4P_ZT.144	5	9.4	65.6	1.02E+07 (R)
788	S3P_ZT_Ro	3	9.27	81	1.54E+06 (R)
791	S2P_ZT_Ro	2	9.26	63.6	8.52E+05 (R)

801 X3P_ZT.15	3	9.2	64	1.64E+06 (R)
812 S2P_ZT_Ro	3	9.14	76.4	4.77E+06 (R)
819 S4P_ZT_Ro	2	9.1	67.8	8.31E+05 (R)
836 X4P_ZT.14	2	9.03	69.2	7.11E+05 (R)
848 X3P_ZT.14	5	8.99	72	1.15E+07 (R)
864 S5P_ZT_Ro	2	8.93	64.6	1.57E+05 (R)
867 X3P_ZT.15	5	8.92	72.5	1.47E+07 (R)
876 X4P_ZT.14	5	8.88	70.5	8.58E+06 (R)
892 S3P_ZT_Ro	3	8.81	71.9	1.54E+06 (R)
918 L3P_ZT.15	3	8.71	70.5	6.56E+06 (R)
924 S5P_ZT_Ro	3	8.65	77.1	7.27E+06 (R)
979 X4P_ZT.15	3	8.44	70.3	1.24E+06 (R)
990 X4P_ZT.14	3	8.41	71.3	5.85E+06 (R)
1001 L3P_ZT.15	5	8.37	64.3	1.49E+07 (R)
1033 S2P_ZT_Ro	3	8.27	70.9	4.77E+06 (R)
1040 X4P_ZT.15	5	8.25	89.7	2.63E+06 (R)
1085 S2P_ZT_Ro	2	8.07	64.8	1.94E+05 (R)
1105 S1P_ZT_Ro	2	8.02	69.7	6.11E+05 (R)
1122 L3P_ZT.16	4	7.95	76.5	3.75E+06 (R)
1143 X3P_ZT.14	2	7.86	63.5	7.68E+05 (R)
1153 L3P_ZT.15	3	7.83	70.1	6.56E+06 (R)
1179 S3P_ZT_Ro	4	7.74	79.7	6.13E+06 (R)
1193 S3P_ZT_Ro	4	7.69	71.8	6.13E+06 (R)
1208 X4P_ZT.14	5	7.65	67.5	1.02E+07 (R)
1227 S5P_ZT_Ro	2	7.56	62.7	1.57E+05 (R)
1278 X3P_ZT.15	5	7.39	62.1	3.13E+06 (R)
1315 S2P_ZT_Ro	4	7.26	77	1.59E+07 (R)
1328 X3P_ZT.14	2	7.21	65.3	5.27E+05 (R)
1349 S2P_ZT_Ro	2	7.15	64.4	8.52E+05 (R)
1442 X3P_ZT.14	3	6.88	86.9	8.99E+06 (R)
1447 X4P_ZT.14	4	6.87	63.4	2.08E+07 (R)
1491 L3P_ZT.15	2	6.77	83.9	8.49E+05 (R)
1497 S4P_ZT_Ro	4	6.75	65.6	1.46E+07 (R)
1566 S3P_ZT_Ro	5	6.6	70.4	5.03E+06 (R)
1611 S1P_ZT_Ro	2	6.49	60.6	1.30E+05 (R)
1661 S5P_ZT_Ro	3	6.37	71.2	7.27E+06 (R)
1755 S5P_ZT_Ro	3	6.18	81.1	7.27E+06 (R)
1782 X3P_ZT.13	2	6.1	70	5.27E+05 (R)
1939 S5P_ZT_Ro	3	5.73	78.7	8.71E+05 (R)
2019 S3P_ZT_Ro	2	5.59	66.9	3.76E+05 (R)
2228 S4P_ZT_Ro	4	5.22	80.3	1.21E+04 (R)
1572 S1P_ZT_Ro	3	6.58	62.1	5.59E+05 (R)
2088 L1P_ZT.21	2	5.46	73.8	1.10E+06 (R)
610 S3P_ZT_Ro	3	10.26	65.6	3.36E+04 (R)
786 X3P_ZT.47	3	9.29	81.6	2.69E+05 (R)
1531 L3P_ZT.56	3	6.69	76.9	7.96E+05 (R)
104 S1P_ZT_Ro	4	15.44	84.2	3.26E+06 (R)

195 S4P_ZT_Ro	4	13.99	87.1	6.21E+06 (R)
229 S3P_ZT_Ro	4	13.56	71.8	1.21E+06 (R)
253 X3P_ZT.55!	4	13.25	80.9	1.42E+06 (R)
426 S5P_ZT_Ro	4	11.63	66	4.17E+06 (R)
514 S2P_ZT_Ro	4	10.94	73.3	2.74E+06 (R)
781 X4P_ZT.55!	4	9.33	63.2	1.34E+06 (R)
797 S4P_ZT_Ro	4	9.22	62.4	6.21E+06 (R)
998 X4P_ZT.55!	3	8.37	60.4	1.23E+06 (R)
1251 X2P_ZT.59!	4	7.48	64	7.61E+04 (R)
541 X4P_ZT.10!	4	10.78	76.8	5.10E+05 (R)
985 S4P_ZT_Ro	4	8.43	69.9	3.35E+05 (R)
1007 S1P_ZT_Ro	5	8.35	65.4	1.19E+06 (R)
1020 S4P_ZT_Ro	5	8.31	67.5	3.81E+05 (R)
1051 S2P_ZT_Ro	5	8.2	64.9	4.42E+05 (R)
1082 X3P_ZT.10!	3	8.07	78.4	1.39E+05 (R)
1177 S4P_ZT_Ro	4	7.74	62.3	3.35E+05 (R)
1284 L3P_ZT.11!	3	7.38	91.3	8.55E+04 (R)
1286 X4P_ZT.10!	3	7.37	91.6	8.76E+04 (R)
1318 S3P_ZT_Ro	5	7.25	71.1	9.65E+04 (R)
1690 S1P_ZT_Ro	5	6.3	69.8	1.19E+06 (R)
1697 S5P_ZT_Ro	5	6.29	78.9	4.29E+05 (R)
1804 S1P_ZT_Ro	5	6.06	100	6.49E+04 (R)
311 L3P_ZT.16!	4	12.59	76.3	1.01E+06 (R)
390 S5P_ZT_Ro	4	11.84	80.5	1.85E+06 (R)
438 S3P_ZT_Ro	3	11.54	72.7	2.63E+04 (R)
504 S3P_ZT_Ro	4	11.02	82.8	3.36E+05 (R)
516 S4P_ZT_Ro	4	10.93	66.9	1.47E+05 (R)
557 X3P_ZT.15!	3	10.66	85.2	6.91E+05 (R)
666 S4P_ZT_Ro	3	9.93	81.6	4.66E+05 (R)
744 S2P_ZT_Ro	3	9.55	75	4.89E+05 (R)
787 S4P_ZT_Ro	3	9.28	82.5	4.66E+05 (R)
792 S1P_ZT_Ro	5	9.26	76.7	1.73E+06 (R)
804 S2P_ZT_Ro	5	9.18	77.8	1.76E+06 (R)
807 S1P_ZT_Ro	5	9.17	67.1	1.62E+05 (R)
831 X4P_ZT.15!	4	9.06	69.4	2.34E+06 (R)
859 X3P_ZT.15!	3	8.95	100	1.45E+05 (R)
873 S2P_ZT_Ro	4	8.89	65.1	1.77E+06 (R)
1030 X4P_ZT.15!	3	8.27	78.2	7.13E+05 (R)
1043 S1P_ZT_Ro	3	8.23	95.4	4.59E+05 (R)
1301 S1P_ZT_Ro	3	7.31	76.2	4.59E+05 (R)
1340 S4P_ZT_Ro	4	7.17	61.7	1.68E+06 (R)
1359 L3P_ZT.16!	4	7.12	100	1.01E+06 (R)
1448 S1P_ZT_Ro	4	6.87	100	2.71E+05 (R)
1479 S2P_ZT_Ro	3	6.78	85.2	4.89E+05 (R)
1481 S1P_ZT_Ro	4	6.78	63.1	6.93E+05 (R)
1612 L3P_ZT.16!	3	6.49	93.1	2.09E+05 (R)
1668 S5P_ZT_Ro	3	6.36	68.7	5.27E+05 (R)

1744 L3P_ZT.156	3	6.21	63.2	6.17E+05 (R)
1998 X4P_ZT.160	3	5.62	67.7	1.90E+05 (R)
2103 L3P_ZT.156	4	5.42	100	4.30E+05 (R)
1392 S4P_ZT_Ro	5	7	62.1	8.98E+05 (K)
2136 S2P_ZT_Ro	5	5.36	73.8	1.15E+05 (K)
1199 L1P_ZT.318	3	7.67	67.5	5.64E+05 (C)
1650 L1P_ZT.156	3	6.41	71.4	2.12E+05 (C)
2169 S4P_ZT_Ro	2	5.3	67.4	1.29E+05 (R)
1838 X1P_ZT.209	2	5.95	82.9	7.73E+06 (K)
1889 S5P_ZT_Ro	2	5.83	66	4.84E+06 (K)
2028 X4P_ZT.209	2	5.57	64.7	2.67E+06 (K)
2113 L4P_ZT.130	2	5.41	71	6.97E+05 (K)
1059 L2P_ZT.200	2	8.15	78	6.62E+07 (K)
1830 X1P_ZT.211	2	5.98	60.3	7.00E+07 (K)
1167 S5P_ZT_Ro	3	7.77	66.7	1.02E+05 (L)
1306 S4P_ZT_Ro	3	7.3	65.7	3.96E+05 (L)
1322 S4P_ZT_Ro	3	7.23	63	3.96E+05 (L)
1347 S4P_ZT_Ro	3	7.15	62.4	3.96E+05 (L)
1571 S5P_ZT_Ro	3	6.58	65.7	1.02E+05 (L)
2097 L1P_ZT.397	4	5.45	68.2	3.50E+04 (K)
837 L4P_ZT.780	2	9.03	66.4	1.70E+06 (P)
1436 X4P_ZT.482	3	6.89	70.6	9.67E+05 (Y)
2131 L1P_ZT.173	2	5.37	71	1.08E+05 (K)
1695 X4P_ZT.482	4	6.29	86.6	2.19E+04 (R)
705 S3P_ZT_Ro	7	9.71	64.9	2.94E+05 (K)
1022 S3P_ZT_Ro	7	8.31	60.4	7.16E+04 (K)
1206 X5P_ZT.558	7	7.65	72.5	1.59E+05 (K)
1408 X2P_ZT.546	7	6.97	100	7.73E+04 (K)
1543 X3P_ZT.549	7	6.65	62.3	2.16E+06 (K)
1622 S4P_ZT_Ro	7	6.47	100	1.03E+05 (K)
1089 L1P_ZT.321	3	8.06	71	1.10E+06 (C)
1605 L3P_ZT.336	3	6.51	68.7	2.35E+06 (C)
2275 L4P_ZT.308	4	5.12	71.6	3.49E+04 (K)
2090 L2P_ZT.213	6	5.46	71.3	4.80E+04 (R)
1859 X1P_ZT.353	4	5.91	65.3	1.03E+05 (R)
1658 L5P_ZT.256	2	6.38	68	8.38E+04 (K)
1014 S1P_ZT_Ro	2	8.33	70.9	5.34E+06 (G)
1403 S4P_ZT_Ro	5	6.98	70.4	7.30E+05 (T)
1587 S3P_ZT_Ro	5	6.55	69.5	5.40E+05 (T)
1795 X5P_ZT.521	5	6.08	68.7	1.06E+06 (T)
1827 S4P_ZT_Ro	3	5.99	63	1.13E+06 (R)
1379 S5P_ZT_Ro	3	7.04	61.9	1.34E+06 (V)
2172 L2P_ZT.116	2	5.3	61.8	5.90E+05 (K)
1987 S3P_ZT_Ro	3	5.65	61.1	5.72E+05 (K)
1769 S2P_ZT_Ro	3	6.14	62	2.44E+04 (K)
2045 L4P_ZT.246	3	5.54	92	1.19E+04 (K)
2117 X2P_ZT.279	4	5.39	67.1	3.19E+05 (K)

1929 X2P_ZT.496	4	5.75	64.7	1.27E+04 (K)
1463 S4P_ZT_Ro	6	6.83	61.5	8.78E+05 (K)
1858 X2P_ZT.288	4	5.91	67.5	2.16E+06 (R)
1982 X2P_ZT.289	5	5.65	71.5	4.27E+06 (R)
2324 X2P_ZT.290	4	5.01	65.6	2.16E+06 (R)
1710 S3P_ZT_Ro	2	6.27	62.7	1.66E+06 (K)
1802 X1P_ZT.318	2	6.06	100	8.96E+05 (K)
2009 S1P_ZT_Ro	2	5.61	71.8	6.34E+05 (K)
2059 S1P_ZT_Ro	2	5.51	83.3	1.26E+06 (K)
2127 S3P_ZT_Ro	2	5.37	61.8	7.48E+05 (K)
2292 S3P_ZT_Ro	2	5.09	62.2	1.58E+06 (K)
1145 S1P_ZT_Ro	2	7.86	68.4	6.98E+05 (K)
1420 S5P_ZT_Ro	4	6.94	72.9	2.18E+06 (K)
1417 L3P_ZT.270	3	6.95	65.1	2.49E+04 (K)
1547 L3P_ZT.488	5	6.65	66.2	2.14E+06 (K)
2225 X4P_ZT.489	6	5.22	61.5	7.27E+05 (K)
2027 L3P_ZT.501	5	5.58	70.8	2.89E+04 (K)
2297 X5P_ZT.290	5	5.08	80.1	9.63E+05 (K)
1698 S5P_ZT_Ro	2	6.29	63.6	4.36E+05 (K)
1902 L3P_ZT.491	2	5.81	66.3	3.43E+05 (K)
1679 X2P_ZT.509	7	6.33	66.8	1.47E+05 (K)
1881 X4P_ZT.497	7	5.86	61.8	1.15E+05 (K)
714 L5P_ZT.459	2	9.68	68.1	5.70E+05 (E)
774 X3P_ZT.274	2	9.37	60.5	9.88E+05 (G)
899 S1P_ZT_Ro	2	8.78	63.7	5.76E+05 (G)
1063 L3P_ZT.250	2	8.14	63.3	5.21E+05 (G)
1188 L3P_ZT.275	2	7.72	100	1.19E+06 (G)
1867 S2P_ZT_Ro	3	5.9	69.5	1.23E+06 (K)
2290 L4P_ZT.247	3	5.1	61.1	1.39E+06 (K)
2313 S5P_ZT_Ro	3	5.04	76.5	3.35E+06 (K)
1226 X2P_ZT.359	3	7.56	87.2	7.66E+04 (E)
1912 L4P_ZT.412	5	5.79	60.9	9.41E+04 (K)
2286 S5P_ZT_Ro	4	5.1	66.3	1.26E+06 (K)
1865 X1P_ZT.240	2	5.9	85.5	5.27E+05 (R)
2327 L2P_ZT.238	2	5.01	77.1	5.11E+05 (R)
2190 S5P_ZT_Ro	2	5.26	66.1	2.27E+04 (R)
2086 S5P_ZT_Ro	3	5.46	78.2	2.59E+05 (K)
2230 S3P_ZT_Ro	5	5.22	100	2.22E+05 (K)
1910 L3P_ZT.172	2	5.79	65.5	8.45E+05 (K)
977 S1P_ZT_Ro	2	8.45	70.8	2.60E+06 (E)
1884 L1P_ZT.490	4	5.85	60.7	3.84E+04 (C)
616 S4P_ZT_Ro	2	10.22	86.8	3.82E+07 (K)
729 S2P_ZT_Ro	2	9.59	85.4	3.94E+07 (K)
853 S3P_ZT_Ro	2	8.98	82.4	2.44E+07 (K)
891 S1P_ZT_Ro	2	8.82	83.5	2.04E+06 (K)
920 S5P_ZT_Ro	2	8.7	93.3	2.83E+07 (K)
1060 X4P_ZT.484	2	8.14	79.5	2.15E+06 (K)

1127 X3P_ZT.479	2	7.92	87.9	8.90E+05 (K)
1160 S2P_ZT_Ro	2	7.8	71	3.94E+07 (K)
1854 S1P_ZT_Ro	2	5.92	100	1.74E+06 (K)
2252 L3P_ZT.567	2	5.18	76.7	8.01E+06 (K)
1702 L2P_ZT.340	2	6.29	64.4	1.74E+04 (K)
1431 L4P_ZT.297	3	6.92	100	4.45E+04 (K)
2212 L4P_ZT.351	2	5.24	87.4	4.37E+04 (K)
2299 L3P_ZT.515	2	5.08	65.9	3.02E+07 (K)
1574 L3P_ZT.403	3	6.58	87.7	1.68E+06 (K)
1926 L4P_ZT.438	3	5.76	72.8	8.32E+06 (K)
2115 S2P_ZT_Ro	3	5.4	61.7	6.76E+06 (K)
2200 S3P_ZT_Ro	3	5.25	75.1	2.49E+06 (K)
2204 L3P_ZT.453	3	5.25	73.3	3.34E+06 (K)
1727 S2P_ZT_Ro	2	6.23	64.5	1.81E+06 (K)
631 S4P_ZT_Ro	2	10.14	81	7.63E+07 (K)
671 S2P_ZT_Ro	2	9.89	83.6	7.60E+07 (K)
741 S5P_ZT_Ro	2	9.56	100	1.23E+08 (K)
832 S1P_ZT_Ro	2	9.06	78.9	1.27E+08 (K)
1006 S3P_ZT_Ro	2	8.36	78.2	4.46E+07 (K)
1427 X4P_ZT.461	2	6.92	100	6.36E+07 (K)
2076 X3P_ZT.464	2	5.47	87.6	1.40E+08 (K)
2304 S5P_ZT_Ro	2	5.06	80.6	1.23E+08 (K)
1131 L5P_ZT.359	3	7.91	70	1.74E+05 (K)
1365 S4P_ZT_Ro	2	7.09	63.1	2.36E+06 (K)
1997 L4P_ZT.401	2	5.63	78.1	7.86E+05 (K)
1869 L3P_ZT.185	2	5.9	88.2	8.62E+04 (K)
2132 L5P_ZT.259	5	5.37	100	1.08E+05 (K)
2261 L4P_ZT.489	4	5.16	63.5	5.30E+04 (K)
1579 X4P_ZT.281	3	6.57	63.2	2.13E+07 (K)
1970 S2P_ZT_Ro	2	5.67	100	2.13E+07 (K)
2256 S5P_ZT_Ro	4	5.17	100	1.00E+05 (K)
2091 L4P_ZT.363	4	5.46	63.8	4.85E+05 (K)
1236 L1P_ZT.360	3	7.54	79.8	1.59E+05 (T)
1026 X3P_ZT.158	6	8.28	63.1	8.51E+04 (K)
649 S5P_ZT_Ro	2	10	67.7	8.40E+05 (R)
737 X4P_ZT.776	2	9.56	76.9	1.49E+06 (R)
883 S1P_ZT_Ro	2	8.86	78.2	2.63E+06 (R)
884 L1P_ZT.842	2	8.86	63.9	1.57E+06 (R)
1140 S3P_ZT_Ro	2	7.87	66	2.39E+06 (R)
1309 S2P_ZT_Ro	2	7.28	64.9	8.13E+05 (R)
1411 L3P_ZT.844	2	6.97	65.7	9.60E+05 (R)
1628 S4P_ZT_Ro	2	6.46	60.1	1.08E+06 (R)
1864 L5P_ZT.811	2	5.91	62.6	9.46E+05 (R)
2030 L2P_ZT.796	2	5.57	63.7	1.71E+06 (R)
2038 L4P_ZT.904	2	5.55	69.9	6.56E+05 (R)
1842 S2P_ZT_Ro	5	5.94	66.4	6.57E+04 (R)
1880 L2P_ZT.266	4	5.87	67.6	1.87E+06 (R)

1992 S3P_ZT_Ro	4	5.64	61.5	1.40E+06 (R)
2119 L1P_ZT.266	4	5.39	62.6	5.67E+06 (R)
1136 L1P_ZT.222	3	7.88	61.9	3.26E+05 (R)
1380 X3P_ZT.658	3	7.03	86.3	1.24E+05 (R)
1921 L5P_ZT.719	3	5.77	85.9	1.46E+05 (R)
2110 X1P_ZT.409	2	5.41	68.9	7.65E+05 (R)
2125 X5P_ZT.169	6	5.37	79	4.47E+05 (R)
1745 S4P_ZT_Ro	3	6.2	100	5.93E+05 (P)
1685 S4P_ZT_Ro	3	6.31	83.8	1.03E+06 (R)
1701 L2P_ZT.252	2	6.29	61.3	4.59E+05 (R)
1836 X1P_ZT.259	2	5.96	75.9	4.57E+05 (R)
2092 X5P_ZT.128	2	5.45	83.7	1.65E+06 (R)
1959 L3P_ZT.410	3	5.71	79.4	7.93E+04 (K)
2157 S5P_ZT_Ro	5	5.32	83.4	1.29E+05 (R)
2320 L2P_ZT.348	4	5.02	89.6	3.83E+07 (R)
1330 S2P_ZT_Ro	5	7.21	77	1.53E+06 (R)
2083 L3P_ZT.326	2	5.47	100	1.51E+05 (R)
1967 L2P_ZT.367	3	5.68	67.1	5.55E+04 (R)
1861 L1P_ZT.525	5	5.91	72.2	3.50E+04 (R)
1258 X1P_ZT.389	2	7.45	76.8	3.65E+06 (L)
1985 S5P_ZT_Ro	6	5.65	78.8	5.04E+05 (R)
1426 X4P_ZT.439	4	6.92	100	2.37E+06 (K)
1117 L3P_ZT.504	5	7.97	80.7	4.44E+05 (N)
1194 X1P_ZT.989	2	7.68	65.4	9.52E+07 (K)
1395 L1P_ZT.913	2	7	66.1	7.15E+07 (K)
1558 L3P_ZT.935	2	6.63	65.3	1.37E+08 (K)
1597 S2P_ZT_Ro	2	6.52	63.8	1.76E+08 (K)
1683 L4P_ZT.100	2	6.32	67	4.60E+07 (K)
1728 S1P_ZT_Ro	2	6.23	87.4	1.06E+08 (K)
1849 X5P_ZT.890	2	5.92	62	1.97E+08 (K)
1905 L4P_ZT.105	2	5.8	67.8	4.60E+07 (K)
2295 L4P_ZT.101	2	5.09	61.2	4.60E+07 (K)
1134 S3P_ZT_Ro	5	7.89	69.2	1.95E+05 (N)
2026 L2P_ZT.378	3	5.58	89	1.01E+06 (L)
2166 S2P_ZT_Ro	4	5.31	88.2	4.20E+04 (K)
1524 S4P_ZT_Ro	2	6.7	100	3.98E+06 (K)
2008 X4P_ZT.553	2	5.61	76.1	1.16E+06 (K)
1501 L3P_ZT.166	3	6.75	100	4.05E+06 (K)
1822 S4P_ZT_Ro	3	6	100	1.73E+06 (K)
1909 L2P_ZT.153	2	5.79	86.5	9.03E+05 (K)
2202 L1P_ZT.156	2	5.25	100	1.59E+06 (K)
1166 X5P_ZT.504	7	7.77	61.9	5.84E+06 (K)
1390 X2P_ZT.516	5	7	78.2	5.27E+04 (K)
2326 L1P_ZT.377	2	5.01	70.4	1.67E+05 (K)
944 X3P_ZT.417	2	8.58	67.9	1.69E+05 (K)
1108 L4P_ZT.402	2	8.01	64.5	1.08E+06 (K)
1110 X1P_ZT.394	2	7.99	62.1	1.72E+06 (K)

1128 S1P_ZT_Ro	2	7.92	63.9	4.76E+06 (K)
1164 L5P_ZT.42C	2	7.79	68.5	9.33E+05 (K)
1292 L2P_ZT.402	2	7.35	64.1	3.08E+06 (K)
1326 S2P_ZT_Ro	2	7.22	73.6	1.47E+06 (K)
1375 L2P_ZT.403	2	7.05	70.2	3.08E+06 (K)
1383 S4P_ZT_Ro	2	7.02	70.3	1.43E+06 (K)
1439 L2P_ZT.393	2	6.89	73	4.85E+06 (K)
1477 X2P_ZT.423	2	6.79	70.9	3.87E+05 (K)
1731 L5P_ZT.43C	2	6.23	71.2	1.08E+07 (K)
1750 X2P_ZT.434	2	6.19	71.2	2.84E+06 (K)
1786 L3P_ZT.415	2	6.1	60.3	3.61E+04 (K)
1968 X4P_ZT.418	2	5.67	70.8	3.25E+06 (K)
2188 X3P_ZT.477	2	5.26	73.3	1.26E+06 (K)
2193 L3P_ZT.359	4	5.26	69.2	2.91E+05 (K)
2281 L5P_ZT.367	4	5.11	61.7	1.03E+05 (K)
1129 L5P_ZT.319	3	7.92	77.6	4.64E+05 (K)
719 S5P_ZT_Ro	2	9.65	70.7	2.15E+06 (N)
882 S3P_ZT_Ro	2	8.86	86.4	1.47E+06 (N)
982 S4P_ZT_Ro	2	8.44	66.8	2.35E+06 (N)
987 X3P_ZT.557	2	8.42	100	5.54E+05 (N)
1325 X2P_ZT.526	4	7.22	100	1.29E+05 (N)
1866 S3P_ZT_Ro	5	5.9	90.3	7.26E+05 (R)
1991 X1P_ZT.47C	5	5.64	87.9	5.51E+05 (R)
2223 X5P_ZT.523	5	5.22	100	7.04E+05 (R)
1192 X2P_ZT.503	5	7.69	65.3	5.56E+04 (A)
1879 S2P_ZT_Ro	5	5.87	60.4	2.30E+05 (A)
2239 X1P_ZT.197	3	5.21	79.1	2.66E+04 (K)

Tandem mass spectrometry for serum amyloid A peptides detected in plasma

sequence	next_aa	sequenceV	modificatic	parent_m_	matched_p
AADILLGVItK	(S)		t:Phosphor	597.3223	1113.688
AAPDGSGTLVRDFVCDVCE DLCQTDDLVLHERK	(S)		C:Carbamic	667.9969	4002.899
AAVAAGTEGAPGFWDITK	(P)			931.9783	1862.928
ADLVREGYLTERTCVAAARSLTPNFQTSFEHLQCVLSEAD	(L)		C:Carbamic	1202.851	4808.352
ADQAANEWGR	(S)			559.2582	1117.502
ADQAAnEWGR	(S)		n:Deamida	559.7488	1117.502
ADQAANEWGR	(S)			559.2585	1117.502
ADQAANEWGR	(S)			559.2581	1117.502
ADQAANEWGR	(S)			559.2508	1117.502
ADQAANEWGR	(S)			559.2595	1117.502
ADQAANEWGR	(S)			559.2592	1117.502
ADQAANEWGR	(S)			559.2582	1117.502
ADQAANEWGR	(S)			559.2551	1117.502
ADQAANEWGR	(S)			559.2563	1117.502
ADQAAnEWGR	(S)		n:Deamida	559.746	1117.502
ADQAAnEWGR	(S)		n:Deamida	559.7488	1117.502
ADQAANEWGR	(S)			559.2586	1117.502
ADQAAnEWGR	(S)		n:Deamida	559.7496	1117.502
ADQAAnEWGR	(S)		n:Deamida	559.7505	1117.502
ADQAANEWGR	(S)			559.2552	1117.502
ADQAAnEWGR	(S)		n:Deamida	559.7465	1117.502
ADQAAnEWGR	(S)		n:Deamida	559.7487	1117.502
ADQAANEWGR	(S)			559.2571	1117.502
ADQAANEWGR	(S)			559.259	1117.502
ADQAAnEWGR	(S)		n:Deamida	559.7499	1117.502
ADQAAnEWGR	(S)		n:Deamida	559.7498	1117.502
ADQAAnEWGR	(S)		n:Deamida	559.7501	1117.502
ADQAANEWGR	(S)			559.2615	1117.502
ADQAANEWGR	(S)			559.2582	1117.502
ADQAANEWGR	(S)			559.2573	1117.502
ADQAAnEWGR	(S)		n:Deamida	559.7488	1117.502
ADQAANEWGR	(S)			559.2568	1117.502
ADQAANEWGR	(S)			559.2571	1117.502
ADQAANEWGRSGKDPNHFRP	(A)			751.6925	2253.054
ADQAANEWGRSGKDPNHFRP	(A)			751.6917	2253.054
ADQAANEWGRSGKDPNHFRP	(A)			751.6953	2253.054
ADQEANQWGRSGNDPNHFRPKGLPD	(K)			702.3219	2806.304
ALVGS LTHILQHLEDCQKEPLEK PmRPsNEG TDEPR	(A)		C:Carbamic	1056.003	4125.049
ANHQN sDQYFYARGnFEAQQRGSGGVWAAK	(I)	ANHQN sDC	s:Phosphor	1146.862	3357.553
ANHQN sDQYFYARGnFEAQQRGSGGVWAAK	(I)	ANHQN sDC	s:Phosphor	1146.861	3357.553
ANHQN sDQYFYARGnFEAQQRGSGGVWAAK	(I)	ANHQN sDC	s:Phosphor	1146.861	3357.553
ANWIGADKYFHAR	(G)			774.8846	1548.771
ANWKNSDKYFHARGNYDAASRGAGGR	(V)			957.1371	2869.363
ANWKNSDKYFHARGNYDAASRGAGGR	(V)			957.1441	2869.363
ATDILVGVISRSRCPRLTEICVGILGNIACFPDTCATLSQNEI	(E)		C:Carbamic	827.7603	4961.474

ATVIFSLKNEV	(G)		610.8601	1220.688	
ATVIFSLKNEV	(G)		610.8589	1220.688	
AVGEDDDDLAIGETIYSkHWIFSTLTR	(L)	k:Acetyl	1032.187	3052.49	
AYHDMR	(E)		396.6759	792.346	
AYHDMR	(E)		264.7873	792.346	
AYHDMR	(E)		396.6769	792.346	
AYHDMR	(E)		264.7874	792.346	
AYHDMR	(E)		396.6767	792.346	
AYHDMR	(E)		264.7868	792.346	
AYHDMR	(E)		264.787	792.346	
AYHDMR	(E)		396.6775	792.346	
AYHDMR	(E)		396.6766	792.346	
AYHDMR	(E)		264.7864	792.346	
AYHDMR	(E)		264.7872	792.346	
AYHDMR	(E)		264.7885	792.346	
AYHDMR	(E)		396.6765	792.346	
AYHDMR	(E)		264.7899	792.346	
AYHDMR	(E)		396.6785	792.346	
AYNDMR	(E)		385.1705	769.33	
AYNDMR	(E)		385.171	769.33	
AYNDMR	(E)		385.1704	769.33	
AYNDMR	(E)		385.1704	769.33	
AYNDMR	(E)		385.1698	769.33	
AYNDMR	(E)		385.1692	769.33	
AYNDMR	(E)		385.1718	769.33	
AYNDMR	(E)		385.1706	769.33	
AYNDMR	(E)		385.1685	769.33	
AYnDMR	(E)	AYnDMR	n:Deamida	385.6588	769.33
AYnDMR	(E)		n:Deamida	385.6613	769.33
AYnDMR	(E)		n:Deamida	385.6635	769.33
AYnDMR	(E)		n:Deamida	385.6613	769.33
AYnDMR	(E)	AYnDMR	n:Deamida	385.6628	769.33
AYnDMR	(E)		n:Deamida	385.6601	769.33
AYnDMR	(E)		n:Deamida	385.6616	769.33
AYnDMR	(E)		n:Deamida	385.6594	769.33
AYnDMR	(E)		n:Deamida	385.6634	769.33
AYnDMR	(E)		n:Deamida	385.661	769.33
AYnDMR	(E)		n:Deamida	385.6616	769.33
AYnDMR	(E)		n:Deamida	385.6637	769.33
AYnDMR	(E)	AYnDMR	n:Deamida	385.6613	769.33
AYnDMR	(E)		n:Deamida	385.6612	769.33
AYnDMR	(E)		n:Deamida	385.6629	769.33
AYnDMR	(E)		n:Deamida	385.6622	769.33
AYnDMR	(E)		n:Deamida	385.6606	769.33
AYnDMR	(E)		n:Deamida	385.6634	769.33
AYnDMR	(E)		n:Deamida	385.6628	769.33
AYNDMR	(E)		385.1747	769.33	

AYQDmkKSNWINGDK	(Y)	AYQDmkKS m:Oxidized	619.6231	1797.859
AYQDMKKS NWINGDK	(Y)	k:Acetyl	920.4453	1797.859
AYS DMKEANYINADkYFHAR	(G)	k:Carbamyl	624.0244	2407.114
AYWNVLTSSHQ NSKRYFYAQGN YDAAER	(G)		835.659	3339.557
AYWNVLTSSHQ NSKRYFYAQGN YDAAER	(G)		668.7291	3339.557
CLESTELPLCSALRRGAESPLR	(A)	C:Carbamic	839.0896	2515.276
CSCAFENLLPFYsPVVEDFLK	(I)	C:Carbamic	886.7296	2535.193
CSCAFknLLPFYsPVIEDFLK	(I)	C:Carbamic	864.7417	2548.262
CSCAFkNLLPLYCsVVKDFLK	(V)	C:Carbamic	909.4358	2562.292
CSCAFK NLLPLYCsVVKDFLK	(V)	C:Carbamic	909.4358	2562.292
CSCAFkNLLPLYCsVVKDFLK	(V)	C:Carbamic	909.445	2562.292
CSCAFQnLLPFyNPVVEDFIK	(I)	C:Carbamic	881.408	2561.22
CSCAFQnLLPFyNPVVEDFIK	(I)	CSCAFQnLL C:Carbamic	881.4121	2561.22
CSCAFQnLLPFyNPVVEDFIK	(I)	C:Carbamic	881.4071	2561.22
CSCAFQnLLPFyNPVVEDFIK	(I)	CSCAFQnLL C:Carbamic	881.408	2561.22
CSCAFQnLLPFyNPVVEDFIK	(I)	C:Carbamic	881.408	2561.22
CSCAFQnLLPFynPVVEDFIK	(I)	C:Carbamic	881.4122	2561.22
CSCAFQnLLPFyNPVVEDFIK	(I)	C:Carbamic	881.077	2561.22
CSCAFQnLLPFyNPVVEDFIK	(I)	CSCAFQnLL C:Carbamic	881.4054	2561.22
CsCAFQnLLPFynPVVEDFIK	(I)	C:Carbamic	661.5513	2561.22
CSCAFQnLLPFYSPmVEDFLk	(I)	C:Carbamic	875.7266	2566.182
CSCAFQnLLPFYsPMVEDFLK	(I)	C:Carbamic	882.7264	2566.182
CSCAFQnLLPFYsPVVEDFLR	(V)	C:Carbamic	881.4034	2562.216
CSCAFQnLLPFYsPVVEDFLR	(V)	C:Carbamic	881.4098	2562.216
CSCAFQnLLPFYsPVVEDFLR	(V)	C:Carbamic	881.3994	2562.216
CSCAFQnLLPFYsPVVEDFLR	(V)	C:Carbamic	881.4122	2562.216
CSCAFQnLLPFYsPVVEDFLR	(V)	C:Carbamic	881.4121	2562.216
CSCAFQnLLPFYsPVVEDFLR	(V)	C:Carbamic	881.4122	2562.216
CSCAFQnLLPFYsPVVEDFLR	(V)	C:Carbamic	881.4122	2562.216
CSCAFQnLLPFYsPVVEDFLR	(V)	C:Carbamic	881.4054	2562.216
CSCAFQnLLPFYsPVVEDFLR	(V)	C:Carbamic	881.3892	2562.216
CSCAFQnLLPFYsPVVEDFLR	(V)	C:Carbamic	881.4122	2562.216
CSCAFQnLLPFYsPVVEDFLR	(V)	C:Carbamic	881.408	2562.216
CSCAFQnLLPFYsPVVEDFLR	(V)	C:Carbamic	881.4122	2562.216
CSCAFQnLLPFYsPVVEDFLR	(V)	C:Carbamic	881.4033	2562.216
CSCAFQnLLPFYsPVVEDFLR	(V)	C:Carbamic	881.4059	2562.216
CSCAFQnLLPFYsPVVEDFLR	(V)	C:Carbamic	881.4074	2562.216
CSCAFQnLLPFYsPVVEDFLR	(V)	C:Carbamic	881.4034	2562.216
CSCAFQnLLPFYsPVVEDFLR	(V)	C:Carbamic	881.4013	2562.216
CSCAFQnLLPFYsPVVEDFLR	(V)	C:Carbamic	881.408	2562.216
CSCAFQnLLPFYsPVVEDFLR	(V)	C:Carbamic	881.408	2562.216
CSCAFQnLLPFYsPVVEDFLR	(V)	C:Carbamic	881.4017	2562.216
CSCAFQnLLPFYsPVVEDFLR	(V)	C:Carbamic	881.4005	2562.216
CSCAFQnLLPFYsPVVEDFLR	(V)	C:Carbamic	881.4121	2562.216
CSCAFQnLLPFYsPVVEDFLR	(V)	C:Carbamic	881.4059	2562.216
CSCAFQnLLPFYsPVVEDFLR	(V)	C:Carbamic	881.4054	2562.216
CSCAFQnLLPFYsPVVEDFLR	(V)	C:Carbamic	881.4054	2562.216
CSCAFQnLLPFYsPVVEDFLR	(V)	C:Carbamic	881.4013	2562.216

CSCAFQNLPPFYsPVVEDFLR	(V)	C:Carbamic	881.4098	2562.216
CSCAFQNLPPFYsPVVEDFLR	(V)	C:Carbamic	881.4029	2562.216
CSCVFQnLLPLYGPVVEDFIK	(I)	C:Carbamic	833.763	2498.246
CSSAFQNLPPFYSPVVEDFIKILREVDKALADDLEKN	(F)	C:Carbamic	1071.815	4284.19
DAAQRGPGGAWAAKVISNARENIQGITDPLFKGMTRDC	(E)		716.6988	4295.221
DAVADLMnKgYLTEk	(T)	k:Acetyl	876.4367	1667.831
DFHLKILKDILCEFLSNIFQALTKETVVQGVK	(E)	C:Carbamic	625.3445	3747.055
DGAEDEQLEtLTEITAELLADLCLHISKDAVADLmNk	(G)	DGAEDEQL C:Carbamic	1408.994	4084.994
DILCEFLSNIFQALTKETVVQGVKEGQLSKQKCSSAFQNL	(F)	C:Carbamic	954.5016	4768.469
DKEEEEVAGGDCIGSTVYSKHWLFGVLsGLIQIVSPENTK	(S)	DKEEEEVAC C:Carbamic	895.2339	4392.17
DKLFDLDEKLMLEWIK	(N)		679.3739	2036.077
DKLFDLDEKLMLEWIK	(N)		679.3542	2036.077
DKLFDLDEKLMLEWIK	(N)		679.3744	2036.077
DLCQAEDLSVVL	(Q)	C:Carbamic	681.3295	1361.662
DLCQAEDLSVVL	(Q)	C:Carbamic	681.3276	1361.662
DLCQAEDLSVVL	(Q)	C:Carbamic	681.3297	1361.662
DLCQAEDLSVVL	(Q)	C:Carbamic	681.3291	1361.662
DLKkANWIGADk	(Y)	k:Acetyl	721.8939	1358.743
DLKksNFIGADK	(Y)	k:Acetyl,s:F	486.5728	1335.727
DLKksNFIGADK	(Y)	k:Acetyl,s:F	486.5743	1335.727
DLKksNFIGADK	(Y)	k:Acetyl,s:F	486.5742	1335.727
DLKksNFIGADK	(Y)	k:Acetyl,s:F	486.5742	1335.727
DLkksNFIGADK	(Y)	k:Acetyl	710.3666	1335.727
DLKksNFIGADK	(Y)	k:Acetyl,s:F	486.5728	1335.727
DLKksNFIGADK	(Y)	k:Acetyl,s:F	486.5758	1335.727
DLKKsNFIGADk	(Y)	DLKKsNFIG s:Phosphor	486.5692	1335.727
DLPSLK	(A)		336.7018	672.393
DLPSLK	(A)		336.7019	672.393
DLPSLK	(A)		336.7014	672.393
DLPSLK	(A)		336.7027	672.393
DLPSLK	(A)		336.6967	672.393
DLPSLK	(A)		336.7026	672.393
DLPSLK	(A)		336.7017	672.393
DLPSLK	(A)		336.7041	672.393
DLPSLK	(A)		336.6937	672.393
DLPSLK	(A)		336.7003	672.393
DLPSLK	(A)		336.7003	672.393
DLPSLK	(A)		336.7009	672.393
DLPSLK	(A)		336.7031	672.393
DLPSLK	(A)		336.7063	672.393
DLPSLK	(A)		336.7025	672.393
DmWKAYSdMKEANyK	(K)	m:Oxidized	996.3973	1879.835
DNPEGLDVYMHILQLLTTADEGIQAIVQCpAAGR	(D)	C:Carbamic	742.575	3708.836
DNPEGLDVYMHILQLLTTADEGIQAIVQCpAAGR	(D)	C:Carbamic	742.5688	3708.836
DPNHFR	(P)		393.1883	785.369
DPNHFR	(P)		393.1885	785.369
DPNHFR	(P)		393.1935	785.369

DPNHFR	(P)		262.4611	785.369
DPNHFR	(P)		393.1883	785.369
DPNHFR	(P)		393.1948	785.369
DPNHFR	(P)		393.1937	785.369
DPNHFR	(P)		262.4621	785.369
DPNHFRPAGLPDK	(Y)		732.3863	1463.739
DPNHFRPAGLPDK	(Y)		488.5869	1463.739
DPNHFRPAGLPDK	(Y)		488.589	1463.739
DPNHFRPAGLPDK	(Y)		488.5875	1463.739
DPNHFRPAGLPDK	(Y)		488.5875	1463.739
DPNHFRPAGLPDK	(Y)		488.5877	1463.739
DPNHFRPAGLPDK	(Y)		488.5877	1463.739
DPNHFRPAGLPDK	(Y)		366.6939	1463.739
DPNHFRPAGLPDK	(Y)		366.6937	1463.739
DPNHFRPAGLPDK	(Y)		732.3858	1463.739
DPNHFRPAGLPDK	(Y)		488.5875	1463.739
DPNHFRPAGLPDK	(Y)		732.3858	1463.739
DPNHFRPAGLPDKY	(-)		542.9395	1626.802
DPNHFRPAGLPDKY	(-)		542.9407	1626.802
DPNHFRPAGLPDKY	(-)		813.9087	1626.802
DPNHFRPAGLPDKY	(-)		407.4577	1626.802
DPNHFRPAGLPDKY	(-)		542.9416	1626.802
DPNHFRPAGLPDKY	(-)		813.9059	1626.802
DPNHFRPAGLPDKY	(-)		813.9092	1626.802
DPNHFRPAGLPDKY	(-)		542.9395	1626.802
DPNHFRPAGLPDKY	(-)		407.4574	1626.802
DPNHFRPAGLPDKY	(-)		813.9073	1626.802
DPnHFRPAGLPDKY	(-)	n:Deamida	814.3993	1626.802
DPNHFRPAGLPDKY	(-)		407.4596	1626.802
DPNHFRPAGLPDKY	(-)		407.4574	1626.802
DPNHFRPAGLPDKY	(-)		542.9417	1626.802
DPNHFRPAGLPDKY	(-)		542.9417	1626.802
DPNHFRPAGLPDKY	(-)		813.9073	1626.802
DPNHFRPAGLPDKY	(-)		542.9412	1626.802
DPnHFRPAGLPDKY	(-)	n:Deamida	543.2724	1626.802
DPNHFRPAGLPDKY	(-)		813.9092	1626.802
DPNHFRPAGLPDKY	(-)		813.909	1626.802
DPnHFRPAGLPDKY	(-)	n:Deamida	814.4062	1626.802
DPNHFRPAGLPDKY	(-)		813.9092	1626.802
DPNHFRPAGLPDKY	(-)		407.4598	1626.802
DPNHFRPAGLPDKY	(-)		813.9087	1626.802
DPNHFRPAGLPDKY	(-)		813.909	1626.802
DPnHFRPAGLPDKY	(-)	n:Deamida	814.4006	1626.802
DPNHFRPAGLPDKY	(-)		542.9425	1626.802
DPnHFRPAGLPDKY	(-)	n:Deamida	814.4063	1626.802
DPNHFRPAGLPDKY	(-)		407.4611	1626.802
DPnHFRPAGLPDKY	(-)	n:Deamida	814.3989	1626.802

DPNHFRPAGLPDKY	(-)		542.943	1626.802
DPNHFRPH	(G)		510.245	1019.481
DPNHFRPH	(G)		510.2438	1019.481
DPNHFRPH	(G)		510.2441	1019.481
DPNHFRPH	(G)		510.2438	1019.481
DPNHFRPH	(G)		510.2469	1019.481
DPNHFRPH	(G)		510.2462	1019.481
DPNHFRPH	(G)		340.4998	1019.481
DPNHFRPH	(G)		340.4994	1019.481
DPNHFRPH	(G)		510.244	1019.481
DPNHFRPH	(G)		340.4995	1019.481
DPNHFRPH	(G)		340.4996	1019.481
DPNHFRPH	(G)		510.2458	1019.481
DPNHFRPH	(G)		510.2475	1019.481
DPNHFRPH	(G)		510.2435	1019.481
DPNHFRPH	(G)		510.244	1019.481
DPNHFRPH	(G)		340.4987	1019.481
DPNHFRPH	(G)		510.245	1019.481
DPNHFRPH	(G)		510.2469	1019.481
DPNHFRPH	(G)		340.4993	1019.481
DPNHFRPH	(G)		340.502	1019.481
DPNHFRPH	(G)		510.2464	1019.481
DPNHFRPH	(G)		510.2469	1019.481
DPNHFRPH	(G)		510.244	1019.481
DPNHFRPH	(G)		510.2442	1019.481
DPNHFRPH	(G)		510.2464	1019.481
DPNHFRPH	(G)		510.2475	1019.481
DPNHFRPH	(G)		510.2431	1019.481
DPNHFRPH	(G)		340.5005	1019.481
DPNHFRPH	(G)		510.2435	1019.481
DPNHFRPHG	(L)		538.7566	1076.502
DPNHFRPHGLPDK	(Y)		765.3851	1529.761
DPNHFRPHGLPDK	(Y)		510.5936	1529.761
DPNHFRPHGLPDK	(Y)		383.1972	1529.761
DPNHFRPHGLPDK	(Y)		510.5929	1529.761
DPNHFRPHGLPDK	(Y)		510.5945	1529.761
DPNHFRPHGLPDK	(Y)		510.5942	1529.761
DPNHFRPHGLPDK	(Y)		510.5944	1529.761
DPNHFRPHGLPDK	(Y)		510.5882	1529.761
DPnHFRPHGLPDK	(Y)	n:Deamida	383.4434	1529.761
DPNHFRPHGLPDK	(Y)		510.593	1529.761
DPNHFRPHGLPDK	(Y)		383.1968	1529.761
DPnHFRPHGLPDK	(Y)	n:Deamida	510.9248	1529.761
DPNHFRPHGLPDK	(Y)		510.5952	1529.761
DPNHFRPHGLPDK	(Y)		765.3873	1529.761
DPNHFRPHGLPDK	(Y)		510.5942	1529.761
DPNHFRPHGLPDK	(Y)		383.1973	1529.761

DPnHFRPHGLPDK	(Y)	n:Deamida	510.9243	1529.761
DPnHFRPHGLPDK	(Y)	n:Deamida	510.9217	1529.761
DPNHFRPHGLPDK	(Y)		383.198	1529.761
DPNHFRPHGLPDK	(Y)		383.1978	1529.761
DPNHFRPHGLPDK	(Y)		510.5936	1529.761
DPNHFRPHGLPDK	(Y)		510.5942	1529.761
DPnHFRPHGLPDK	(Y)	n:Deamida	383.4431	1529.761
DPNHFRPHGLPDK	(Y)		510.5941	1529.761
DPNHFRPHGLPDK	(Y)		383.197	1529.761
DPNHFRPHGLPDK	(Y)		510.5952	1529.761
DPNHFRPHGLPDK	(Y)		510.5936	1529.761
DPNHFRPHGLPDK	(Y)		765.387	1529.761
DPNHFRPHGLPDK	(Y)		383.2031	1529.761
DPnHFRPHGLPDK	(Y)	n:Deamida	383.4478	1529.761
DPnHFRPHGLPDK	(Y)	n:Deamida	383.4442	1529.761
DPnHFRPHGLPDK	(Y)	n:Deamida	383.4448	1529.761
DPNHFRPHGLPDKY	(-)		846.9084	1692.824
DPNHFRPHGLPDKY	(-)		846.919	1692.824
DPNHFRPHGLPDKY	(-)		846.9199	1692.824
DPNHFRPHGLPDKY	(-)		846.9178	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	565.2749	1692.824
DPNHFRPHGLPDKY	(-)		423.9643	1692.824
DPNHFRPHGLPDKY	(-)		846.9199	1692.824
DPNHFRPHGLPDKY	(-)		564.9498	1692.824
DPNHFRPHGLPDKY	(-)		564.947	1692.824
DPNHFRPHGLPDKY	(-)		846.9178	1692.824
DPNHFRPHGLPDKY	(-)		423.9638	1692.824
DPNHFRPHGLPDKY	(-)		423.9648	1692.824
DPNHFRPHGLPDKY	(-)		846.9174	1692.824
DPNHFRPHGLPDKY	(-)		564.9481	1692.824
DPNHFRPHGLPDKY	(-)		564.9492	1692.824
DPNHFRPHGLPDKY	(-)		423.963	1692.824
DPNHFRPHGLPDKY	(-)		564.9488	1692.824
DPNHFRPHGLPDKY	(-)		423.9632	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	565.2761	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	565.2761	1692.824
DPNHFRPHGLPDKY	(-)		423.963	1692.824
DPNHFRPHGLPDKY	(-)		846.9175	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	565.2792	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	565.2775	1692.824
DPNHFRPHGLPDKY	(-)		846.92	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	424.2107	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	565.2764	1692.824
DPNHFRPHGLPDKY	(-)		564.9483	1692.824
DPNHFRPHGLPDKY	(-)		423.963	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	847.4077	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	847.4094	1692.824

DPnHFRPHGLPDKY	(-)	n:Deamida	565.2764	1692.824
DPNHFRPHGLPDKY	(-)		564.95	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	424.21	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	847.4118	1692.824
DPNHFRPHGLPDKY	(-)		846.9083	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	424.2092	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	847.4075	1692.824
DPNHFRPHGLPDKY	(-)		846.9218	1692.824
DPNHFRPHGLPDKY	(-)		846.9231	1692.824
DPNHFRPHGLPDKY	(-)		846.9218	1692.824
DPNHFRPHGLPDKY	(-)		846.9178	1692.824
DPNHFRPHGLPDKY	(-)		423.9643	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	847.4114	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	847.4109	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	565.2764	1692.824
DPNHFRPHGLPDKY	(-)		564.9474	1692.824
DPNHFRPHGLPDKY	(-)		564.9483	1692.824
DPNHFRPHGLPDKY	(-)		846.9218	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	847.4077	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	847.4119	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	565.2735	1692.824
DPNHFRPHGLPDKY	(-)		423.9637	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	847.4094	1692.824
DPNHFRPHGLPDKY	(-)		846.919	1692.824
DPNHFRPHGLPDKY	(-)		423.9632	1692.824
DPNHFRPHGLPDKY	(-)		564.9498	1692.824
DPNHFRPHGLPDKY	(-)		846.9218	1692.824
DPNHFRPHGLPDKY	(-)		564.9481	1692.824
DPNHFRPHGLPDKY	(-)		846.919	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	565.2749	1692.824
DPNHFRPHGLPDKY	(-)		564.9492	1692.824
DPNHFRPHGLPDKY	(-)		846.9199	1692.824
DPNHFRPHGLPDKY	(-)		846.9284	1692.824
DPNHFRPHGLPDKY	(-)		564.9488	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	565.2761	1692.824
DPNHFRPHGLPDKY	(-)		564.9481	1692.824
DPNHFRPHGLPDKY	(-)		846.919	1692.824
DPNHFRPHGLPDKY	(-)		564.9472	1692.824
DPNHFRPHGLPDKY	(-)		846.9084	1692.824
DPNHFRPHGLPDKY	(-)		846.9284	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	847.4094	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	424.2113	1692.824
DPNHFRPHGLPDKY	(-)		846.9175	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	424.2117	1692.824
DPNHFRPHGLPDKY	(-)		846.9252	1692.824
DPNHFRPHGLPDKY	(-)		846.9199	1692.824
DPNHFRPHGLPDKY	(-)		564.9502	1692.824

DPnHFRPHGLPDKY	(-)	n:Deamida	847.4109	1692.824
DPNHFRPHGLPDKY	(-)		846.919	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	847.4109	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	847.4077	1692.824
DPNHFRPHGLPDKY	(-)		846.9218	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	847.4094	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	565.2792	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	565.2703	1692.824
DPNHFRPHGLPDKY	(-)		846.9284	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	424.2132	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	565.2759	1692.824
DPNHFRPHGLPDKY	(-)		564.9488	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	847.4119	1692.824
DPNHFRPHGLPDKY	(-)		846.919	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	847.4075	1692.824
DPNHFRPHGLPDKY	(-)		564.9488	1692.824
DPNHFRPHGLPDKY	(-)		423.9652	1692.824
DPNHFRPHGLPDKY	(-)		423.963	1692.824
DPNHFRPHGLPDKY	(-)		564.95	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	565.2703	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	565.2735	1692.824
DPnHFRPHGLPDKY	(-)	n:Deamida	565.2792	1692.824
DPNPFRPAGLPDK	(Y)		712.3773	1423.733
DPNYyRPPGLPDK	(Y)	y:Phosphor	827.8633	1531.754
DPNYRPPGLPDKY	(-)		424.4603	1694.817
DPPIILQEQKTVLASVSVLSAIYASR	(A)		741.1581	2961.63
DQWRSRSDSIVPLIGNVLRVCQYHR	(E)	C:Carbamic	1018.869	3054.58
DSGHGAEDSR	(A)		515.7149	1030.418
DSGHGAEDSR	(A)	DSGHGAEDSR DSGHG	515.7148	1030.418
DSGHGAEDSR	(A)	DSGHGAEDSR DSGHG	515.7204	1030.418
DTVADLmnkGYLTEKTCCLAAASCLHHK	(F)	DTVADLmn C:Carbamic	1036.145	3047.475
DTWNLFLDLVCHEFCQSDDPPIILQEQKTVLASVFSVLSAI	(A)	C:Carbamic	819.417	4911.426
DVSCCELLSnVFQDLTKEnIIQALKEDHLnk	(Q)	DVSCCELLSn C:Carbamic	721.3436	3513.789
DVSCCELLSnVFQDLTKEnIIQALKEDHLnk	(Q)	DVSCCELLSn C:Carbamic	721.3521	3513.789
DVSCCELLSnVFQDLTKEnIIQALKEDHLnk	(Q)	DVSCCELLSn C:Carbamic	721.3457	3513.789
DVSCCELLSnVFQDLTKEnIIQALKEDHLnk	(Q)	DVSCCELLSn C:Carbamic	721.3522	3513.789
DVTVFLFTLCPFGRVLSFPGTWDMMLRAY	(N)	C:Carbamic	662.536	3308.664
DVTVFLFTLCPFGRVLSFPGTWDMMLRAY	(N)	C:Carbamic	662.538	3308.664
DVTVFLFTLCPFGRVLSFPGTWDMMLRAY	(N)	C:Carbamic	662.5335	3308.664
DVTVFLFTLCPFGRVLSFPGTWDMMLRAY	(N)	C:Carbamic	662.5334	3308.664
DVTVFLFTLCPFGRVLSFPGTWDMMLRAY	(N)	C:Carbamic	662.5352	3308.664
DVTVFLFTLCPFGRVLSFPGTWDMMLRAY	(N)	C:Carbamic	662.5319	3308.664
DVTVFLFTLCPFGRVLSFPGTWDMMLRAY	(N)	C:Carbamic	662.5358	3308.664
DVTVFLFTLCPFGRVLSFPGTWDMMLRAY	(N)	C:Carbamic	662.5353	3308.664
DVTVFLFTLCPFGRVLSFPGTWDMMLRAY	(N)	C:Carbamic	662.5311	3308.664
DVTVFLFTLCPFGRVLSFPGTWDMMLRAY	(N)	C:Carbamic	662.5353	3308.664
DVTVFLFTLCPFGRVLSFPGTWDMMLRAY	(N)	C:Carbamic	662.5333	3308.664

DVTVFLFTLCPFGRVLSFPGTWDMMLRAY	(N)	C:Carbamic	662.5319	3308.664
DVTVFLFTLCPFGRVLSFPGTWDMMLRAY	(N)	C:Carbamic	662.5352	3308.664
EEAQQAWDMWRAYSMDREANYIGADKYFHARGNYEA	(Q)		1429	4284.904
EAARGTWDMIRAYHDMREANYIGADK	(Y)	EAARGTWDMIRAYHDM	1014.163	3040.415
EALQGAGDLGRAYWNVLtSSHQnSkR	(Y)	t:Phosphor	994.8002	2858.429
EALQGAGDLGRAYWNVLtSSHQNSKRYFYAQGNYPDAE	(L)		1192.417	7149.51
EALQGITDPLFkGMTRDQVR	(E)	k:Carbanyl	773.3908	2275.186
EALQGITDPLFkGMTRDQVR	(E)	k:Carbanyl	773.3908	2275.186
EANWKKSDKYFHARGNYDA	(A)	EANWKKSDKYFHARGN	1150.534	2300.084
EANWKKSDKYFHARGNYDA	(A)		1150.532	2300.084
EANWKKSDKYFHARGNYDA	(A)		1150.55	2300.084
EANYIGADK	(Y)		490.7417	980.468
EANYIGADK	(Y)		490.7406	980.468
EANYIGADK	(Y)		490.7407	980.468
EANYIGADK	(Y)		490.7415	980.468
EANYIGADK	(Y)	EANYIGADK	490.7392	980.468
EANYIGADK	(Y)		490.74	980.468
EAnYIGADK	(Y)	n:Deamida	491.2316	980.468
EANYIGADK	(Y)		490.7404	980.468
EANYIGADK	(Y)		490.7359	980.468
EAnYIGADK	(Y)	n:Deamida	491.2348	980.468
EAnYIGADK	(Y)	n:Deamida	491.2312	980.468
EAnYIGADK	(Y)	n:Deamida	491.23	980.468
EAnYIGADK	(Y)	n:Deamida	491.2324	980.468
EAnYIGADK	(Y)	n:Deamida	491.2302	980.468
EAnYIGADK	(Y)	n:Deamida	491.2376	980.468
EAnYIGADK	(Y)	n:Deamida	491.2333	980.468
EANYIGADK	(Y)		490.742	980.468
EAnYIGADK	(Y)	n:Deamida	491.2343	980.468
EANYIGADK	(Y)		490.7413	980.468
EANYIGADK	(Y)	EANYIGADK	490.7367	980.468
EANYIGADKY	(F)		572.2716	1143.532
EANYIGADKY	(F)		572.2721	1143.532
EANYIGADKY	(F)		572.2722	1143.532
EANYIGADKY	(F)		572.2711	1143.532
EANYIGADKY	(F)		572.2708	1143.532
EANYIGADKY	(F)		572.2713	1143.532
EANYIGADKY	(F)		572.2768	1143.532
EANYIGADKY	(F)		572.2722	1143.532
EANYIGADKYF	(H)		645.8126	1290.6
EANYIGADKYF	(H)		645.8136	1290.6
EANYIGADKYF	(H)		645.8109	1290.6
EANYIGADKYF	(H)		645.8133	1290.6
EANYIGADKYF	(H)		645.8098	1290.6
EANYIGADKYFHAR	(G)		414.4587	1654.797
EANYIGADKYFHARGNYDAAQRGPGGAWAAKVISDGRE	(G)		819.2575	5728.724
EANYIGADKYFHARGNYDAARRGPGGVWAA	(K)		814.1455	3253.568

EANYINADKYFHAR	(G)		428.7138	1711.819
EANYINADKYFHAR	(G)		428.713	1711.819
EANYINADKYFHAR	(G)		428.713	1711.819
EANYINADKYFHAR	(G)		571.2787	1711.819
EANYINADKYFHAR	(G)		428.7138	1711.819
EANYINADKYFHAR	(G)		571.2779	1711.819
EANYINADKYFHAR	(G)		428.7138	1711.819
EANYINADKYFHAR	(G)		571.2787	1711.819
EANYINADKYFHAR	(G)		428.7133	1711.819
EANYKNADKYFHARGNYDAAQRGPGDTWAAKVISDA	(R)		794.9967	3970.886
EANYRGADKYFHARGNYDAARRGPGGAWAAKVISNARI	(Q)		730.8744	4380.188
ECKHEATSKGGAEDGQLETLAEITAEFLADLCLDISKDTVA	(T)	C:Carbamic	819.2588	5728.755
ECKHEATSKGGAEDGQLETLAEITAEFLADLCLDISKDTVA	(T)	C:Carbamic	819.2588	5728.755
EDEKDEQLETLAEITAEFLADLFVHIQKDTVADLVKKV	(Y)		1086.572	4343.255
EEEEEVAGGDCIGSTVYSKHWLFGVLSGLIQDVALFLQEF	(S)	C:Carbamic	955.7926	5728.823
EEEEEVAGGDCIGSTVYSKHWLFGVLSGLIQVSPENTKSS	(E)	C:Carbamic	818.9724	5726.67
EFkRPKtVIWtFTYK	(L)	EFkRPKtVIV	k:Carbamyl	689.6934 1944.074
EFkRPKtVIWtFTYK	(L)		k:Acetyl,t:F	689.3438 1944.074
EFTkTIR	(R)		k:Acetyl	468.7626 894.504
EFTKTIRRPFGVKYNPYTRSIQ	(I)			676.1064 2701.457
EGQLSKEK	(C)			459.7501 918.489
EGQLSkEkCSSAFQnLLPFYSLV	(-)	C:Carbamic	683.3486	2645.328
EGQLsKQkCSSAFQnLLPFYSPVISLR	(I)	C:Carbamic	1074.19	3097.614
EGYLTERTC	(V)	C:Carbamic	564.7452	1128.499
EGYLTERTCVAAARSLTPNFQT	(S)	C:Carbamic	829.0861	2485.214
EGYLTERTCVAAARSLTPNFQT	(S)	C:Carbamic	829.0875	2485.214
EGYLTERTCVAAARSLTPNFQT	(S)	C:Carbamic	829.0861	2485.214
EGYLTERTCVAAARSLTPNFQT	(S)	C:Carbamic	829.0902	2485.214
EGYLTERTCVAAARSLTPNFQT	(S)	C:Carbamic	829.0886	2485.214
EHsLERGRATVIFsLK	(N)	EHsLERGRAs	:Phosphor	501.5007 1843.018
EICVSISSDKNLGQMLLHCLYD	(S)	C:Carbamic	865.7502	2595.225
EKHVNLLHIEsR	(K)		s:Phosphor	777.9037 1474.812
EmLLLTCLSQTEVASVWVER	(I)	C:Carbamic	595.8077	2364.194
EnAQRVTDLFK	(F)		n:Deamida	441.2357 1320.691
ENFQRfDRLK	(F)		t:Phosphor	511.922 1453.755
ENPAIYDsICFIMSSSTNVDLLVKVGEVVDKLFDLDEK	(L)		C:Carbamic	1096.54 4303.14
ENPAVYDSICFImsSSTNVDLLVKVGEVVDKLFDLDEK	(L)	ENPAVYDSI	C:Carbamic	1489.042 4289.124
ENPAVYDSICFImsSSTNVDLLVKVGEVVDKLFDLDEK	(L)	ENPAVYDSI	C:Carbamic	1489.038 4289.124
ENPAVYDSICFImsSSTNVDLLVKVGEVVDKLFDLDEK	(L)	ENPAVYDSI	C:Carbamic	1489.044 4289.124
ENPAVYESICFIMsSSTNVDLLVKVGEVVDKLFDLDEK	(L)	ENPAVYESI	C:Carbamic	1096.551 4303.14
EPLKPMRPSnEGTDEPRAPEEDFHLk	(I)		n:Deamida	798.8841 3148.5
EPLKPMRPSnEGTDEPRAPEEDFHLk	(I)		n:Deamida	798.8834 3148.5
EQLNDIFHLLKSHtNVLSVTPPDNFTMK	(E)	EQLNDIFHL	t:Phosphor	1106.874 3238.657
EQLNDIFHLLKsHTNVLSVTPPDNFTMK	(E)	EQLNDIFHL	s:Phosphor	1106.872 3238.657
EQLNDIFHLLKSHtNVLSVTPPDNFTMK	(E)	EQLNDIFHL	t:Phosphor	1106.874 3238.657
EQLNDIFHLLKSHtNVLSVTPPDNFTMK	(E)	EQLNDIFHL	t:Phosphor	1106.874 3238.657
EQLNDIFHLLKsHTNVLSVTPPDNFTMK	(E)	EQLNDIFHL	s:Phosphor	1106.875 3238.657

EQLNDIFHLLKsHTNVLSVTPPDNFTMK	(E)	EQLNDIFHL s:Phosphor	1106.869	3238.657
EQLNDIFHLLKShHTNVLSVTPPDNFTMK	(E)	EQLNDIFHL t:Phosphor	1106.872	3238.657
ESFEDAKEKMREFTKTIRRPFGVKYNPYTRSIQILKDRSIT:	(V)		1017.519	7116.667
ESFFAALHEADQSIENLAKEFPSLR	(P)		974.1662	2920.448
ESFFAALHEADQSIENLAKEFPSLR	(P)		974.153	2920.448
ESFFAALHEADQSIENLAKEFPSLR	(P)		974.1634	2920.448
ESFQEFF	(G)		467.2088	933.399
ESFQEFFGRGHED	(T)		528.8963	1584.671
ESFQEFFGRGHED	(T)		528.9042	1584.671
ESFQEFFGRGHED	(T)		528.9052	1584.671
ESFQEFFGRGHED	(T)		528.9057	1584.671
ESFQEFFGRGHED	(T)		528.8999	1584.671
ESFQEFFGRGHED	(T)		528.9049	1584.671
ESFQEFFGRGHED	(T)		528.9051	1584.671
ETVAQGLKEGQLSKQKCSCVFQNLPLYGPVVEDFIKILHE	(S)	C:Carbamic	1430.538	7148.741
ETVAQGLKEGQLSKQKCSCVFQNLPLYGPVVEDFIKILHE	(S)	C:Carbamic	1022.104	7148.741
ETVTKGLKEGQLsk	(Q)	k:Acetyl,s:F	841.4348	1517.853
EVDKALAEDLKESFSLK	(V)		679.0465	2035.096
EVDKALAEDLKESFSLK	(V)		679.0391	2035.096
EVDKALAEDLKESFSLK	(V)		679.0465	2035.096
EVDKALAEDLKESFSLK	(V)		679.0448	2035.096
EVDKTLAGNLEESFPSLKR	(S)		711.7013	2133.119
EWLTLK	(E)		468.7635	936.519
EYPAIYDSICFIMSSSTNVDLLmkIGEVDkLFDLDEK	(L)	C:Carbamic	1125.788	4398.148
FDLTQDYFHLLKILKDISCEFLSNIFQALTKETVTKG	(L)	C:Carbamic	1066.541	4263.205
FGDSGHGAEDSR	(A)		617.7593	1234.508
FGDSGHGAEDSR	(A)		617.7584	1234.508
FGDSGHGAEDSR	(A)		617.7591	1234.508
FGDSGHGAEDSR	(A)		617.7579	1234.508
FGDSGHGAEDSR	(A)	FGDSGHGAEDSR FGDS	617.7581	1234.508
FGDSGHGAEDSR	(A)	FGDSGHGAEDSR FGDS	412.1777	1234.508
FGDSGHGAEDSR	(A)		617.7619	1234.508
FGDSGHGAEDSR	(A)	FGDSGHGAEDSR FGDS	617.7595	1234.508
FGDSGHGAEDSR	(A)	FGDSGHGAEDSR FGDS	412.1765	1234.508
FGDSGHGAEDSR	(A)	FGDSGHGAEDSR FGDS	617.761	1234.508
FGDSGHGAEDSR	(A)	FGDSGHGAEDSR FGDS	412.1761	1234.508
FGDSGHGAEDSR	(A)	FGDSGHGAEDSR FGDS	412.1766	1234.508
FGDSGHGAEDSR	(A)		617.7621	1234.508
FGDSGHGAEDSR	(A)		617.7586	1234.508
FGDSGHGAEDSR	(A)		617.7601	1234.508
FGDSGHGAEDSR	(A)	FGDSGHGAEDSR FGDS	617.7599	1234.508
FGDSGHGAEDSR	(A)	FGDSGHGAEDSR FGDS	617.7611	1234.508
FGDSGHGAEDSR	(A)	FGDSGHGAEDSR FGDS	412.1825	1234.508
FGDSGHGAEDSR	(A)	FGDSGHGAEDSR FGDS	412.1813	1234.508
FGDSGHGAEDSR	(A)	FGDSGHGAEDSR FGDS	617.761	1234.508
FGDSGHGAEDSR	(A)	FGDSGHGAEDSR FGDS	617.7592	1234.508
FGDSGHGAEDSR	(A)	FGDSGHGAEDSR FGDS	617.761	1234.508

FGDSGHGAEDSR	(A)	FGDSGHGAEDSR FGDS	412.1812	1234.508
FGDSGHGAEDSR	(A)		617.7611	1234.508
FGDSGHGAEDSR	(A)	FGDSGHGAEDSR FGDS	412.1784	1234.508
FGDSGHGAEDSR	(A)	FGDSGHGAEDSR FGDS	412.1789	1234.508
FGDSGHGAEDSR	(A)	FGDSGHGAEDSR FGDS	412.18	1234.508
FGDSGHGAEDSRADQAANEWGR	(S)	FGDSGHGAAs:Phosphor	804.9957	2332.993
FGDSGHGEADSR	(A)		617.7592	1234.508
FGDSGHGEADSR	(A)		617.7608	1234.508
FGDSGHGEADSR	(A)		617.7579	1234.508
FGDSGHGEADSR	(A)		412.1755	1234.508
FGDSGHGEADSR	(A)		412.1755	1234.508
FGDSGHGEADSR	(A)		412.176	1234.508
FGDSGHGVEDSK	(A)		412.1796	1234.534
FIGEAVR	(G)		396.2186	791.441
FKNSFQHLQTMLSEADPQLADVIRTQCPV	(-)	C:Carbamic	1139.217	3373.667
FLGEAAR	(G)		382.216	763.41
FLQEFK	(A)		406.2282	811.435
FSFGGSGR	(G)		407.6995	814.384
FSFGGSGR	(G)		407.7005	814.384
FSFGGSGR	(G)		407.697	814.384
FSFGGSGR	(G)		407.6991	814.384
FSFGGSGR	(G)		407.6998	814.384
FSFGGSGR	(G)		407.6996	814.384
FSFGGSGR	(G)		407.6998	814.384
FSFGGSGR	(G)		407.6983	814.384
FSFGGSGR	(G)		407.697	814.384
FSFGGSGR	(G)		407.6958	814.384
FSFGGSGR	(G)		407.6953	814.384
FSFGGSGR	(G)		407.697	814.384
FSFGGSGR	(G)		407.6974	814.384
FSFGGSGR	(G)		407.6972	814.384
FSFGGSGR	(G)		407.6945	814.384
FSFGGSGR	(G)		407.6971	814.384
FSFGGSGR	(G)		407.6978	814.384
FSFGGSGR	(G)		407.6986	814.384
GADKYFHAKGNFDAAQRG	(P)		651.6559	1952.936
GADKYFHARGNYDAAKRGPGGAWAAEVIR	(L)		776.8861	3104.556
GADKYFHARGNYDAAQRGPGGAWAAKVISNARETIQGI	(T)	GADKYFHARGNYDAAQ	804.1945	4017.023
GAEDSR	(A)		317.6436	634.279
GAESPLRAGIVPK	(Y)		432.2569	1294.748
GAESPLRAGIVPK	(Y)		432.2464	1294.748
GAGGRVAAAVISnTWEGIQRAR	(G)	n:Deamida	747.7291	2240.201
GDAIGATIYSkHWLFGVLSsLIQLInPEK	(A)	GDAIGATIY k:Carbamyl	1098.911	3170.725
GDAIGATIYSkHWLFGVLSsLIQLInPEK	(A)	GDAIGATIY k:Carbamyl	1098.914	3170.725
GDAIGATIYSkHWLFGVLSsLIQLInPEK	(A)	GDAIGATIY k:Carbamyl	1098.914	3170.725
GDAIGATIYSkHWLFGVLSsLIQLInPEK	(A)	GDAIGATIY k:Carbamyl	1098.908	3170.725
GDEsDtPLDLTLCLLEAVKQLR	(S)	C:Carbamic	530.0562	2486.281

GDSGHGAEDSR	(A)		544.2245	1087.44
GDSGHGAEDSR	(A)		544.2271	1087.44
GDSGHGAEDSR	(A)	GDSGHGAEDSR GDSG	544.2246	1087.44
GDSGHGAEDSR	(A)	GDSGHGAEDSR GDSG	544.2254	1087.44
GDSGHGAEDSR	(A)	GDSGHGAEDSR GDSG	544.2277	1087.44
GDSGHGAEDSR	(A)	GDSGHGAEDSR GDSG	544.2261	1087.44
GDSGHGAEDSR	(A)	GDSGHGAEDSR GDSG	544.2271	1087.44
GDSGHGAEDSR	(A)	GDSGHGAEDSR GDSG	544.2284	1087.44
GDSGHGAEDSR	(A)		544.2253	1087.44
GDSGHGAEDSR	(A)	GDSGHGAEDSR GDSG	544.2256	1087.44
GDSGHGAEDSR	(A)	GDSGHGAEDSR GDSG	544.2291	1087.44
GGAWAAK	(V)		330.6788	660.346
GGAWAAK	(V)		330.6805	660.346
GGAWAAK	(V)		330.6789	660.346
GGAWAAK	(V)		330.6795	660.346
GGAWAAK	(V)		330.6771	660.346
GLIQIVSPENAK	(S)		634.8693	1268.721
GLKEGQLskQK	(C)	s:Phosphor	669.8346	1215.706
GLKEGQLskQK	(C)	s:Phosphor	669.8324	1215.706
GLKEGQLskQK	(C)	s:Phosphor	669.8309	1215.706
GLKEGQLskQK	(C)	s:Phosphor	669.8325	1215.706
GLKEGQLskQK	(C)	s:Phosphor	669.8327	1215.706
GLKEGQLskQK	(C)	s:Phosphor	669.8325	1215.706
GLKEGQLskQK	(C)	s:Phosphor	669.8308	1215.706
GLKEGQLskQK	(C)	s:Phosphor	669.8321	1215.706
GLKEGQLskQK	(C)	s:Phosphor	669.8318	1215.706
GLKEGQLskQK	(C)	s:Phosphor	669.8487	1215.706
GLKEGQLskQK	(C)	s:Phosphor	669.8306	1215.706
GLKEGQLskQK	(C)	s:Phosphor	669.8317	1215.706
GLKEGQLskQK	(C)	s:Phosphor	669.8325	1215.706
GLKEGQLskQK	(C)	s:Phosphor	669.8301	1215.706
GLKEGQLskQk	(C)	GLKEGQLsk:s:Phosphor	669.8302	1215.706
GLKEGQLskQK	(C)	s:Phosphor	669.8326	1215.706
GLKEGQLskQK	(C)	s:Phosphor	669.8351	1215.706
GLKEGQLskQK	(C)	s:Phosphor	669.8306	1215.706
GLKEGQLskQK	(C)	s:Phosphor	669.8351	1215.706
GLKEGQLskQK	(C)	s:Phosphor	669.8293	1215.706
GLKEGQLskQK	(C)	s:Phosphor	669.8346	1215.706
GLKEGQLskQK	(C)	s:Phosphor	669.8325	1215.706
GLKEGQLskQK	(C)	s:Phosphor	669.8327	1215.706
GLLSFLGEAAR	(G)		567.3217	1133.631
GLLSFLGEAAR	(G)		567.3119	1133.631
GLLSFLGEAAR	(G)		567.3129	1133.631
GLLSFLGEAAR	(G)		567.3209	1133.631
GLLSFLGEAAR	(G)		567.3111	1133.631
GLLSFLGEAAR	(G)		567.3211	1133.631
GLLSFLGEAAR	(G)		567.3194	1133.631

GLLSFLGEAAR	(G)		567.308	1133.631
GLLSFLGEAAR	(G)		567.3227	1133.631
GLLSFLGEAAR	(G)		567.3234	1133.631
GLLSFLGEAAR	(G)		567.321	1133.631
GLLSFLGEAAR	(G)		567.322	1133.631
GLLSFLGEAAR	(G)		567.3155	1133.631
GLLSFLGEAAR	(G)		567.318	1133.631
GLLSFLGEAAR	(G)		567.3111	1133.631
GLLSFLGEAAR	(G)		567.318	1133.631
GLLSFLGEAAR	(G)		567.3224	1133.631
GLLSFLGEAAR	(G)		567.3137	1133.631
GLPKY	(-)		346.685	692.361
GLPKY	(-)		346.6844	692.361
GLPKY	(-)		346.6853	692.361
GLPKY	(-)		346.686	692.361
GLPKY	(-)		346.6863	692.361
GLPKY	(-)		346.6857	692.361
GLPKY	(-)		346.6851	692.361
GLPKY	(-)		346.6867	692.361
GLPKY	(-)		346.6877	692.361
GLPKY	(-)		346.6875	692.361
GLPKY	(-)		346.6875	692.361
GLPKY	(-)		346.6867	692.361
GLPKY	(-)		346.6846	692.361
GLPKY	(-)		346.6863	692.361
GLPKY	(-)		346.6869	692.361
GLPKY	(-)		346.6881	692.361
GLPKY	(-)		346.6877	692.361
GLPKY	(-)	GLPKY GLPKY	346.685	692.361
GNFDAARRGPGGVWAAEVI	(S)		971.9999	1942.988
GNWIIQKPRGTCQVLR	(N)	C:Carbamic	729.4014	2186.202
GNYDAAQR	(G)		447.7074	894.406
GNYDAAQR	(G)		447.7096	894.406
GNYDAAQR	(G)		447.7077	894.406
GNYDAAQR	(G)		447.7082	894.406
GNYDAAQR	(G)		447.7086	894.406
GNYDAAQR	(G)		447.7084	894.406
GNYDAAQR	(G)		447.7093	894.406
GNYDAAQR	(G)		447.7075	894.406
GnYDAAQR	(G)	n:Deamida	448.2001	894.406
GNYDAAQR	(G)		447.7121	894.406
GnYDAAQR	(G)	n:Deamida	448.2024	894.406
GNYDAAR	(R)		383.679	766.348
GNYDAAR	(R)		383.6781	766.348
GNYDAAR	(R)		383.6775	766.348
GNYDAAR	(R)		383.679	766.348
GNYDAAR	(R)		383.679	766.348

GNYDAAR	(R)		383.6793	766.348
GNYDAAR	(R)		383.6794	766.348
GPGGAWAAEVIRLkCHGmIMAHCNLDLPGLK	(R)	GPGGAWA C:Carbamic	572.7788	3372.695
GPGGAWAAEVISNAREDLQKFMGHAE	(D)		576.4849	2878.369
GPGGAWAAEVISNAREDLQKFMGHAE	(D)		576.4849	2878.369
GPGGAWAAEVISNAREDYQKFMG	(H)		818.7295	2454.151
GPGGAWAAK	(V)		407.7172	814.421
GPGGAWAAK	(V)		407.7167	814.421
GPGGAWAAK	(V)	GPGGAWAAK	407.7174	814.421
GPGGAWAAK	(V)		407.7161	814.421
GPGGAWAAK	(V)		407.7165	814.421
GPGGAWAAK	(V)		407.7165	814.421
GPGGAWAAK	(V)		407.7153	814.421
GPGGAWAAK	(V)		407.7169	814.421
GPGGAWAAK	(V)		407.7131	814.421
GPGGAWAAK	(V)		407.719	814.421
GPGGAWAAK	(V)		407.717	814.421
GPGGAWAAK	(V)		407.7147	814.421
GPGGAWAAK	(V)		407.7178	814.421
GPGGAWAAK	(V)		407.7169	814.421
GPGGAWAAK	(V)		407.7174	814.421
GPGGAWAAK	(V)		407.7196	814.421
GPGGAWAAK	(V)		407.7212	814.421
GPGGAWAAK	(V)		407.7174	814.421
GPGGAWAAK	(V)		407.7212	814.421
GPGGAWAAKVIR	(G)		394.8972	1182.674
GPGGAWAAKVISDAR	(E)	k:CarbamyI	500.2667	1455.77
GPGGAWAAKVISDAR	(E)	k:CarbamyI	500.2654	1455.77
GPGGAWAAKVISDAR	(E)	k:CarbamyI	500.2669	1455.77
GPGGAWAAKVISDAR	(E)	k:CarbamyI	500.2686	1455.77
GPGGAWAAKVISDAR	(E)	k:CarbamyI	500.2657	1455.77
GPGGAWAAKVISDAR	(E)	k:CarbamyI	500.266	1455.77
GPGGAWAAKVISDAR	(E)	k:CarbamyI	749.8948	1455.77
GPGGAWAAKVISDAR	(E)	k:CarbamyI	749.8908	1455.77
GPGGAWAAKVISDAREGFK	(R)	k:CarbamyI	654.014	1916.998
GPGGAWAAKVISDARENIQRFTDPLFKGTTSG	(Q)		670.3355	3347.713
GPGGAWAAKVISDARENVQRFTDRFSF	(G)		746.3734	2982.497
GPGGAWAAKVISDARENVQRFTDRFSF	(G)		746.3832	2982.497
GPGGAWAAKVISDARENVQRFTDRFSF	(G)		746.3838	2982.497
GPGGAWAAKVISDARENVQRFTDRFSF	(G)		746.3781	2982.497
GPGGAWAAKVISNARETIQGITDPLFKMTRDQVRE	(D)	C:Carbamic	795.4004	3973.017
GPGGAWAAKVISNARETIQGITDPLLK	(G)	k:CarbamyI	468.6013	2763.515
GPGGPWAAKmISGAR	(E)	m:Oxidized	491.2542	1455.753
GPGGPWAAKmISGAR	(E)	m:Oxidized	491.2525	1455.753
GPGGPWAAKmISGAR	(E)	m:Oxidized	491.2501	1455.753
GPGGPWAAKmISGAR	(E)	m:Oxidized	491.2574	1455.753
GPGGPWAAKmISGAR	(E)	m:Oxidized	491.2574	1455.753

GPGGPWAAKmISGAR	(E)	m:Oxidized	491.262	1455.753
GPGGRWAATVISNGR	(E)		500.2644	1498.787
GPGGVWAAEVISDARENIQkLLGHGAEDTLADQAAAnEW(S)		k:Carbamyl	708.5168	4202.065
GPGGVWAAEVISDAREnIQkLLGHGAEDTLADQAANEW(S)		GPGGVWA n:Deamida	708.5168	4202.065
GPGGVWAAKVISDVREDLQRL	(M)		378.5465	2266.23
GPWAAK	(M)		315.176	629.341
GSEAEAEAAAGGDAIGATlySkHWLFGVLGSLIQLInPEk(D)	(D)	GSEAEAEAty:Phosphor	730.8706	4213.145
GSEAEAEAAAGGDAIGATlySkHWLFGVLGSLIQLINPEk(D)	(D)	GSEAEAEAts:Phosphor	730.3663	4213.145
GSEAEAEAAAGGDAIGATlySkHWLFGVLGSLIQLINPEk(D)	(D)	GSEAEAEAty:Phosphor	730.3744	4213.145
GSGGIWAAkIISrK	(Y)	GSGGIWAAk:Acetyl,t:F	898.4575	1631.923
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7172	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7136	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7159	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7105	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7169	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7164	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7174	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7164	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7174	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7162	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7165	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7135	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7164	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7174	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7169	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7167	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7104	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7174	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7172	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7187	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7174	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7153	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7174	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7113	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7217	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7186	878.419
GTWDMIR	(A)	GTWDMIR m:Oxidized	447.7134	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7205	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7167	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7128	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.717	878.419
GTWDMIR	(A)	GTWDMIR GTWDMLR	439.7217	878.419
HALSGHAKVkpFDpkItCK	(Q)	C:Carbamic	575.7836	2134.159
HEATSKGGAEDGQLETlAEITAeFLADLCLDISKDTVADL	(M)	C:Carbamic	607.5855	4247.055
HFRPAGLPDKY	(-)		434.2341	1300.68
HFRPAGLPDKY	(-)		650.8461	1300.68
HFRPAGLPDKY	(-)		434.2274	1300.68

HFRPAGLPDKY	(-)		434.2346	1300.68
HFRPAGLPDKY	(-)		434.2342	1300.68
HFRPAGLPDKY	(-)		650.8436	1300.68
HFRPAGLPDKY	(-)		434.2344	1300.68
HFRPAGLPDKY	(-)		434.2344	1300.68
HFRPAGLPDKY	(-)		434.2344	1300.68
HFRPAGLPDKY	(-)		434.2337	1300.68
HFRPHGLPDK	(Y)		301.6657	1203.638
HFRPHGLPDKY	(-)		342.4326	1366.701
HFRPHGLPDKY	(-)		342.4338	1366.701
HFRPHGLPDKY	(-)		683.859	1366.701
HFRPHGLPDKY	(-)		342.4318	1366.701
HFRPHGLPDKY	(-)		683.8553	1366.701
HFRPHGLPDKY	(-)		683.8567	1366.701
HFRPHGLPDKY	(-)		683.8564	1366.701
HFRPHGLPDKY	(-)		456.2414	1366.701
HFRPHGLPDKY	(-)		342.4332	1366.701
HFRPHGLPDKY	(-)		683.8548	1366.701
HFRPHGLPDKY	(-)		342.4329	1366.701
HFRPHGLPDKY	(-)		683.8567	1366.701
HFRPHGLPDKY	(-)		342.4326	1366.701
HFRPHGLPDKY	(-)		342.4338	1366.701
HFRPHGLPDKY	(-)		456.2389	1366.701
HFRPHGLPDKY	(-)		342.4315	1366.701
HFRPHGLPDKY	(-)		683.8552	1366.701
HFRPHGLPDKY	(-)		342.4337	1366.701
HFRPHGLPDKY	(-)		456.2409	1366.701
HFRPHGLPDKY	(-)		342.4332	1366.701
HFRPHGLPDKY	(-)		456.2424	1366.701
HPAIYDSICFIMSSTNVDLLVKVGEVVDK	(L)	C:Carbamic	834.9197	3336.685
HPAIYDSICFIMSSTNVDLLVKVGEVVDK	(L)	C:Carbamic	834.9227	3336.685
HPAIYDSICFIMSSTNVDLLVKVGEVVDK	(L)	C:Carbamic	834.9205	3336.685
HPAIYDSICFIMSSTNVDLLVKVGEVVDK	(L)	C:Carbamic	834.9169	3336.685
HWLFGVLSrLIQDVALFLQEFNAPDIFmGVLAKSR	(C)	s:Phosphor	1043.306	4031.173
HWVFGVLSGF	(I)		574.793	1148.589
HWVFGVLSGFIQIVSPENTk	(S)	k:Acetyl	575.8011	2258.197
IACFPDTCVTLKEDLCAVLLLLLGADPPTLLETSR	(L)	C:Carbamic	607.3051	4245.149
IACFPDTCVTLKEDLCAVLLLLLGADPPTLLETSR	(L)	C:Carbamic	607.3056	4245.149
IDEGIRVFAASDGPVK	(S)		544.6089	1631.839
IDSLIRVLQNMEQCQKKPENSTESNTGETK	(K)	C:Carbamic	696.3477	3477.695
IEEDLPLI	(D)		471.2689	941.519
IEEDLPLI	(D)		471.2709	941.519
IEEDLPLI	(D)		471.2687	941.519
IEEDLPLI	(D)		471.2547	941.519
IEEDLPLI	(D)		471.2702	941.519
IEEDLPLI	(D)		471.2701	941.519
IEEDLPLI	(D)		471.2624	941.519

IEEDLPLI	(D)		471.2696	941.519
IEEDLPLI	(D)		471.2604	941.519
IEEDLPLI	(D)		471.2687	941.519
IEEDLPLI	(D)		471.2721	941.519
IEEDLPLI	(D)		471.2648	941.519
IEEDLPLI	(D)		471.2698	941.519
IEEDLPLI	(D)		471.2654	941.519
IEEDLPLI	(D)		471.2696	941.519
IEEDLPLI	(D)		471.2718	941.519
IEEDLPLI	(D)		471.2561	941.519
IEEDLPLI	(D)		471.2602	941.519
IEEGKYHL	(P)		494.765	988.51
IEEGKYHLPLID	(S)		713.8702	1426.758
IEEGKYHLPLID	(S)		476.2561	1426.758
IEEGKYHLPLID	(S)		713.8797	1426.758
IEEGKYHLPLID	(S)		713.8797	1426.758
IEEGKYHLPLID	(S)		476.2592	1426.758
IEEGKYHLPLID	(S)		476.2615	1426.758
IEEGKYHLPLID	(S)		713.8702	1426.758
IEEGKYHLPLID	(S)		476.2592	1426.758
IEEGKYHLPLID	(S)		476.2592	1426.758
IEEGKYHLPLID	(S)		476.2592	1426.758
IEEGKYHLPLID	(S)		713.8755	1426.758
IEKDLPLIDSL	(I)		628.3601	1255.714
IEKSLPL	(V)		400.2464	799.492
IEKVDL	(P)		358.7133	716.419
IFCSLVLGVHSQWLSFLGEAYEGAK	(D)	C:Carbamic	937.8031	2811.417
IFQDLTK	(E)		432.7453	864.482
IFQDLTK	(E)		432.7479	864.482
IFQEKHVN	(L)		507.7631	1014.537
IFQEKHVN	(L)		338.8461	1014.537
IFQEKHVN	(L)		338.8447	1014.537
IFQEkHVnLLHIESRK	(S)	k:Carbamyl	679.0417	1991.119
IFQEkHVnLLHIEsRK	(S)	k:Carbamyl	529.2688	1991.119
IGADKYFHARGNYDAAKRGPGGAWAAEVISNAREDLQK	(F)		821.4269	4103.059
IGADKYFPPRGKYDAAR	(R)	IGADKYFPPRGKYDAAR	642.3282	1925.003
IGkGkYnLPLIDsLIR	(V)	IGkGkYnLP k:Acetyl,n:l	655.6792	1800.074
IGkGkYnLPLIDsLIR	(V)	k:Acetyl,s:F	655.3468	1800.074
IIFCFLILGVNSR	(E)	C:Carbamic	517.958	1551.872
IIFCFLILGVNSR	(E)	C:Carbamic	517.9563	1551.872
IIFCFLILGVNSR	(E)	C:Carbamic	517.9592	1551.872
IIFQRMIFPK	(V)		431.5833	1292.755
IIFQRMIFPK	(V)		431.5834	1292.755
IISTGRkyFQGLMnR	(Y)	k:Carbamyl	609.9789	1783.964
IKILHEVDKALADDLEKSFPGLK	(V)		645.6137	2579.444
ILEAAKQVR	(S)		343.2076	1027.626
ILEAAKQVR	(S)		343.2152	1027.626

ILEAAKQVR	(S)		343.2166	1027.626
ILEAAKQVR	(S)		343.2184	1027.626
ILGVNSREWLTLFLKEAGQGAK	(D)		773.0992	2317.266
ILGVSSQGWGTFLKEAGQGAK	(D)		712.0616	2134.129
ILHEVDKALANDLEKSFPS	(L)		532.2791	2126.113
ILHEVDKAV	(A)		512.297	1023.583
ILHEVDKAVAS	(D)		394.5632	1181.652
ILHEVDkTLADDLEESFPSLkVQt	(-)	ILHEVDkTL k:Carbamyl	724.096	2727.409
ILHEVDkTLADDLEESFPSLkVQt	(-)	ILHEVDkTL k:Carbamyl	724.0899	2727.409
ILHEVDkTLADDLEESFPSLkVQt	(-)	k:Carbamyl	724.0976	2727.409
ILHEVDkTLADDLEESFPSLkVQt	(-)	ILHEVDkTL k:Carbamyl	724.0935	2727.409
ILHEVDktLADDLEESFPSLkVQT	(-)	k:Carbamyl	579.4783	2727.409
ILHEVDKTLAGNLE	(E)		517.9582	1551.838
ILHEVDKTLAGNLE	(E)		517.954	1551.838
ILHEVDKTLAGNLE	(E)		517.954	1551.838
ILHEVDKtLAGnLEESFPSLkR	(S)	t:Phosphor	874.1056	2496.346
ILHEVDKTLAGnLEEsFPSLkR	(S)	n:Deamida	874.1036	2496.346
ILHEVDKtLAGnLEESFPSLkR	(S)	ILHEVDKtL/t:Phosphor	874.102	2496.346
ILHEVDKtLAGnLEESFPSLkR	(S)	ILHEVDKtL/t:Phosphor	874.1065	2496.346
ILHEVDKtLAGnLEESFPSLkR	(S)	ILHEVDKtL/t:Phosphor	874.1065	2496.346
ILHEVDKTLAGNLEESFPSLkVQT	(-)	k:Acetyl	904.1571	2668.419
ILHEVDKVLADYLE	(E)		552.9601	1656.884
ILHEVDKVLADYLE	(E)		552.9596	1656.884
ILHEVDKVLADYLE	(E)		552.959	1656.884
ILHEVDKVLADYLE	(E)		552.9603	1656.884
ILHEVDkVLADYLEENFPSLKEK	(H)	k:Carbamyl	555.2904	2729.44
ILHEVDkVLADYLEENfPSLKEK	(H)	n:Deamida	925.1369	2729.44
ILHEVDkVLADYLEENFPSLKEK	(H)	ILHEVDkVL k:Carbamyl	555.2842	2729.44
ILHEVDkVLADyLEENFPSLKEK	(H)	ILHEVDkVL k:Acetyl,y:f	724.1028	2729.44
ILHEVDkVLADYLEENFPSLKEK	(H)	k:Carbamyl	555.2862	2729.44
ILHEVDkVLADYLEENfPSLKEK	(H)	ILHEVDkVL n:Deamida	925.1382	2729.44
ILHEVDkVLADYLEENfPSLKEK	(H)	ILHEVDkVL n:Deamida	925.1383	2729.44
ILHEVDkVLADyLEENFPSLKEK	(H)	k:Acetyl,y:f	579.4835	2729.44
ILHEVDkVLADYLEENfPsLKEVALSACGFK	(G)	C:Carbamic	610.6434	3534.819
ILHEVDnVLADDLQESFPTLkDQS	(-)	n:Deamida	693.3401	2726.352
ILILGVDSQR	(W)		371.894	1113.663
ILIVGTEAVDLNFPIQAIQGGHDMWKAYR	(D)		814.687	3255.698
ILKDILCE	(F)	C:Carbamic	502.2757	1003.549
ILKDILCEFLSNI	(F)	C:Carbamic	526.6153	1577.861
ILkDILCEFLSNIFQALTK	(E)	C:Carbamic	577.813	2266.252
ILKDILCEFLsNIFQALTkETVVQGvK	(E)	ILKDILCEFL: C:Carbamic	808.1815	3106.722
ILKDILCEFLsNIFQALTkETVVQGvK	(E)	ILKDILCEFL: C:Carbamic	808.173	3106.722
ILKDISCEFLsIIFQVLTkEtVAQGLK	(E)	C:Carbamic	814.1851	3093.727
ILkDISCEFLSnIFQALTkETVAQGLK	(E)	C:Carbamic	631.5455	3066.654
ILKDISCEFLSNIFQALTkETVT	(K)	C:Carbamic	890.8017	2670.406
ILKDIscEFLSNIFQALTkETVTK	(G)	ILKDIscEFL: C:Carbamic	576.4906	2798.501
ILKDISCEFLSNIFQVLTkETVAQGVKEG	(Q)	C:Carbamic	817.4507	3266.734

ILKDISCEFLSNIFQVLTKETVAQGVKEG	(Q)		C:Carbamic	817.4534	3266.734
ILKDISCEFLSNIFQVLTKETVAR	(G)		C:Carbamic	581.6935	2824.528
ILKDISCEFLSnILQALTKETVTQGLK	(E)		C:Carbamic	621.9383	3062.681
ILKDISCEFLSNILQALTKETVTQGLK	(E)		C:Carbamic	621.9479	3062.681
ILKDISCEFLSnILQALTKETVTQGLK	(E)		C:Carbamic	621.9304	3062.681
ILKDISCEFLSSIFQTLTK	(E)		C:Carbamic	762.4054	2243.199
ILKDISCEFLSSIFQTLTKETVAQGLKEGQLSKQKCSCVFQN	(K)		C:Carbamic	1193.115	7153.734
ILQEQK	(T)	ILQEQK		379.7222	758.441
ILREVDk	(A)		k:Acetyl	457.7689	872.52
ILREVDKA	(L)			472.2905	943.557
ILREVDKA	(L)			472.2837	943.557
ILREVDKTLAGNLE	(E)			524.29	1570.88
ILRVCQYHR	(E)		C:Carbamic	415.5568	1244.668
ILRVCQYHR	(E)		C:Carbamic	415.5538	1244.668
IQEHPAIYDSICFIMSSSTNVDLLVKVGEVVDK	(L)		C:Carbamic	618.6512	3706.871
IREHPAIYDSMCFIMSSSTNVDLLVKVG	(E)		C:Carbamic	637.3263	3182.568
IREnPAIYDSICFIMSSSTnVDLLVK	(V)		C:Carbamic	996.4893	2985.506
IRENPAVY	(E)			481.2564	961.51
IRENPAVYDSI	(C)			638.8226	1276.653
IRENPAVYDSI	(C)			638.8233	1276.653
IRENPAVYDSI	(C)			638.8256	1276.653
IRENPAVYDSICFI	(M)		C:Carbamic	848.9159	1696.836
IRENPAVYDSICFI	(M)		C:Carbamic	848.9195	1696.836
IRENPAVYDSICFI	(M)		C:Carbamic	848.9076	1696.836
IRENPsVYVSFCFImSSSTsADLLVKVGEVVDK	(L)	IRENPsVYV	C:Carbamic	1284.926	3676.86
IREYPAIYDSICFIMSSSTNVDLLVKVGEVVDKFLDLDEKLM	(Q)		C:Carbamic	876.4383	6129.143
IRQQTsVCPNLCFIMSSSTNTDLEK	(V)		C:Carbamic	761.3643	3042.469
ISCEFLSSIFQTLTK	(E)		C:Carbamic	591.9802	1773.909
ISCEFLSSIFQTLTK	(E)		C:Carbamic	591.979	1773.909
ISCEFLSSIFQTLTK	(E)		C:Carbamic	591.9803	1773.909
ISCEFLSSIFQTLTK	(E)		C:Carbamic	591.9841	1773.909
ISCEFLSSIFQTLTK	(E)		C:Carbamic	591.9794	1773.909
ISCEFLSSIFQTLTK	(E)		C:Carbamic	591.9818	1773.909
ISCEFLSSIFQTLTK	(E)		C:Carbamic	591.9796	1773.909
ISCEFLSSIFQTLTK	(E)		C:Carbamic	591.979	1773.909
ISDAREAVQKFTGHGAEDSRADQFANEWGR	(S)			670.5321	3348.574
ISDAREKSQRITDLFK	(F)			636.3454	1907.034
ISDAREKSQRITDLFK	(F)			636.3439	1907.034
ISDAREKSQRITDLFK	(F)			636.3473	1907.034
ISDAREKSQRITDLFK	(F)			636.343	1907.034
ISDAREKSQRITDLFK	(F)			636.3463	1907.034
ISDAREKSQRITDLFK	(F)			636.3464	1907.034
ISDAREKSQRITDLFK	(F)			636.3435	1907.034
ISDAREKSQRITDLFK	(F)			636.3435	1907.034
ISDAREKSQRITDLFK	(F)			636.3449	1907.034
ISDAREKSQRITDLFK	(F)			636.3545	1907.034
ISDAREKSQRITDLFK	(F)			636.3408	1907.034

ISDGRENFQRFTDRFSFGGSGR	(G)		634.8181	2536.208
ISDLDHCANRVLMYGSELDA	(D)	C:Carbamic	760.3447	2279.043
ITDLIKYGDS	(G)		562.7987	1124.583
ITDLIKYGDSGHGVEDsK	(A)	s:Phosphor	671.9899	1933.95
ITDLIKYGDSGHGVEDsK	(A)	s:Phosphor	671.9834	1933.95
ITDLIKYGDSGHGVEDsK	(A)	s:Phosphor	671.9856	1933.95
ITDLIKYGDSGHGVEDsK	(A)	s:Phosphor	671.9858	1933.95
ITDLIKYGDSGHGVEDSK	(A)	ITDLIKYGDS:s:Phosphor	671.9858	1933.95
ITDLIKYGDSGHGVEDsK	(A)	s:Phosphor	671.9871	1933.95
ITDLIKYGDSGHGVEDsK	(A)	s:Phosphor	671.9823	1933.95
ITDLIKYGDSGHGVEDsK	(A)	s:Phosphor	671.9814	1933.95
ITDLLK	(F)	ITDLLK ITDLIK	351.7246	702.44
ITDLLK	(F)	ITDLLK ITDLIK	351.7235	702.44
ITDLLK	(F)	ITDLLK ITDLIK	351.7256	702.44
ITDLLK	(F)	ITDLLK ITDLIK	351.7273	702.44
ITDLLK	(F)	ITDLLK ITDLIK	351.727	702.44
ITDLLK	(F)	ITDLLK ITDLIK	351.7256	702.44
ITDLLK	(F)	ITDLLK ITDLIK	351.7228	702.44
ITDLLK	(F)	ITDLLK ITDLIK	351.7241	702.44
ITDLLK	(F)	ITDLLK ITDLIK	351.7241	702.44
ITDLLK	(F)	ITDLLK ITDLIK	351.7233	702.44
ITDLLK	(F)	ITDLLK ITDLIK	351.7246	702.44
ITDLLK	(F)	ITDLLK ITDLIK	351.7232	702.44
ITDLLK	(F)	ITDLLK ITDLIK	351.7245	702.44
ITDLLK	(F)	ITDLLK ITDLIK	351.727	702.44
ITDLLK	(F)	ITDLLK ITDLIK	351.726	702.44
ITDLLK	(F)	ITDLLK ITDLIK	351.723	702.44
ITDLLR	(F)		365.7257	730.446
ITDLLRFGDS	(G)		568.8053	1136.595
ITDRLK	(F)		373.2352	745.457
ITDRLKFGDS	(G)		576.2958	1151.605
ITGHGAEDSKADQAANEW	(G)		950.4142	1899.847
ITILREVDK	(A)		543.822	1086.652
ITILREVDK	(A)		362.8849	1086.652
ITSEFLADLCIHIPK	(E)	C:Carbamic	586.313	1756.93
IVFCSLVMGVTSESWHSFFK	(E)	C:Carbamic	787.716	2361.141
IVLALLVEANAQSGRFMK	(Q)		654.0518	1960.105
IVPCILEAAKQVRSEnPEGLDVYmHILQLLTTVDDGIEAIVC	(D)	C:Carbamic	773.539	5348.721
IVPCILEAAKQVRSENTEGLDVYMHILQLLTTVDDGIIQAIV	(Q)	C:Carbamic	761.7388	4565.399
IVPCLLEAAR	(Q)	C:Carbamic	381.2205	1141.64
IVPCLLEAAR	(Q)	C:Carbamic	381.2196	1141.64
IVPCLLEAAR	(Q)	C:Carbamic	381.2125	1141.64
IVPCVLEAAK	(Q)	C:Carbamic	571.3176	1099.618
IVPCVLEAAK	(Q)	C:Carbamic	571.3116	1099.618
IVPCVLEAAKQIRSDNPVGLDVYMHILQLLTTVD	(D)	C:Carbamic	956.0106	3821.034
IVPCVLEAAKQVRSEnLEGLDVYMHILQLLTTVDDGMK	(A)	C:Carbamic	869.0514	4298.223
IVPCVLEAAKQVRSEnLEGLDVYMHILQLLTTVDDGMK	(A)	C:Carbamic	869.0449	4298.223

IVPCVLEAAKQVRSEnLEGLDVYMHILQLLTTVDDGMk	(A)	C:Carbamic	869.0601	4298.223
IVPCVLEAAKQVRSEnLEGLDVYMHILQLLTTVDDGMk	(A)	C:Carbamic	869.0412	4298.223
IVPCVLEAAKQVRSEnLEGLDVYMHILQLLTTVDDGMk	(A)	C:Carbamic	869.0577	4298.223
IVPCVLEAAKQVRSEnLEGLDVYMHILQLLTTVDDGMk	(A)	C:Carbamic	869.0651	4298.223
IVPCVLEAAKQVRSEnLEGLDVYMHILQLLTTVDDGMk	(A)	C:Carbamic	1086.054	4298.223
IVPCVLEAAKQVRSEnLEGLDVYMHILQLLTTVDDGMk	(A)	C:Carbamic	869.2465	4298.223
IVPCVLEAAKQVRSEnLEGLDVYMHILQLLTTVDDGMk	(A)	C:Carbamic	869.0524	4298.223
IVPCVLEAAKQVRSEnLEGLDVYMHILQLLTTVDDGMk	(A)	C:Carbamic	869.0661	4298.223
IVPCVLEAAKQVRSEnLEGLDVYMHILQLLTTVDDGMk	(A)	C:Carbamic	869.0385	4298.223
IVsCVLEAAK	(Q)	C:Carbamic	585.2952	1089.597
IVSPENTKSR	(S)		377.5469	1130.616
IVSPENTKSR	(S)		565.8075	1130.616
IWDmsMDHDVALFLQEFnAPEILLGVMAK	(S)	m:Oxidized	695.5305	3333.636
IWDMsmDHDVALFLQEFnAPEILLGVMAK	(S)	s:Phosphor	695.5286	3333.636
IWDMsMDHDVALFLQEFnAPEILLGVMAK	(S)	s:Phosphor	1138.867	3333.636
IWDMsMDHDVALFLQEFnAPEILLGVMAksK	(C)	n:Deamida	918.951	3548.763
KAnWIGADK	(Y)	n:Deamida	502.2649	1002.537
KANWIGADKYFHA	(R)		507.5842	1520.764
kAnWIGADkYFHAR	(G)	k:Acetyl,n:l	881.4327	1676.866
KDGAEDGQLEtLAEITAEFLADLCLDISKDTVADLmNK	(G)	KDGAEDGC:C:Carbamic	607.8673	4153.02
KFDLtQDYFHLK	(I)	t:Phosphor	545.6001	1554.795
KFDLTQDyFHLK	(I)	KFDLTQDyf y:Phosphor	545.6006	1554.795
KFDLTQDyFHLK	(I)	KFDLTQDyf y:Phosphor	545.6024	1554.795
KFDLtQDYFHLK	(I)	t:Phosphor	545.6016	1554.795
KFDLTQDyFHLK	(I)	KFDLTQDyf y:Phosphor	545.6017	1554.795
KFDLTQDyFHLK	(I)	KFDLTQDyf y:Phosphor	545.6024	1554.795
KNLLPLYCSVVKDFLKVLEADKALVDNLEKDFPSLK	(A)	C:Carbamic	1075.571	4299.346
KNLPLLSKYCGYREDNIPQLEDVSNFLKERTGFSIR	(P)	C:Carbamic	1075.809	4300.218
KNLPLLSKYCGYREDNIPQLEDVSNFLKERTGFSIR	(P)	C:Carbamic	1075.813	4300.218
KNLPLLSKYCGYREDNIPQLEDVSNFLKERTGFSIR	(P)	C:Carbamic	1075.809	4300.218
KNLPLLSKYCGYREDNIPQLEDVSNFLKERTGFSIR	(P)	C:Carbamic	1075.809	4300.218
KNSDKYFHARGNYDAAQRGPGGAWAAKVISDAREGFKF	(M)		600.1723	4195.108
KPENSVESNTEETKKSDDLQEDFHLKILKDISCEF	(L)	C:Carbamic	690.6872	4139.012
KVISNARETIQGITDPLFKGMTRDQVREDSK	(A)		589.653	3532.854
LADETPRLFPSLR	(S)		505.6112	1514.833
LADETPRLFPSLR	(S)		505.6073	1514.833
LCQADDPPIIVQEQTVLASIFSVLSAMYASRVEQEYLKIEI	(S)	C:Carbamic	962.9252	4810.505
LDAIGETIYSKHWIFSTLTRLINMVSEHSEENTEGQMQLSI	(V)	C:Carbamic	819.104	5727.641
LDLPGLK	(R)		378.237	755.466
LDLPGLK	(R)		378.2367	755.466
LDLPGLK	(R)		378.2375	755.466
LDLPGLK	(R)		378.2388	755.466
LDVYMHILQLLTTVDDGIQAIVQSPDTGK	(D)		637.5451	3183.661
LEESFPSLK	(V)		525.2841	1049.551
LEESFPSLK	(V)		525.2774	1049.551
LEESFPSLK	(V)		525.2805	1049.551
LEESFPSLK	(V)		525.2821	1049.551

LENVEHCQKK	(P)	C:Carbamic	428.8878	1284.637
LENVEHCQKK	(P)	C:Carbamic	428.8859	1284.637
LESLQSTQK	(A)		517.2751	1033.552
LESLQSTQK	(A)		517.2771	1033.552
LFDLDEELmGSWITSSSEnKEDDDENQLDVIFCLLEAAk	(Q)	LFDLDEELn C:Carbamic	956.8396	4679.1
LFDLDEELMLnWIKnGTCRSVGPSVDDSPPEELPDFK	(I)	C:Carbamic	834.3954	4165.973
LFDLDEELMLnWIKnGTCRSVGPSVDDSPPEELPDFK	(I)	C:Carbamic	834.3912	4165.973
LFDLDEkLmLDWIRsGAAAPLDQPQEDSEEQPVFK	(I)	k:Acetyl,m:	1043.006	4030.974
LFDLDEkLmLEWIK	(N)	k:Carbamyl	617.9978	1792.955
LFDLDEkLmLEWVRNGAAQPLDQPQEESEEQPVFR	(L)	m:Oxidized	835.4179	4157.028
LFDLDETLMLD	(W)		662.8192	1324.634
LFDLDETLMLD	(W)		662.8168	1324.634
LFDLDETLMLD	(W)		662.8172	1324.634
LFPGLLFCSLVLGVsGQWYSFVSEAAQGAWDMWRAYSc	(E)	LFPGLLFCsI C:Carbamic	783.7032	4601.188
LFPsLRSCFK	(S)	C:Carbamic	627.8436	1254.666
LFTGIVFCsLVMGVTSEnWFSFFkEALQGAGDLGRAYWN	(R)	LFTGIVFCsI C:Carbamic	810.0992	5499.693
LFTGIVFCsLVMGVTSESWSFFk	(E)	C:Carbamic	953.1398	2798.404
LFTGIVFCsLVMGVTSESWSFFk	(E)	C:Carbamic	953.1445	2798.404
LFTGIVFCsLVMGVTSESWSFFk	(E)	C:Carbamic	953.121	2798.404
LFTGIVFCsLVMGVTSESWSFFkEALQGVGDmGR	(A)	C:Carbamic	794.9896	3911.928
LFTGLIFcSLVLGVHSQWLSFLGEAYEGKTHG	(G)	C:Carbamic	892.4633	3566.814
LFTGLIFcSLVLGVsSQWYSFIGEAAQGAWDMYRAYSDM	(Y)	LFTGLIFcSL C:Carbamic	827.7328	4881.34
LFTGLILcSLVLGVHSQWWSFFGEAYEGAK	(D)	LFTGLILcSL C:Carbamic	708.3419	3415.718
LFTGLILcSLVLGVHSQWWSFFGEAYEGAK	(D)	LFTGLILcSL C:Carbamic	708.5406	3415.718
LFTGLVFCsLVLGVsSEWYSFLGEAAQGAWDMWRAYSD	(Y)	LFTGLVFCsI C:Carbamic	810.0857	5567.617
LFVAGVLLILIVETnAQWYK	(F)	n:Deamida	570.069	2276.305
LGEAAR	(G)		308.6745	616.341
LGEAAR	(G)		308.6745	616.341
LGEAAR	(G)		308.6746	616.341
LGEAAR	(G)		308.6754	616.341
LGEAAR	(G)		308.6751	616.341
LGEAAR	(G)		308.6745	616.341
LGEAAR	(G)		308.6744	616.341
LGEVVDKLF	(D)	LGEVVDKLF IGEVDKL	510.2955	1019.577
LGEVVDKLF	(D)	LGEVVDKLF IGEVDKL	510.2977	1019.577
LGEVVDKLF	(D)	LGEVVDKLF IGEVDKL	510.2971	1019.577
LGEVVDKLF	(D)	LGEVVDKLF IGEVDKL	510.2967	1019.577
LGEVVDKLF	(D)	LGEVVDKLF IGEVDKL	510.296	1019.577
LGEVVDKLF	(D)	LGEVVDKLF IGEVDKL	510.2908	1019.577
LGEVVDKLF	(D)	LGEVVDKLF IGEVDKL	510.294	1019.577
LGEVVDKLF	(D)	LGEVVDKLF IGEVDKL	510.2989	1019.577
LGEVVDKLF	(D)	LGEVVDKLF IGEVDKL	510.2908	1019.577
LGEVVDKLF	(D)	LGEVVDKLF IGEVDKL	510.2921	1019.577
LGEVVDKLF	(D)	LGEVVDKLF IGEVDKL	510.2964	1019.577
LGEVVDKLF	(D)	LGEVVDKLF IGEVDKL	510.2989	1019.577
LGEVVDKLF	(D)	LGEVVDKLF IGEVDKL	510.2971	1019.577
LGEVVDKLF	(D)	LGEVVDKLF IGEVDKL	510.3024	1019.577

LGEVVDKLF	(D)	LGEVVDKLF IGEVDKLF	510.294	1019.577
LGEVVDKLFDLDEKLMLEWIRHGAVQPLDPPQEDSE	(E)		1041.006	4161.085
LGEVVDKLFDLDEKLMLEWIRHGAVQPLDPPQEDSE	(E)		1041.007	4161.085
LGEVVDKLFDLDEKLMLEWIRHGAVQPLDPPQEDSE	(E)		1041.007	4161.085
LGEVVDKLFDLDEKLMLEWIRHGAVQPLDPPQEDSE	(E)		1041.006	4161.085
LGsNSRPQVIHPPRPPK	(V)	LGsNSRPQ`s:Phosphor	490.7721	1880.061
LGsNSRPQVIHPPRPPK	(V)	LGsNSRPQ`s:Phosphor	490.7697	1880.061
LGsNSRPQVIHPPRPPK	(V)	LGsNSRPQ`s:Phosphor	654.0185	1880.061
LGVNSRSWFsFLGEAYDGARDMWRAYSMDKEANYINAI	(G)		1217.583	6083.815
LGVSSQGWGTFLEAGQGTKDMWRAYR	(D)		1019.832	3057.511
LHERKSVLVQAFSVLQALYRCQDQWCSR	(S)	C:Carbamic	580.4779	3477.763
LHEVDKTLADDLEKSFPSLK	(A)		762.3973	2285.202
LHEVDKTLADDLEKSFPSLK	(A)		762.4081	2285.202
LHEVDKTLADDLEKSFPSLK	(A)		762.4039	2285.202
LHFALmLLRtEKPWIK	(M)	m:Oxidized	698.0513	1996.157
LHFALmLLRtEKPWIK	(M)	m:Oxidized	698.0547	1996.157
LHFALmLLRtEKPWIK	(M)	m:Oxidized	698.0521	1996.157
LHFALmLLRtEKPWIK	(M)	m:Oxidized	698.0521	1996.157
LHFALmLLRtEKPWIK	(M)	m:Oxidized	698.0525	1996.157
LHFALmLLRtEKPWIK	(M)	m:Oxidized	698.0526	1996.157
LHFALmLLRtEKPWIK	(M)	m:Oxidized	698.0526	1996.157
LHFALmLLRtEKPWIK	(M)	m:Oxidized	698.0522	1996.157
LIHmVSELSEENPEAQVk	(L)	m:Oxidized	704.3583	2053.027
LIQDVA	(L)		329.6983	658.377
LIQDVA	(L)		329.698	658.377
LIQDVA	(L)		329.6983	658.377
LIQDVA	(L)		329.6978	658.377
LIQDVA	(L)		329.6978	658.377
LIQDVA	(L)		329.6917	658.377
LIQDVA	(L)		329.6978	658.377
LIQIVSPEnTkSSSDDEEQQMELDEEMENEICRVWDMSM	(S)	C:Carbamic	1214.549	7238.28
LIQIVSPENTkSSSDDEEQQMELDEEMENEICRVWDMSM	(S)	C:Carbamic	1457.058	7238.28
LIQIVSPENTkSSSDDEEQQMELDEEMENEICRVWDMSM	(S)	C:Carbamic	1214.389	7238.28
LIQIVSPENTkSSSDDEEQQMELDEEMENEICRVWDMSM	(S)	C:Carbamic	1214.219	7238.28
LISRSR	(V)		366.2367	731.452
LISRSR	(V)		366.2337	731.452
LISRSRV	(Y)		415.7563	830.521
LISRSRVYLQGLIDY	(Y)		599.3298	1796.006
LKVLREADESLADELMGNFPSLK	(V)		859.1119	2575.344
LKVLREADESLADELMGNFPSLK	(V)		859.1113	2575.344
LLADDLEK	(D)		458.7545	916.499
LLADDLEK	(D)		458.7525	916.499
LLADDLEK	(D)		458.7528	916.499
LLADDLEK	(D)		458.7557	916.499
LLADDLEK	(D)		458.755	916.499
LLADDLEK	(D)		458.7538	916.499
LLADDLEkDLPsLk	(A)	k:Carbamyl	868.4359	1569.873

LLADDEKDLpLk	(A)	k:CarbamyI	868.4424	1569.873
LLADDEKDLpLk	(A)	k:CarbamyI	868.4374	1569.873
LLASILSVLSAMFASETQQEYVNIGKNR	(A)		514.6194	3082.624
LLASILSVLSAMFASETQQEYVNIGKNR	(A)		514.6202	3082.624
LLASILSVLSAMFASETQQEYVNIGKNR	(A)		514.6201	3082.624
LLASILSVLSAMFASETQQEYVNIGKNR	(A)		514.617	3082.624
LLASILSVLSAMFASETQQEYVNIGKNR	(A)		514.6178	3082.624
LLASILSVLSAMFASETQQEYVNIGKNR	(A)		514.6201	3082.624
LLASILSVLSAMFASETQQEYVNIGKNR	(A)		514.6201	3082.624
LLASILSVLSAMFASETQQEYVNIGKNR	(A)		514.6189	3082.624
LLEAVK	(Q)		336.7219	672.429
LLFDLVCHEFCQSDPPPIILQEQTVLASAFSVLSAIYASQT	(L)	C:Carbamic	1424.539	7118.538
LLGRGAEDTLA	(D)		558.3166	1115.605
LLGRGAEDTLAD	(Q)		410.8826	1230.632
LLGRGAEDTLAD	(Q)		410.8823	1230.632
LLGRGAEDTLAD	(Q)		410.8845	1230.632
LLGRGAEDTLAD	(Q)		615.8242	1230.632
LLGRGAEDTLAD	(Q)		410.8818	1230.632
LLGRGAEDTLAD	(Q)		615.8249	1230.632
LLGRGAEDTLAD	(Q)		615.8214	1230.632
LLIDSLIRVLQNMEQCQK	(K)	C:Carbamic	734.4024	2201.178
LLIDSLIRVLQNMEQCQK	(K)	C:Carbamic	734.4062	2201.178
LLIDSLIRVLQNMEQCQK	(K)	C:Carbamic	734.4024	2201.178
LLIDSLIRVLQNMEQCQK	(K)	C:Carbamic	734.4001	2201.178
LLIGILFCT	(L)	C:Carbamic	525.2971	1049.606
LLIGILFCT	(L)	C:Carbamic	525.3037	1049.606
LLLAGLALILIVGTEAVDLnFPIQAIQGGHDMWKAYRDLk	(K)	LLLAGLALIL n:Deamida	1473.796	4376.42
LLLAGLALILIVGTEAVDLnFPIQAIQGGHDMWkAYRDLK	(K)	LLLAGLALIL n:Deamida	1473.789	4376.42
LLLTCLSHk	(D)	C:Carbamic	564.311	1084.618
LLLTCLSHk	(D)	C:Carbamic	563.8168	1084.618
LLLTCLSHk	(D)	C:Carbamic	563.8168	1084.618
LLLTCLSHk	(D)	C:Carbamic	564.311	1084.618
LLLTCLSQAEEVAS	(V)	C:Carbamic	468.9181	1404.74
LLLtCLSQAEEVASVWVERIR	(E)	LLLtCLSQAIE C:Carbamic	808.4063	2343.285
LLLTCLSQAEEVASVWVERIR	(E)	C:Carbamic	808.4295	2343.285
LLLTCLsQAEEVASVWVERIR	(E)	LLLTCLsQAIE C:Carbamic	808.4063	2343.285
LLLTCLsQAEEVASVWVERIR	(E)	LLLTCLsQAIE C:Carbamic	808.4063	2343.285
LLLTCLsQAEEVASVWVERIR	(E)	LLLTCLsQAIE C:Carbamic	808.4223	2343.285
LLLtCLSQAEEVASVWVERIR	(E)	LLLtCLSQAIE C:Carbamic	808.4068	2343.285
LLLTCLsQAEEVASVWVERIR	(E)	LLLTCLsQAIE C:Carbamic	808.4071	2343.285
LLLtCLSQAEEVASVWVERIR	(E)	C:Carbamic	808.4091	2343.285
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2909	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2927	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2935	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2936	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2921	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2931	1075.618

LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2927	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2927	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2909	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2896	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2901	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.296	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2899	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2911	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.299	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2912	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2931	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2918	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2955	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2949	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2888	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2906	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.294	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2928	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2923	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2924	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2908	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.294	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2935	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2901	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2935	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.292	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2933	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2927	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2901	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2901	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2924	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2928	1075.618
LLLTCLSQk	(D)	LLLTCLSQk C:Carbamic	559.8062	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2949	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2921	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2931	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2924	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2925	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.291	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.293	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2947	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.2947	1075.618
LLLtCLSQK	(D)	LLLtCLSQK C:Carbamic	578.296	1075.618
LLLTCLSQKDVCSLWLQR	(I)	LLLTCLSQKI C:Carbamic	579.0426	2233.183
LLLTCLSQKDVCSLWLQRIRRQQTSMCSNLCFI	(M)	C:Carbamic	795.1967	3971.979
LLLTCLSQP	(Q)	C:Carbamic	522.8002	1044.576
LLLTCLSQPQVANIWIERR	(E)	C:Carbamic	808.4478	2423.359

LLLTCLSQPQVANIWIERIR	(E)	C:Carbamic	808.4565	2423.359
LLLTCLSQPQVANIWIERIR	(E)	C:Carbamic	808.464	2423.359
LLLTCLSQPQVANIWIERIREnPAVYEsICFIMSSSTnVDLLV(V)		LLLTCLSQP C:Carbamic	868.0951	5120.662
LLLTCLSQPQVANVWVER	(I)	C:Carbamic	532.2875	2126.143
LLLTCLSQPQVANVWVER	(I)	C:Carbamic	532.29	2126.143
LLLTCLSQPQVANVWVER	(I)	C:Carbamic	532.2962	2126.143
LLLTCLSQPQVANVWVER	(I)	C:Carbamic	532.2949	2126.143
LLLTCLSQPQVANVWVER	(I)	C:Carbamic	532.2865	2126.143
LLLTCLSQPQVANVWVER	(I)	C:Carbamic	532.298	2126.143
LLLTCLSQPQVANVWVER	(I)	C:Carbamic	532.2985	2126.143
LLLTCLSQPQVANVWVERIRENPAVYDSICFIMSSSTNVDI(D)		C:Carbamic	795.4235	5561.885
LLLTCLsQTEVANVWVERIREHPAIYDSICFIMSSSTnVDLL(V)		LLLTCLsQTE C:Carbamic	867.757	5120.626
LLLTCLSQTEVASV	(W)	C:Carbamic	767.4108	1533.819
LLPLYCSVVKDFLK	(V)	C:Carbamic	565.6613	1694.955
LLSFLGEAAR	(G)		538.8106	1076.61
LLSFLGEAAR	(G)		538.8135	1076.61
LLSFLGEAAR	(G)		538.8026	1076.61
LLSFLGEAAR	(G)		538.8126	1076.61
LLSFLGEAAR	(G)		538.8133	1076.61
LLSFLGEAAR	(G)		538.8087	1076.61
LLSFLGEAAR	(G)		538.8124	1076.61
LLSFLGEAAR	(G)		538.8081	1076.61
LLSFLGEAAR	(G)		538.8119	1076.61
LLSFLGEAAR	(G)		538.8138	1076.61
LLSFLGEAAR	(G)		538.8106	1076.61
LLSFLGEAAR	(G)		538.8111	1076.61
LLSFLGEAAR	(G)		538.8141	1076.61
LLSFLGEAAR	(G)		538.8098	1076.61
LLSFLGEAAR	(G)		538.7983	1076.61
LLSFLGEAAR	(G)		538.8097	1076.61
LLSFLGEAAR	(G)		538.8022	1076.61
LLSFLGEAAR	(G)		538.8122	1076.61
LLSFLGEAAR	(G)		538.8115	1076.61
LLSFLGEAAR	(G)		538.8123	1076.61
LLSFLGEAAR	(G)		538.8091	1076.61
LLSFLGEAAR	(G)		538.8108	1076.61
LLSFLGEAAR	(G)		538.8097	1076.61
LLSFLGEAAR	(G)		538.8106	1076.61
LLSFLGEAAR	(G)		538.8104	1076.61
LLSFLGEAAR	(G)		538.8088	1076.61
LLSFLGEAAR	(G)		538.8145	1076.61
LLSFLGEAAR	(G)		538.8081	1076.61
LLSFLGEAAR	(G)		538.8112	1076.61
LLSFLGEAAR	(G)		538.8128	1076.61
LLSFLGEAAR	(G)		538.8116	1076.61
LLSFLGEAAR	(G)		538.8089	1076.61
LLSFLGEAAR	(G)		538.8117	1076.61

LLSFLGEAAR	(G)	538.8097	1076.61
LLSFLGEAAR	(G)	538.8112	1076.61
LLSFLGEAAR	(G)	538.8112	1076.61
LLSFLGEAAR	(G)	538.8112	1076.61
LLSFLGEAAR	(G)	538.8113	1076.61
LLSFLGEAAR	(G)	538.8097	1076.61
LLSFLGEAAR	(G)	538.8097	1076.61
LLSFLGEAAR	(G)	538.8121	1076.61
LLSFLGEAAR	(G)	538.8052	1076.61
LLSFLGEAAR	(G)	538.8091	1076.61
LLSFLGEAAR	(G)	538.8113	1076.61
LLSFLGEAAR	(G)	538.8097	1076.61
LLSFLGEAAR	(G)	538.8121	1076.61
LLSFLGEAAR	(G)	538.8128	1076.61
LLSFLGEAAR	(G)	538.8128	1076.61
LLSFLGEAAR	(G)	538.8103	1076.61
LLSFLGEAAR	(G)	538.8099	1076.61
LLSFLGEAAR	(G)	538.8085	1076.61
LLSFLGEAAR	(G)	538.8065	1076.61
LLSFLGEAAR	(G)	538.8097	1076.61
LLSFLGEAAR	(G)	538.8096	1076.61
LLSFLGEAAR	(G)	538.8116	1076.61
LLSFLGEAAR	(G)	538.8114	1076.61
LLSFLGEAAR	(G)	538.8095	1076.61
LLSFLGEAAR	(G)	538.809	1076.61
LLSFLGEAAR	(G)	538.8082	1076.61
LLSFLGEAAR	(G)	538.8097	1076.61
LLSFLGEAAR	(G)	538.8112	1076.61
LLSFLGEAAR	(G)	538.8082	1076.61
LLSFLGEAAR	(G)	538.8088	1076.61
LLSFLGEAAR	(G)	538.81	1076.61
LLSFLGEAAR	(G)	538.8123	1076.61
LLSFLGEAAR	(G)	538.8065	1076.61
LLSFLGEAAR	(G)	538.8112	1076.61
LLSFLGEAAR	(G)	538.8089	1076.61
LLSFLGEAAR	(G)	538.8128	1076.61
LLSFLGEAAR	(G)	538.8106	1076.61
LLSFLGEAAR	(G)	538.808	1076.61
LLSFLGEAAR	(G)	538.8121	1076.61
LLSFLGEAAR	(G)	538.8097	1076.61
LLSFLGEAAR	(G)	538.8097	1076.61
LLSFLGEAAR	(G)	538.8097	1076.61
LLSFLGEAAR	(G)	538.809	1076.61
LLSFLGEAAR	(G)	538.8092	1076.61
LLSFLGEAAR	(G)	538.8123	1076.61
LLSFLGEAAR	(G)	538.8097	1076.61
LLSFLGEAAR	(G)	538.807	1076.61

LLSFLGEAAR	(G)	538.8102	1076.61
LLSFLGEAAR	(G)	538.8085	1076.61
LLSFLGEAAR	(G)	538.8112	1076.61
LLSFLGEAAR	(G)	538.8085	1076.61
LLSFLGEAAR	(G)	538.8121	1076.61
LLSFLGEAAR	(G)	538.8082	1076.61
LLSFLGEAAR	(G)	538.8097	1076.61
LLSFLGEAAR	(G)	538.8065	1076.61
LLSFLGEAAR	(G)	538.8122	1076.61
LLSFLGEAAR	(G)	538.8065	1076.61
LLSFLGEAAR	(G)	538.8065	1076.61
LLSFLGEAAR	(G)	538.8092	1076.61
LLSFLGEAAR	(G)	538.8128	1076.61
LLSFLGEAAR	(G)	538.8065	1076.61
LLSFLGEAAR	(G)	538.8123	1076.61
LLSFLGEAAR	(G)	538.8113	1076.61
LLSFLGEAAR	(G)	538.8128	1076.61
LLSFLGEAAR	(G)	538.8116	1076.61
LLSFLGEAAR	(G)	538.8121	1076.61
LLSFLGEAAR	(G)	538.8061	1076.61
LLSFLGEAAR	(G)	538.8112	1076.61
LLSFLGEAAR	(G)	538.8077	1076.61
LLSFLGEAAR	(G)	538.8065	1076.61
LLSFLGEAAR	(G)	538.8089	1076.61
LLSFLGEAAR	(G)	538.8112	1076.61
LLSFLGEAAR	(G)	538.8121	1076.61
LLSFLGEAAR	(G)	538.8114	1076.61
LLSFLGEAAR	(G)	538.8052	1076.61
LLSFLGEAAR	(G)	538.8122	1076.61
LLSFLGEAAR	(G)	538.8128	1076.61
LLSFLGEAAR	(G)	538.8088	1076.61
LLSFLGEAAR	(G)	538.8096	1076.61
LLSFLGEAAR	(G)	538.8097	1076.61
LLSFLGEAAR	(G)	538.8082	1076.61
LLSFLGEAAR	(G)	538.8128	1076.61
LLSFLGEAAR	(G)	538.81	1076.61
LLSFLGEAAR	(G)	538.8106	1076.61
LLSFLGEAAR	(G)	538.8121	1076.61
LLSFLGEAAR	(G)	538.8139	1076.61
LLSFLGEAAR	(G)	538.8128	1076.61
LLSFLGEAAR	(G)	538.809	1076.61
LLSFLGEAAR	(G)	538.8103	1076.61
LLSFLGEAAR	(G)	538.8097	1076.61
LLSFLGEAAR	(G)	538.8052	1076.61
LLSFLGEAAR	(G)	538.8112	1076.61
LLSFLGEAAR	(G)	538.81	1076.61
LLSFLGEAAR	(G)	538.8121	1076.61

LLSFLGEAAR	(G)	538.8092	1076.61
LLSFLGEAAR	(G)	538.8114	1076.61
LLSFLGEAAR	(G)	538.8095	1076.61
LLSFLGEAAR	(G)	538.8112	1076.61
LLSFLGEAAR	(G)	538.8112	1076.61
LLSFLGEAAR	(G)	538.8085	1076.61
LLSFLGEAAR	(G)	538.8065	1076.61
LLSFLGEAAR	(G)	538.8112	1076.61
LLSFLGEAAR	(G)	538.8094	1076.61
LLSFLGEAAR	(G)	538.8113	1076.61
LLSFLGEAAR	(G)	538.8097	1076.61
LLSFLGEAAR	(G)	538.8121	1076.61
LLSFLGEAAR	(G)	538.8097	1076.61
LLSFLGEAAR	(G)	538.8052	1076.61
LLSFLGEAAR	(G)	538.809	1076.61
LLSFLGEAAR	(G)	538.8112	1076.61
LLSFLGEAAR	(G)	538.8112	1076.61
LLSFLGEAAR	(G)	538.809	1076.61
LLSFLGEAAR	(G)	538.8088	1076.61
LLSFLGEAAR	(G)	538.8106	1076.61
LLSFLGEAAR	(G)	538.8112	1076.61
LLSFLGEAAR	(G)	538.8128	1076.61
LLSFLGEAAR	(G)	538.8121	1076.61
LLSFLGEAAR	(G)	538.8065	1076.61
LLSFLGEAAR	(G)	538.8082	1076.61
LLSFLGEAAR	(G)	538.8112	1076.61
LLSFLGEAAR	(G)	538.8121	1076.61
LLSFLGEAAR	(G)	538.8085	1076.61
LLSFLGEAAR	(G)	538.8109	1076.61
LLSFLGEAAR	(G)	538.8141	1076.61
LLSFLGEAAR	(G)	538.8085	1076.61
LLSFLGEAAR	(G)	538.8112	1076.61
LLSFLGEAAR	(G)	538.8052	1076.61
LLSFLGEAAR	(G)	538.8089	1076.61
LLSFLGEAAR	(G)	538.8097	1076.61
LLSFLGEAAR	(G)	538.8101	1076.61
LLSFLGEAAR	(G)	538.8123	1076.61
LLSFLGEAAR	(G)	538.8112	1076.61
LLSFLGEAAR	(G)	538.8109	1076.61
LLSFLGEAAR	(G)	538.808	1076.61
LLSFLGEAAR	(G)	538.8128	1076.61
LLSFLGEAAR	(G)	538.8065	1076.61
LLSFLGEAAR	(G)	538.8069	1076.61
LLSFLGEAAR	(G)	538.8089	1076.61
LLSFLGEAAR	(G)	538.8085	1076.61
LLSFLGEAAR	(G)	538.8112	1076.61
LLSFLGEAAR	(G)	538.8097	1076.61

LLSFLGEAAR	(G)		538.8065	1076.61
LLSFLGEAAR	(G)		538.8112	1076.61
LLSFLGEAAR	(G)		538.8085	1076.61
LLSFLGEAAR	(G)		538.8097	1076.61
LLSFLGEAAR	(G)		538.8112	1076.61
LLSFLGEAAR	(G)		538.8112	1076.61
LLSFLGEAAR	(G)		538.8097	1076.61
LLSFLGEAAR	(G)		538.8065	1076.61
LLSFLGEAAR	(G)		538.8126	1076.61
LLSFLGEAAR	(G)		538.8096	1076.61
LLSFLGEAAR	(G)		538.8123	1076.61
LLSFLGEAAR	(G)		538.8112	1076.61
LLSFLGEAAR	(G)		538.8022	1076.61
LLSFLGEAAR	(G)		538.8097	1076.61
LLSFLGEAAR	(G)		538.8097	1076.61
LLSFLGEAAR	(G)		538.8128	1076.61
LLSFLGEAARG	(T)		567.3111	1133.631
LLSFLGEAARG	(T)		567.316	1133.631
LLSFLGEAARG	(T)		567.3129	1133.631
LLSFLGEAARG	(T)		567.3129	1133.631
LLSFLGEAARG	(T)		567.3222	1133.631
LLSFLGEAARG	(T)		567.308	1133.631
LLSFLGEAARG	(T)		567.3177	1133.631
LLSFLGEAARG	(T)		567.3222	1133.631
LLSFLGEAARG	(T)		567.308	1133.631
LLSFLGEAARG	(T)		567.308	1133.631
LLSFLGEAARGTWMIR	(A)		646.0105	1936.011
LLSFLGEAARGTWMIR	(A)		646.0123	1936.011
LLSTCLSHSEVATTWVERV	(Q)	C:Carbamic	730.0308	2188.107
LLTGLVFC	(S)	C:Carbamic	461.7584	922.507
LLTGLVFC	(S)	C:Carbamic	461.7529	922.507
LLTGLVFC	(S)	C:Carbamic	461.7515	922.507
LLTGLVFCSLVLGVNSRSWFS	(F)	C:Carbamic	785.7519	2355.253
LLTGLVFCSLVLGVNSRSWFSFLGEAYDGARD	(M)	C:Carbamic	888.1946	3549.784
LLTGLVFCSLVLGVNSRSWFSFLGEAYDGARD	(M)	C:Carbamic	888.1942	3549.784
LLTGLVFCSLVLGVNSRSWFSFLGEAYDGARD	(M)	C:Carbamic	888.1921	3549.784
LLTGLVFCSLVLGVNSRSWFSFLGEAYDGARD	(M)	C:Carbamic	888.1899	3549.784
LLTGLVFCSLVLGVSSr	(S)	LLTGLVFC C:Carbamic	634.3255	1821.03
LLVAVVLAAVAAG	(T)		633.4221	1265.819
LLVAVVLAAVAAGTEGAPGFWDITKPFSSFAKEAVQGA	(N)	k:Acetyl	814.687	5654.845
LLVGILLCSLVLGSSQS	(W)	C:Carbamic	620.0167	1858.072
LLVGILLCSLVLGSSQS	(W)	C:Carbamic	620.0167	1858.072
LLVGILLCSLVLGvsSQSWWTFLEAGQGtR	(D)	LLVGILLCSL C:Carbamic	895.4649	3418.856
LLVVLHERKSILVQAFSVLQALYRCQDQWCSR	(S)	C:Carbamic	653.5262	3916.084
LLWSKTVD	(M)		481.2714	961.535
LMEICVGILGNMACFQEICVSISNDkNIGQTLHCLYDLDP	(L)	C:Carbamic	965.2963	5663.775
LmEICVGILGNmACFQELCVSISNDKNIGR	(T)	C:Carbamic	695.5275	3441.646

LmLDWIRSGAAAPLDQPQEDSEEQPVFKIVPCVLEAAK	(Q)	C:Carbamic	871.0543	4251.146	
LmLEWIKNGAVQPLDPPQEDSEEQPVFKIVPCVLEAAK	(Q)	C:Carbamic	876.2478	4318.214	
LmLEWIKNGAVQPLDPPQEDSEEQPVFKIVPCVLEAAK	(Q)	C:Carbamic	876.2662	4318.214	
LmLEWIKNGAVQPLDPPQEDSEEQPVFKIVPCVLEAAK	(Q)	C:Carbamic	876.2623	4318.214	
LmLEWIKnGAVQPLDPPQEDSEEQPVFKIVPCVLEAAK	(Q)	C:Carbamic	876.4595	4318.214	
LMLEWIKnGAVQPLDPPQEDSEEQPVFKIVPCVLEAAK	(Q)	C:Carbamic	1080.561	4318.214	
LmLEWIKNGAVQPLDPPQEDSEEQPVFKIVPCVLEAAK	(Q)	C:Carbamic	876.2608	4318.214	
LmLEWIKNGAVQPLDPPQEDSEEQPVFKIVPCVLEAAK	(Q)	C:Carbamic	876.2576	4318.214	
LmLEWIKNGAVQPLDPPQEDSEEQPVFKIVPCVLEAAK	(Q)	C:Carbamic	876.2653	4318.214	
LmLEWIKNGAVQPLDPPQEDSEEQPVFKIVPCVLEAAK	(Q)	C:Carbamic	876.25	4318.214	
LmLEWIRHGAVQPLDPPQEDSEEQPVFK	(I)	m:Oxidized	837.4256	3288.636	
LmLEWIRHGAVQPLDPPQEDSEEQPVFK	(I)	m:Oxidized	837.4213	3288.636	
LMLEWIRHGAVQPLDPPQEDsEEQPVFKIVPCVLEAAK	(Q)	C:Carbamic	1134.577	4369.236	
LMLEWIRIGAVQALDQPQEDsEQQPVFRIVPCVLEAAK	(Q)	C:Carbamic	743.7187	4377.273	
LMLEWIRnAPAQPVDQAQENSEEQPAFR	(I)	n:Deamida	817.9106	3267.585	
LPGLKRSSHFSLLNNWDCR	(C)	C:Carbamic	575.7894	2300.172	
LPLCSALRRGAESPLR	(A)	C:Carbamic	599.3344	1795.996	
LQEKTVLASVFSVLCAIYASQTEQEYLKIEK	(V)	C:Carbamic	744.1854	3716.945	
LQGGSSGRGVEDSMADQEANRWGRSGKDPNRYRPKGL	(-)		756.691	4535.198	
LQGGSSGRGVEDSMADQEANRWGRSGKDPNRYRPKGL	(-)		756.7109	4535.198	
LQGWGLEVV	(F)		500.7725	1000.546	
LQGWGLEVVFLSFK	(N)		811.9393	1622.894	
LQGWGLEVVFLSFK	(N)		541.6331	1622.894	
LQGWGLEVVFLSFK	(N)		541.6268	1622.894	
LQGWGLEVVFLSFK	(N)		541.6295	1622.894	
LQGWGLEVVFLSFK	(N)		541.6276	1622.894	
LRDVTVFLFTLCPFGRVLSFPGTWDMLRAYNDMREANYI	(G)	C:Carbamic	955.8196	5729.84	
LREAGQGAKDMWRAYRDMKEANYKGADKYFHARGNY	(G)		1202.849	4808.307	
LREICVGILGnMACFQEICVsISNDKnLGEVLLHCLYDSDPF	(L)	LREICVGILC	C:Carbamic	819.6828	5649.752
LREICVGILGNmACFR	(E)	C:Carbamic	642.3276	1908.96	
LREICVGILGNmACFR	(E)	C:Carbamic	642.3259	1908.96	
LREICVGILGNMACFR	(E)	C:Carbamic	637.0014	1908.96	
LREICVGILGNmACFR	(E)	C:Carbamic	642.3252	1908.96	
LREICVGILGNmACFR	(E)	C:Carbamic	642.3244	1908.96	
LREICVGILGNMtCFQEICVSISSDKnLGEVLLHCLYDsDPP	(I)	LREICVGILC	C:Carbamic	818.9672	5565.72
LREICVGILGNMtCFQEICVSISSDKnLGEVLLHCLYDsDPP	(I)	LREICVGILC	C:Carbamic	818.9655	5565.72
LREICVGILGnMtCFQEICVSISSDKnLGEVLLHCLYDsDPP	(I)	LREICVGILC	C:Carbamic	818.9668	5565.72
LREICVGILGnmTCFQEICVSISSDKnLGEVLLHCLYDsDPP	(I)	LREICVGILC	C:Carbamic	809.8246	5565.72
LREICVGILGNMtCFQEICVSISSDKnLGEVLLHCLYDsDPP	(I)	LREICVGILC	C:Carbamic	818.9632	5565.72
LREICVGILGnMtCFQEICVSISSDKnLGEVLLHCLYDsDPP	(I)	LREICVGILC	C:Carbamic	818.9686	5565.72
LRTAGGAVGGVPPGAPGALALGCPSSPPQLPARPS	(S)	C:Carbamic	647.552	3233.721	
LSACGFKGNWIIQK	(P)	C:Carbamic	578.9827	1734.936	
LSEADPNLAEVTR	(T)		472.2519	1414.717	
LSEADPNLAEVTR	(T)		472.2475	1414.717	
LSFLGEAAR	(G)		482.2741	963.526	
LSFLGEAAR	(G)		482.2698	963.526	
LSFLGEAAR	(G)		482.2573	963.526	

LSFLGEAAR	(G)		482.2573	963.526
LSFLGEAAR	(G)		482.2687	963.526
LSFLGEAAR	(G)		482.2579	963.526
LSFLGEAAR	(G)		482.2579	963.526
LSFLGEAAR	(G)		482.2573	963.526
LSIGIIFCFLILGVnsREWLTfLK	(E)	C:Carbamic	584.9036	2839.594
LSIGIIFCFLILGVnsREWLTFLK	(E)	C:Carbamic	584.9124	2839.594
LSIGIIFCFLILGVnsREWLTFLkEAGQGAK	(D)	C:Carbamic	721.373	3480.908
LSIGIIFCSL	(V)	C:Carbamic	561.8099	1122.623
LSIGIIFCSL	(V)	C:Carbamic	561.8079	1122.623
LSIGIIFCSL	(V)	C:Carbamic	561.8117	1122.623
LSIGIIFCSL	(V)	C:Carbamic	561.8097	1122.623
LSKQKCSCAFQNLFPYNPVVEDFIKILHEVDKAVASDL EE (-)		C:Carbamic	826.8635	5781.955
LSQSEVASVWVERIREHPAIYDSMCFIMSSSTNVDLLVKV (L)		C:Carbamic	1217.591	6084.044
LSQTEVANVWVER	(I)		510.9378	1530.791
LSQTEVASVWVER	(I)		501.9277	1503.78
LStGIIFCFLILGVsSQR	(W)	LStGIIFCFLI C:Carbamic	724.3606	2011.104
LStGIIFCSLVLGVSQGWLTFLKAAGQGtKDMWK	(A)	LStGIIFCSL\ C:Carbamic	654.6785	3799.991
LTCLSQKDVCSLWLQRIRQQTSLCSNL CFIMSSSTR	(T)	C:Carbamic	626.1774	4377.139
LTCLSQKDVCSLWLQRIRQQTSLCSNL CFIMSSSTR	(T)	C:Carbamic	876.249	4377.139
LTCLSQKDVCSLWLQRIRQQTSLCSNL CFIMSSSTR	(T)	C:Carbamic	626.1774	4377.139
LTCLSQKDVCSLWLQRIRQQTSLCSNL CFIMSSSTR	(T)	C:Carbamic	730.3767	4377.139
LTCLSQKDVCSLWLQRIRQQTSLCSNL CFIMSSSTR	(T)	C:Carbamic	876.2434	4377.139
LTEICVGILGNIA	(C)	C:Carbamic	686.8725	1372.751
LTEICVGILGNIA	(C)	C:Carbamic	686.8725	1372.751
LTEICVGILGNIA	(C)	C:Carbamic	686.8708	1372.751
LTEICVGILGNIA	(C)	C:Carbamic	686.8708	1372.751
LTEICVGILGNIA	(C)	C:Carbamic	686.8703	1372.751
LtEICVGILGnmACFQDICmSISkDES LGQVLLQRLCDS DSf (L)		C:Carbamic	819.397	5573.676
LTEICVGILGnmACFQDICMSISkDES LGQVLLQRLC DS (L)		LTEICVGIL C:Carbamic	1418.437	5573.676
LTEICVGILGnmACFQDICmSISkDES LGQVLLQRLC DS (L)		LTEICVGIL C:Carbamic	819.2539	5573.676
LTKVEDFLK	(I)		546.8168	1092.63
LTKVEDFLK	(I)		546.8162	1092.63
LTKVEDFLK	(I)		546.8162	1092.63
LTKVEDFLK	(I)		546.8205	1092.63
LTKVEDFLK	(I)		546.8119	1092.63
LTKVEDFLK	(I)		546.821	1092.63
LTKVEDFLK	(I)		546.8202	1092.63
LTKVEDFLK	(I)		546.8218	1092.63
LTKVEDFLK	(I)		546.8213	1092.63
LTKVEDFLK	(I)		546.8172	1092.63
LTKVEDFLK	(I)		546.8184	1092.63
LVAVVVLAAVAAGTEGAPGFWDTITKPF SFAK	(E)		809.1879	3233.761
LVAVVVLAAVAAGTEGAPGFWDTITKPF SFAK	(E)		809.1856	3233.761
LVAVVVLAAVAAGTEGAPGFWDTITKPF SFAK	(E)		809.1895	3233.761
LVAVVVLAAVAAGTEGAPGFWDTITKPF SFAK	(E)		647.5512	3233.761
LVAVVVLAAVAAGTEGAPGFWDTITKPF SFAK	(E)		647.5516	3233.761

LVAVVVLAAVAAGTEGAPGFWDTITKPFSAK	(E)		809.185	3233.761
LVDKLFDLDEELMK	(T)		569.9596	1707.887
LVDNLEK	(D)		415.7351	830.462
LVLGVDSQRWFQFMK	(E)		618.6556	1853.973
LVLGVHSWFSFIGEAFGGAR	(D)		717.3799	2150.118
LVLGVHSWFSFIGEAFGGAR	(D)		717.3841	2150.118
LVLGVHSWFSFIGEAFGGAR	(D)		717.385	2150.118
LVLGVHSWFSFIGEAFGGAR	(D)		717.3905	2150.118
LVLGVHSWFSFIGEAFGGAR	(D)		717.3897	2150.118
LVLGVHSWFSFIGEAFGGAR	(D)		717.3777	2150.118
LVLGVHSWFSFIGEAFGGAR	(D)		717.3892	2150.118
LVLGVHSWFSFIGEAFGGAR	(D)		717.3768	2150.118
LVLGVHSWFSFIGEAFGGAR	(D)		717.3841	2150.118
LVLGVHSWFSFIGEAFGGAR	(D)		717.3633	2150.118
LVLGVHSWFSFIGEAFGGAR	(D)		717.3859	2150.118
LVLGVHSWFSFIGEAFGGAR	(D)		717.3854	2150.118
LVLGVHSWFSFIGEAFGGAR	(D)		717.3892	2150.118
LVLGVHSWFSFIGEAFGGAR	(D)		717.3825	2150.118
LVLGVHSWFSFIGEAFGGAR	(D)		717.3837	2150.118
LVLGVHSWFSFIGEAFGGAR	(D)		717.3841	2150.118
LVLGVHSWFSFIGEAFGGAR	(D)		717.3854	2150.118
LVLGVSSREWFTFLK	(E)		594.6581	1781.995
LVLGVSSREWFTFLK	(E)		594.6581	1781.995
LVPLHCPDTGKDIWNLLFDLVCHEFC	(Q)	C:Carbamic	800.3711	3198.521
LYCSVVKDFLKVLEADKALVDNLEKDFPSLK	(A)	C:Carbamic	623.1802	3733.987
LYPTHACREYLkNLPLLSk	(Y)	C:Carbamic	813.4302	2316.253
MDRNPSPPPPGRDKEEEEVAGGDCIGSTVYSKHWLFG\	(V)	C:Carbamic	981.2087	6862.29
MDRNPSPPPPGRDQEEEEVAGGDCIGStVYSK	(H)	C:Carbamic	909.3761	3474.554
MDRNPSPPPPGRDQEEEEVAGGDCIGStVYSK	(H)	C:Carbamic	909.3746	3474.554
MDRNPSPPPPGRDQEEEEVAGGDCIGSTVYsK	(H)	MDRNPSP C:Carbamic	909.3686	3474.554
MEEGKYHSNLPLIDSLI	(R)		653.6753	1958.989
MEGFFSFVHEAFQGAGDMWRAYTDMKEANWKKSDKY	(N)		697.4759	4876.228
mEKNLPLIGSLIRVLHNMEDCQQR	(S)	C:Carbamic	984.8293	2894.48
mEKNLPLIGSLIRVLHNMEDCQQR	(S)	C:Carbamic	984.8289	2894.48
mENGCTIDLPLIGtLIRVLQnMEHCEkR	(S)	C:Carbamic	870.9092	3340.663
MKLFTGLILCSLVLGVHSQWMSFLGEAYEGAKDMWRA	(Y)	C:Carbamic	1062.035	4245.116
MKLFTGLILCSLVLGVHSQWWSFFGEAYEGAK	(D)	MkLFTGLIL C:Carbamic	744.3856	3674.854
MKLFTGLILCSLVLGVHSQWWSFFGEAYEGAK	(D)	MkLFTGLIL C:Carbamic	760.1834	3674.854
MKLLLAGIVLIFMAGsEAQWYnYPVQAAQGAGDMWRA	(K)	MkLLLAGIV k:Acetyl,s:F	694.9132	4735.333
MKLLLAGIVLIFMAGsEAQWYnYPVQAAQGAGDMWRA	(K)	MkLLLAGIV k:Acetyl,s:F	694.9133	4735.333
MKLLLAGIVLIFMAGsEAQWYNYPVQAAQGAGDMWRA	(K)	MkLLLAGIV k:Carbamyl	694.9033	4735.333
MKLLAVLVMFMVVEAQAQWYRFPGEAAGG	(A)		1109.236	3325.73
mKLLTGLVFCSLVLGVHSWFSFIGEAFGGARDMWR	(A)	mKLLTGLV C:Carbamic	668.1707	3988.022
MKLLTGLVFCSLVLGVSSRSFFSFLGEAFDG	(A)	C:Carbamic	677.7627	3384.737
MKLLTSLVFCSLLLGVCHGGFFSFIGEAFQGAGDMWRAY	(E)	C:Carbamic	697.6222	4861.347
MKLLVAVVVLAAVAAGtEGAPGFWDTItKPFSAK	(E)	MKLLVAVV t:Phosphor	753.9845	3605.98
MKLLVAVVVLAAVAAGtEGAPGFWDTItKPFSAK	(E)	MKLLVAVV t:Phosphor	753.9842	3605.98

MKLLVAVVVLAAVAAGTEGAPGFWDtItKPFSFAK	(E)	t:Phosphor	753.9836	3605.98
MKLLVAVVVLAAVAAGtEGAPGFWDtItKPFSFAK	(E)	MKLLVAVV t:Phosphor	753.9874	3605.98
MKLLVAVVVLAAVAAGtEGAPGFWDtItKPFSFAK	(E)	MKLLVAVV t:Phosphor	753.9864	3605.98
MKLSTGIIFCSLVLGVsSQGWLTFLkAAGQGTK	(D)	MKLSTGIIF C:Carbamic	725.1918	3498.885
mKPFLAIIFCFLILGVDSQRWFQFMkEAGQGsR	(D)	C:Carbamic	812.6041	3921.017
mNLSTGIIFCFLILGVSSQGWGtFLKEAGQGAKDMWK	(A)	C:Carbamic	1410.362	4091.059
MNLSTGIIFCFLILGVSSQGWGtFLRE	(A)	C:Carbamic	1016.207	3046.553
mNLsTGIIFCFLILGVSSQGWGtFLREAGQGAKDMWR	(A)	mNLsTGIIF C:Carbamic	1429.002	4147.071
MRSLGVFLNGH	(F)		615.8235	1230.641
MTCRDSRAPDQLFSSP	(L)	C:Carbamic	655.6438	1964.895
MTCRDSRAPDQLFSSP	(L)	C:Carbamic	655.6454	1964.895
mWkAyQDMREAnYK	(G)	m:Oxidized	987.392	1833.841
NFPSLKVQ	(T)		466.7548	932.52
NGAVQPLDPPQ	(E)		568.2999	1135.574
NGAVQPLDPPQ	(E)		568.295	1135.574
NGDAQPLDQSAGDAEPPVfK	(I)	k:Carbamyl	1114.527	2185.004
NKEEEEVAGGDCIGSTVySkHWLFGVLSGLIQIVSPEnTk	(S)	NKEEEEVA C:Carbamic	1140.302	4391.186
nKEEEEVAGGDCIGSTVYskHWLFGVLSGLIQIVSPEStk	(S)	nKEEEEVA C:Carbamic	755.7086	4364.176
NKGYLTEK	(T)	k:Acetyl	497.7629	952.51
NKGYLTEKCLAAASCLHHK	(F)	C:Carbamic	1172.582	2302.143
NLGKsLYIRER	(E)	s:Phosphor	714.8718	1348.77
NLGKsLYIRER	(E)	s:Phosphor	714.8721	1348.77
NLGKsLYIRER	(E)	s:Phosphor	714.8704	1348.77
nLLPFYsPVIEdFLKILHEVDkTLADDLEESFPSLK	(V)	nLLPFYsPVI n:Deamida	1075.546	4175.184
nLLPFYSPVIEdFLKILHEVDkTLADDLEESFPSLK	(V)	nLLPFYSPV n:Deamida	1075.543	4175.184
NLLPLYCSVVKDFLK	(V)	C:Carbamic	905.0083	1808.998
NLLPLYCSVVKDFLK	(V)	C:Carbamic	905.0124	1808.998
NLLPLYCSVVKDFLK	(V)	C:Carbamic	905.0104	1808.998
NLLPLYCSVVKDFLK	(V)	C:Carbamic	905.0124	1808.998
NLLPLYCSVVKDFLK	(V)	C:Carbamic	905.013	1808.998
NLLPLYCSVVKDFLK	(V)	NLLPLYCSV C:Carbamic	617.9961	1808.998
NLLPLYCSVVKDFLK	(V)	C:Carbamic	905.0128	1808.998
NLLPLYCSVVKDFLK	(V)	NLLPLYCSV C:Carbamic	617.9941	1808.998
NLLPLYITEVEtFLk	(V)	NLLPLYITEV t:Phosphor	958.511	1793.009
NLLPLYITEVEtFLk	(V)	NLLPLYITEV t:Phosphor	958.4879	1793.009
NLPLIGsLIR	(V)	s:Phosphor	588.3335	1095.688
NLPLLSKYCGYREDNIP	(Q)	C:Carbamic	684.6778	2052.022
nmPLIGsLIRILQYmEGCGKR	(S)	C:Carbamic	854.7421	2449.288
nmPLIGsLIRILQYmEGCGKR	(S)	nmPLIGsLIF C:Carbamic	854.7436	2449.288
nmPLIGsLIRILQYmEGCGKR	(S)	C:Carbamic	854.7418	2449.288
nmPLIGsLIRILQYmEGCGKR	(S)	C:Carbamic	854.7429	2449.288
nmPLIGsLIRILQYmEGCGKR	(S)	C:Carbamic	854.7402	2449.288
nmPLIGsLIRILQYmEGCGKR	(S)	C:Carbamic	854.7426	2449.288
nmPLIGsLIRILQYmEGCGKR	(S)	C:Carbamic	854.7401	2449.288
nmPLIGsLIRILQYmEGCGKR	(S)	nmPLIGsLIF C:Carbamic	854.7436	2449.288
nmPLIGsLIRILQYmEGCGKR	(S)	C:Carbamic	854.7437	2449.288
nmPLIGsLIRILQYmEGCGKR	(S)	nmPLIGsLIF C:Carbamic	854.7318	2449.288

nmPLIGsLIRILQYmEGCGKR	(S)	nmPLIGsLIF C:Carbamic	854.7457	2449.288
NPSPPPEEGDQEAEDADAIGDTVYskHWLFLSTLR	(L)	k:Carbamyl	795.3803	3929.81
NPSPPSPGRDKEEEEVAGGDCIGSTVYskHWLFGVLSGL	(I)	C:Carbamic	835.2138	4172.003
NPSPPWRGSEAEAEAEAAAGGDAIGA	(T)		804.021	2410.091
NQsVYDHICFImSSSTNVELLVkvGEVVDK	(L)	C:Carbamic	888.1697	3410.697
NQsVYDHICFImSSSTNVELLVkvGEVVDK	(L)	NQsVYDHIC:Carbamic	888.1825	3410.697
NQSVYDHICFImSSSTNVELLVkvGEVVDK	(L)	NQSVYDHIC:Carbamic	702.1271	3410.697
NVEEQLTELDEEMENEICKVWDMMSMDKDVALFLYEFNA	(T)	C:Carbamic	818.9475	5726.64
NVEEQLTELDEEMENEICKVWDMMSMDKDVALFLYEFNA	(T)	C:Carbamic	818.9672	5726.64
PAGLPDK	(Y)		349.2013	697.388
PAGLPDK	(Y)		349.1909	697.388
PAGLPDK	(Y)		349.1925	697.388
PAGLPDK	(Y)		349.1982	697.388
PAGLPDK	(Y)		349.1972	697.388
PAGLPDK	(Y)		349.1981	697.388
PAGLPDK	(Y)		349.1925	697.388
PAGLPDK	(Y)		349.1925	697.388
PAGLPDKY	(-)		430.7301	860.451
PAGLPDKY	(-)		430.7295	860.451
PAGLPDKY	(-)		430.731	860.451
PAGLPDKY	(-)		430.7272	860.451
PAGLPDKY	(-)		430.7304	860.451
PAGLPDKY	(-)		430.7313	860.451
PAGLPDKY	(-)		430.7328	860.451
PAGLPDKY	(-)		430.7307	860.451
PAGLPDKY	(-)		430.7359	860.451
PAGLPDKY	(-)		430.7335	860.451
PAGLPDKY	(-)		430.7329	860.451
PGDTWAAKVISDAREK	(S)		581.9751	1743.902
PGGAWAAK	(V)		379.2047	757.399
PGGAWAAK	(V)		379.2065	757.399
PGGAWAAK	(V)		379.208	757.399
PGGAWAAK	(V)		379.2071	757.399
PGGAWAAK	(V)		379.2071	757.399
PGGAWAAK	(V)		379.2069	757.399
PGGAWAAK	(V)		379.2071	757.399
PHGLPDK	(Y)		255.1418	763.41
PHGLPDK	(Y)		382.208	763.41
PHGLPDK	(Y)		255.1437	763.41
PHGLPDK	(Y)		255.1449	763.41
PHGLPDK	(Y)		382.2101	763.41
PHGLPDK	(Y)		382.2011	763.41
PHGLPDKY	(-)		463.7399	926.473
PHGLPDKY	(-)		463.7399	926.473
PHGLPDKY	(-)		463.7418	926.473
PHGLPDKY	(-)		463.7411	926.473
PHGLPDKY	(-)		463.7424	926.473

PHGLPDKY	(-)		309.4967	926.473
PHGLPDKY	(-)		309.4963	926.473
PHGLPDKY	(-)		463.7415	926.473
PHGLPDKY	(-)		309.4956	926.473
PHGLPDKY	(-)		463.7421	926.473
PHGLPDKY	(-)		463.7415	926.473
PHGLPDKY	(-)		309.4959	926.473
PHGLPDKY	(-)		309.4966	926.473
PHGLPDKY	(-)		463.7431	926.473
PHGLPDKY	(-)		463.7397	926.473
PHGLPDKY	(-)		463.7411	926.473
PHGLPDKY	(-)		309.4958	926.473
PHGLPDKY	(-)		309.4965	926.473
PHGLPDKY	(-)		309.4965	926.473
PHGLPDKY	(-)		463.743	926.473
PHGLPDKY	(-)		309.4968	926.473
PHGLPDKY	(-)		309.4979	926.473
PNHFRPHGLPDKY	(-)		395.2096	1577.797
PNHFRPHGLPDKY	(-)		526.6046	1577.797
PPGAPGALALGCRSSPPQLPARPSSAERGK	(V)	C:Carbamic	597.3098	2982.569
PPGAPGALALGCRSSPPQLPARPSSAERGK	(V)	C:Carbamic	597.3118	2982.569
PQEDSEEQPVFKIVPCVLEAAKQVR	(S)	C:Carbamic	966.162	2896.487
PQEDSEEQPVFKIVPCVLEAAKQVR	(S)	C:Carbamic	966.1644	2896.487
PQEDSEEQPVFKIVPCVLEAAKQVR	(S)	C:Carbamic	966.1676	2896.487
PQEDSEEQPVFKIVPCVLEAAKQVR	(S)	C:Carbamic	966.1562	2896.487
QKCFCAFKNLLPL	(Y)	C:Carbamic	819.9214	1638.85
QKCFCAFKNLLPL	(Y)	C:Carbamic	819.9266	1638.85
qkCSCAFKNLLPLYCSVVK	(D)	C:Carbamic	781.069	2315.171
QkCsCAFkNLLPLYITEVETFLK	(V)	C:Carbamic	989.5051	2802.457
qkCSCAFQnLLPFYnPVVEDFIKILHEVDK	(A)	C:Carbamic	930.9657	3651.834
QKCSAFQnLLPFYSPmVEDFLKILYEVDK	(T)	QKCSAFQ C:Carbamic	1274.912	3682.799
qkCSSAFQnLLPFYSPVISLRImFQR	(M)	C:Carbamic	793.6653	3130.633
qkCSSAFQnLLPFYSPVISLRImFQR	(M)	qkCSSAFQr C:Carbamic	814.134	3130.633
QKCSAFQnLLPFYSPVVEDFIK	(I)	C:Carbamic	680.108	2717.364
qKCSsAFQnLLPFYSPVVEDFIKILHEVDK	(A)	qKCSsAFQn C:Carbamic	1219.618	3551.824
qKCsSAFQnLLPFYSPVVEDFIKILHEVDK	(A)	qKCsSAFQn C:Carbamic	1219.617	3551.824
QLRSENPEGLDVYmHILQLLTTVDDGIQAIVQCPDTGK	(D)	C:Carbamic	1071.537	4267.137
QLRSESPNGVEIYLHILQLLTTIEE	(G)		965.8467	2895.546
QQTSMCSNLCFIMSSSTKTDLLEKVGELVDKFLDLDEELM	(S)	C:Carbamic	963.0831	4811.296
QVRSEnLEGLDVYmHILQLLTTVDDGmKAIVQCPNTGK	(D)	C:Carbamic	1076.561	4286.162
QVRSEnLEGLDVYmHILQLLTTVDDGMKAIVQCPNTGK	(D)	QVRSEnLEC C:Carbamic	1076.546	4286.162
QVRSEnLEGLDVYmHILQLLTTVDDGMKAIVQCPNTGK	(D)	QVRSEnLEC C:Carbamic	1076.561	4286.162
QVRSEnLEGLDVYmHILQLLTTVDDGmKAIVQCPNTGK	(D)	C:Carbamic	1076.546	4286.162
REANYIGADKYFHARGNYDAAKR	(G)		672.3321	2686.323
REANYIGADKYFHARGNYDAAKR	(G)		672.3332	2686.323
REANYIGADKYFHARGNYDAAKR	(G)		672.3308	2686.323
REANYIGADKYFHARGNYDAAKR	(G)		672.3336	2686.323

REANYIGADKYFHARGNYDAAKR	(G)		672.3325	2686.323
REANYIGADKYFHARGNYDAAKR	(G)		672.3347	2686.323
REANYIGADKYFHARGNYDAAKR	(G)		672.332	2686.323
REANYIGADKYFHARGNYDAAKR	(G)		672.3326	2686.323
REANYIGADKYFHARGNYDAAKR	(G)		672.3329	2686.323
REANYIGADKYFHARGNYDAAKR	(G)		672.334	2686.323
REANYIGADKYFHARGNYDAAKR	(G)		672.331	2686.323
REANYIGADKYFHARGNYDAAKR	(G)		672.3331	2686.323
REANYIGADKYFHARGNYDAAKR	(G)		672.3342	2686.323
REANYIGADKYFHARGNYDAAKR	(G)	REANYIGADKYFHARGN	672.336	2686.323
RGNYDAAKRGP GGAWAAKVISDAR	(E)		829.7742	2487.296
RGPGGAWAAK	(V)		324.1795	970.522
RGPGGAWAAK	(V)		324.1799	970.522
RGPGGAWAAK	(V)		324.1785	970.522
RGPGGAWAAK	(V)		324.1774	970.522
RGPGGAWAAK	(V)		324.179	970.522
RGPGGAWAAK	(V)		485.7665	970.522
RGPGGAWAAK	(V)		485.7622	970.522
RGPGGAWAAK	(V)		324.1815	970.522
RGPGGAWAAK	(V)		485.7651	970.522
RGPGGAWAAK	(V)		324.1805	970.522
RGPGGAWAAK	(V)		485.7673	970.522
RGPGGAWAAK	(V)		485.7669	970.522
RGPGGAWAAK	(V)		324.1786	970.522
RGPGGAWAAK	(V)		485.7677	970.522
RGPGGAWAAK	(V)		324.1819	970.522
RGPGGAWAAK	(V)		324.1792	970.522
RGPGGAWAAK	(V)		485.7689	970.522
RGPGGAWAAK	(V)		485.7659	970.522
RGPGGAWAAK	(V)		485.7662	970.522
RGPGGAWAAK	(V)		485.7647	970.522
RGPGGAWAAK	(V)		324.1734	970.522
RGPGGAWAAK	(V)		485.7552	970.522
RGPGGAWAAK	(V)		485.7694	970.522
RGPGGAWAAK	(V)		485.769	970.522
RNsEFEIFVDCDInR	(E)	RNsEFEIFVI C:Carbamic	665.616	1913.881
RVLQNMEQCQKKPENSTESNTGETKK	(T)	C:Carbamic	1022.179	3064.479
RYFYAQGNYDAAERGP GGVWA	(A)		1174.569	2348.084
RYFYAQGNYDAAERGP GGVWA	(A)		1174.554	2348.084
SAFSVLSSIYASQAEQEDVRVGK	(E)		824.4176	2471.241
SDARENSQRVTDFFRHGNSGHGAEDSKADQEANEWGR	(Y)		992.7872	5951.724
SDLTQDDFHLKILKDISCEFLSNIFQVLTKETVAQGVK	(E)	C:Carbamic	730.8763	4380.28
SDMREANYIGADK	(Y)		490.5681	1469.669
SDSIVPLIGNVLRVCQYHRECKHEATSKGGAEDGQLETLA	(V)	C:Carbamic	925.6082	6473.17
SENLEGLDVYmHILQLLTTVDDGMk	(A)	m:Oxidized	724.098	2834.395
SENLEGLDVYmHILQLLTTVDDGMk	(A)	m:Oxidized	724.1004	2834.395
SENPEWLDVYM HILQLLTTVDDGIQAIVDLPLIDSLIRVLQ	(K)	C:Carbamic	955.9819	5606.858

SEnPEWLDVYMHIQLLTTVDDGIQAIVDLPLIDSLIRVLQI (K)		C:Carbamic	956.1261	5606.858
sEnPEWLDVYMHIQLLTTVDDGIQAIVDLPLIDSLIRVLQI (K)		sEnPEWLD' C:Carbamic	955.9734	5606.858
sEnPEWLDVYMHIQLLTTVDDGIQAIVDLPLIDSLIRVLQI (K)		sEnPEWLD' C:Carbamic	955.9733	5606.858
SEVtEDDFHlTVLkDVSCeLLSnVFQDLTK	(E)	SEVtEDDFH C:Carbamic	721.9481	3481.704
SFLGEAAR	(G)		425.7314	850.442
SFLGEAAR	(G)		425.726	850.442
SFLGEAAR	(G)		425.7248	850.442
SFLGEAAR	(G)		425.7237	850.442
SFLGEAAR	(G)		425.726	850.442
SFLGEAAR	(G)		425.7314	850.442
SFLGEAAR	(G)		425.7287	850.442
SFLGEAAR	(G)		425.7257	850.442
SFLGEAAR	(G)		425.7299	850.442
SFPSLKVQ	(T)		453.2512	905.509
SGFIQIVSPENTK	(S)		473.9167	1419.748
SGKDPNHFR	(P)		353.1787	1057.517
SGKDPNHFR	(P)		265.136	1057.517
SGKDPNHFR	(P)		353.1792	1057.517
SGKDPNHFR	(P)		265.1361	1057.517
SGKDPNHFR	(P)		265.137	1057.517
SGKDPNHFR	(P)		265.1368	1057.517
SGKDPNHFR	(P)		353.1777	1057.517
SGKDPNHFR	(P)		529.2725	1057.517
SGKDPNHFR	(P)		529.2632	1057.517
SGKDPNHFR	(P)		353.1791	1057.517
SGKDPNHFR	(P)		529.2656	1057.517
SGKDPNHFR	(P)		265.138	1057.517
SGKDPNHFRPAGLPDK	(Y)		579.3049	1735.887
SGKDPNHFRPAGLPDK	(Y)		579.3028	1735.887
SGKDPNHFRPAGLPDK	(Y)		579.3012	1735.887
SGKDPnHFRPAGLPDK	(Y)	n:Deamida	434.9762	1735.887
SGKDPNHFRPAGLPDK	(Y)		434.7296	1735.887
SGKDPNHFRPAGLPDK	(Y)		579.2938	1735.887
SGKDPNHFRPAGLPDK	(Y)		579.3012	1735.887
SGKDPNHFRPAGLPDK	(Y)		579.2938	1735.887
SGKDPNHFRPAGLPDK	(Y)		579.3007	1735.887
SGKDPNHFRPAGLPDK	(Y)		434.7321	1735.887
SGKDPnHFRPAGLPDK	(Y)	n:Deamida	434.9814	1735.887
SGKDPNHFRPAGLPDK	(Y)		868.4482	1735.887
SGKDPnHFRPAGLPDK	(Y)	n:Deamida	434.981	1735.887
SGKDPNHFRPAGLPDK	(Y)		434.7285	1735.887
SGKDPNHFRPAGLPDK	(Y)		347.9864	1735.887
SGKDPNHFRPAGLPDK	(Y)		347.9836	1735.887
SGKDPNHFRPAGLPDK	(Y)		868.4488	1735.887
SGKDPnHFRPAGLPDK	(Y)	n:Deamida	434.9817	1735.887
SGKDPNHFRPAGLPDK	(Y)		434.7278	1735.887
SGKDPnHFRPAGLPDK	(Y)	n:Deamida	434.9762	1735.887

SGKDPNHFRPAGLPDKY	(-)		633.6591	1898.951
SGKDPNHFRPAGLPDKY	(-)		475.4959	1898.951
SGKDPNHFRPAGLPDKY	(-)		475.4949	1898.951
SGKDPNHFRPAGLPDKY	(-)		633.6582	1898.951
SGKDPnHFRPAGLPDKY	(-)	n:Deamida	475.745	1898.951
SGKDPNHFRPAGLPDKY	(-)		380.5988	1898.951
SGKDPNHFRPAGLPDKY	(-)		380.5991	1898.951
SGKDPnHFRPAGLPDKY	(-)	n:Deamida	633.9862	1898.951
SGKDPNHFRPAGLPDKY	(-)		949.9853	1898.951
SGKDPNHFRPAGLPDKY	(-)		633.6576	1898.951
SGKDPNHFRPAGLPDKY	(-)		633.6582	1898.951
SGKDPNHFRPAGLPDKY	(-)		633.6582	1898.951
SGKDPNHFRPAGLPDKY	(-)		475.4962	1898.951
SGKDPNHFRPAGLPDKY	(-)		475.4966	1898.951
SGKDPNHFRPAGLPDKY	(-)		633.6591	1898.951
SGKDPNHFRPAGLPDKY	(-)		380.5986	1898.951
SGKDPnHFRPAGLPDKY	(-)	n:Deamida	475.7429	1898.951
SGKDPnHFRPAGLPDKY	(-)	n:Deamida	950.4774	1898.951
SGKDPNHFRPAGLPDKY	(-)		633.6574	1898.951
SGKDPNHFRPAGLPDKY	(-)		475.4968	1898.951
SGKDPNHFRPAGLPDKY	(-)		949.9809	1898.951
SGKDPNHFRPAGLPDKY	(-)		949.9853	1898.951
SGKDPNHFRPAGLPDKY	(-)		949.9851	1898.951
SGKDPNHFRPAGLPDKY	(-)		949.9851	1898.951
SGKDPNHFRPAGLPDKY	(-)		380.5981	1898.951
SGKDPnHFRPAGLPDKY	(-)	n:Deamida	633.9867	1898.951
SGKDPNHFRPAGLPDKY	(-)		949.9841	1898.951
SGKDPNHFRPAGLPDKY	(-)		475.4959	1898.951
SGKDPNHFRPAGLPDKY	(-)		949.9842	1898.951
SGKDPNHFRPAGLPDKY	(-)		949.9797	1898.951
SGKDPNHFRPAGLPDKY	(-)		949.9809	1898.951
SGKDPNHFRPAGLPDKY	(-)		949.9809	1898.951
SGKDPNHFRPAGLPDKY	(-)		380.5991	1898.951
SGKDPNHFRPAGLPDKY	(-)		475.4953	1898.951
SGKDPNHFRPAGLPDKY	(-)		380.5986	1898.951
SGKDPnHFRPAGLPDKY	(-)	n:Deamida	950.4758	1898.951
SGKDPNHFRPAGLPDKY	(-)		633.6592	1898.951
SGKDPNHFRPAGLPDKY	(-)		475.4937	1898.951
SGKDPnHFRPAGLPDKY	(-)	n:Deamida	950.4666	1898.951
SGKDPNHFRPH	(G)		431.2157	1291.629
SGKDPNHFRPH	(G)		431.216	1291.629
SGKDPNHFRPH	(G)		431.2158	1291.629
SGKDPNHFRPH	(G)		431.2151	1291.629
SGKDPNHFRPH	(G)		431.2146	1291.629
SGKDPNHFRPH	(G)		431.2144	1291.629
SGKDPNHFRPH	(G)		431.2144	1291.629
SGKDPNHFRPH	(G)		431.2167	1291.629

SGKDPNHFRPH	(G)		431.2146	1291.629
SGKDPNHFRPH	(G)		431.2163	1291.629
SGKDPNHFRPH	(G)		431.2212	1291.629
SGKDPNHFRPH	(G)		323.6645	1291.629
SGKDPNHFRPH	(G)		323.6645	1291.629
SGKDPNHFRPH	(G)		431.2201	1291.629
SGKDPNHFRPHG	(L)		337.919	1348.65
SGKDPNHFRPHGLPDK	(Y)		451.2369	1801.909
SGKDPNHFRPHGLPDK	(Y)		451.2363	1801.909
SGKDPNHFRPHGLPDK	(Y)		601.3146	1801.909
SGKDPNHFRPHGLPDK	(Y)		601.3146	1801.909
SGKDPNHFRPHGLPDK	(Y)		451.236	1801.909
SGKDPNHFRPHGLPDK	(Y)		361.1905	1801.909
SGKDPNHFRPHGLPDK	(Y)		451.236	1801.909
SGKDPNHFRPHGLPDK	(Y)		451.2345	1801.909
SGKDPnHFRPHGLPDK	(Y)	n:Deamida	451.4822	1801.909
SGKDPnHFRPHGLPDK	(Y)	n:Deamida	451.4866	1801.909
SGKDPNHFRPHGLPDK	(Y)		901.4645	1801.909
SGKDPNHFRPHGLPDK	(Y)		601.3194	1801.909
SGKDPNHFRPHGLPDK	(Y)		361.1921	1801.909
SGKDPNHFRPHGLPDK	(Y)		361.1865	1801.909
SGKDPNHFRPHGLPDK	(Y)		451.236	1801.909
SGKDPNHFRPHGLPDK	(Y)		601.3108	1801.909
SGKDPNHFRPHGLPDK	(Y)		601.3194	1801.909
SGKDPNHFRPHGLPDK	(Y)		601.3194	1801.909
SGKDPnHFRPHGLPDK	(Y)	n:Deamida	451.4808	1801.909
SGKDPnHFRPHGLPDK	(Y)	n:Deamida	361.3861	1801.909
SGKDPNHFRPHGLPDKY	(-)		655.6642	1964.973
SGKDPnHFRPHGLPDKY	(-)	n:Deamida	655.9943	1964.973
SGKDPNHFRPHGLPDKY	(-)		655.6659	1964.973
SGKDPNHFRPHGLPDKY	(-)		655.6665	1964.973
SGKDPnHFRPHGLPDKY	(-)	n:Deamida	655.9921	1964.973
SGKDPNHFRPHGLPDKY	(-)		655.6667	1964.973
SGKDPNHFRPHGLPDKY	(-)		655.6643	1964.973
SGKDPNHFRPHGLPDKY	(-)		393.8017	1964.973
SGKDPNHFRPHGLPDKY	(-)		655.6644	1964.973
SGKDPNHFRPHGLPDKY	(-)		655.6645	1964.973
SGKDPNHFRPHGLPDKY	(-)		982.9959	1964.973
SGKDPnHFRPHGLPDKY	(-)	n:Deamida	492.2477	1964.973
SGKDPNHFRPHGLPDKY	(-)		655.665	1964.973
SGKDPnHFRPHGLPDKY	(-)	n:Deamida	655.9884	1964.973
SGKDPNHFRPHGLPDKY	(-)		655.6642	1964.973
SGKDPnHFRPHGLPDKY	(-)	n:Deamida	655.9993	1964.973
SGKDPNHFRPHGLPDKY	(-)		655.6665	1964.973
SGKDPnHFRPHGLPDKY	(-)	n:Deamida	655.9926	1964.973
SGKDPNHFRPHGLPDKY	(-)		491.9999	1964.973
SGKDPNHFRPHGLPDKY	(-)		492.0017	1964.973

SGKDPNHFRPHGLPDKY	(-)		492.0007	1964.973
SGKDPNHFRPHGLPDKY	(-)		655.6642	1964.973
SGKDPNHFRPHGLPDKY	(-)		492.0008	1964.973
SGKDPNHFRPHGLPDKY	(-)		393.8036	1964.973
SGKDPnHFRPHGLPDKY	(-)	n:Deamida	655.9965	1964.973
SGKDPnHFRPHGLPDKY	(-)	n:Deamida	983.4878	1964.973
SGKDPnHFRPHGLPDKY	(-)	n:Deamida	492.2534	1964.973
SGKDPNHFRPHGLPDKY	(-)		492.0026	1964.973
SGKDPNHFRPHGLPDKY	(-)		982.996	1964.973
SGKDPNHFRPHGLPDKY	(-)		393.8022	1964.973
SGKDPnHFRPHGLPDKY	(-)	n:Deamida	655.9921	1964.973
SGKDPNHFRPHGLPDKY	(-)		393.8053	1964.973
SGKDPNHFRPHGLPDKY	(-)		492.0018	1964.973
SGKDPNHFRPHGLPDKY	(-)		982.991	1964.973
SGKDPNHFRPHGLPDKY	(-)		655.6643	1964.973
SGKDPNHFRPHGLPDKY	(-)		982.9959	1964.973
SGKDPNHFRPHGLPDKY	(-)		492.0006	1964.973
SGKDPnHFRPHGLPDKY	(-)	n:Deamida	492.2478	1964.973
SGKDPnHFRPHGLPDKY	(-)	n:Deamida	983.4829	1964.973
SGKDPNHFRPHGLPDKY	(-)		393.8023	1964.973
SGKDPnHFRPHGLPDKY	(-)	n:Deamida	492.2483	1964.973
SGKDPNHFRPHGLPDKY	(-)		393.8005	1964.973
SGKDPNHFRPHGLPDKY	(-)		491.9999	1964.973
SGKDPNHFRPHGLPDKY	(-)		982.991	1964.973
SGKDPNHFRPHGLPDKY	(-)		393.8029	1964.973
SGKDPNHFRPHGLPDKY	(-)		492.0008	1964.973
SGKDPNHFRPHGLPDKY	(-)		491.9999	1964.973
SGKDPnHFRPHGLPDKY	(-)	n:Deamida	492.2485	1964.973
SGKDPnHFRPHGLPDKY	(-)	n:Deamida	492.2527	1964.973
SGKDPNHFRPHGLPDKY	(-)		655.6642	1964.973
SGKDPNHFRPHGLPDKY	(-)		982.99	1964.973
SGKDPnHFRPHGLPDKY	(-)	n:Deamida	655.9884	1964.973
SGKDPNHFRPHGLPDKY	(-)		393.8012	1964.973
SGKDPnHFRPHGLPDKY	(-)	n:Deamida	492.2496	1964.973
SGKDPnHFRPHGLPDKY	(-)	n:Deamida	492.2483	1964.973
SGKDPNHFRPHGLPDKY	(-)		393.8022	1964.973
SGKDPNHFRPHGLPDKY	(-)		655.6645	1964.973
SGKDPNHFRPHGLPDKY	(-)		655.6665	1964.973
SGKDPNHFRPHGLPDKY	(-)		492.0006	1964.973
SGKDPNHFRPHGLPDKY	(-)		492.0006	1964.973
SGKDPNHFRPHGLPDKY	(-)		492.0017	1964.973
SGKDPNHFRPHGLPDKY	(-)		492.0007	1964.973
SGKDPNHFRPHGLPDKY	(-)		655.6643	1964.973
SGKDPnHFRPHGLPDKY	(-)	n:Deamida	655.993	1964.973
SGKDPNHFRPHGLPDKY	(-)		393.8053	1964.973
SGKDPNHFRPHGLPDKY	(-)		655.665	1964.973
SGKDPNHFRPHGLPDKY	(-)		982.9911	1964.973

SGKDPnHFRPHGLPDKY	(-)	n:Deamida	655.9921	1964.973
SGKDPNHFRPHGLPDKY	(-)		655.6659	1964.973
SGKDPNHFRPHGLPDKY	(-)		982.991	1964.973
SGKDPNHFRPHGLPDKY	(-)		982.9944	1964.973
SGKDPNHFRPHGLPDKY	(-)		393.8012	1964.973
SGKDPNHFRPHGLPDKY	(-)		982.9959	1964.973
SGKDPNHFRPHGLPDKY	(-)		393.801	1964.973
SGKDPNHFRPHGLPDKY	(-)		393.8042	1964.973
SGKDPNHFRPHGLPDKY	(-)		655.6656	1964.973
SGKDPNHFRPHGLPDKY	(-)		655.6637	1964.973
SGKDPNHFRPHGLPDKY	(-)		655.6645	1964.973
SGKDPnHFRPHGLPDKY	(-)	n:Deamida	655.9951	1964.973
SGKDPNHFRPHGLPDKY	(-)		655.6665	1964.973
SGKDPNHFRPHGLPDKY	(-)		393.8022	1964.973
SGKDPNHFRPHGLPDKY	(-)		655.6659	1964.973
SGKDPnHFRPHGLPDKY	(-)	n:Deamida	394.0015	1964.973
SGKDPnHFRPHGLPDKY	(-)	n:Deamida	983.4882	1964.973
SGKDPNHFRPHGLPDKY	(-)		982.996	1964.973
SGKDPnHFRPHGLPDKY	(-)	n:Deamida	492.2483	1964.973
SGKDPNHFRPHGLPDKY	(-)		982.9936	1964.973
SGKDPNHFRPHGLPDKY	(-)		655.6644	1964.973
SGKDPNHFRPHGLPDKY	(-)		492.0021	1964.973
SGKDPNHFRPHGLPDKY	(-)		492.0021	1964.973
SGKDPNHFRPHGLPDKY	(-)		393.8053	1964.973
SGKDPNHFRPHGLPDKY	(-)		982.9959	1964.973
SGKDPnHFRPHGLPDKY	(-)	n:Deamida	393.9995	1964.973
SGKDPNHFRPHGLPDKY	(-)		492.0017	1964.973
SGKDPNHFRPHGLPDKY	(-)		982.9907	1964.973
SGKDPNHFRPHGLPDKY	(-)		982.9911	1964.973
SGKDPNHFRPHGLPDKY	(-)		655.6642	1964.973
SGKDPNHFRPHGLPDKY	(-)		492.0026	1964.973
SGKDPNHFRPHGLPDKY	(-)		982.99	1964.973
SGKDPNHFRPHGLPDKY	(-)		491.9999	1964.973
SGKDPNHFRPHGLPDKY	(-)		393.8033	1964.973
SGKDPnHFRPHGLPDKY	(-)	n:Deamida	983.489	1964.973
SGKDPNHFRPHGLPDKY	(-)		655.6645	1964.973
SGKDPNHFRPHGLPDKY	(-)		655.6645	1964.973
SGKDPNHFRPHGLPDKY	(-)		982.9892	1964.973
SGKDPnHFRPHGLPDKY	(-)	n:Deamida	655.9943	1964.973
SGKDPNHFRPHGLPDKY	(-)		982.9924	1964.973
SGkDPnHVRPDGLPEK	(Y)	k:Carbamyl	448.2298	1745.893
SGKDPnYYRPPGLPAKY	(-)	n:Deamida	656.0041	1922.976
SGkDPnYYRPPGLPDK	(Y)	k:Carbamyl	924.4663	1803.902
SGRDPNHFR	(P)		362.5161	1085.524
SGRDPNHFR	(P)		362.5132	1085.524
SGRDPNHFR	(P)		362.5164	1085.524
SGRDPNHFRPH	(G)		330.6647	1319.635

SGRDPNHFRPH	(G)		330.667	1319.635
SGRDPNHFRPH	(G)		330.6671	1319.635
SGRDPNHFRPH	(G)		330.6655	1319.635
SGRDPNHFRPH	(G)		330.667	1319.635
SGRDPNHFRPH	(G)		330.6661	1319.635
SGRDPNHFRPH	(G)		330.667	1319.635
SGRDPNHFRPH	(G)		330.667	1319.635
SGRDPNHFRPH	(G)		440.5528	1319.635
SGRDPNHFRPH	(G)		330.6658	1319.635
SGRDPNHFRPHGLPDK	(Y)		458.2383	1829.915
SGRDPNHFRPHGLPDK	(Y)		458.241	1829.915
SGRDPNHFRPHGLPDK	(Y)		366.7904	1829.915
SGRDPNHFRPHGLPDK	(Y)		366.7912	1829.915
SGRDPNHFRPHGLPDK	(Y)		366.7897	1829.915
SGRDPNHFRPHGLPDK	(Y)		610.6452	1829.915
SGRDPNHFRPHGLPDK	(Y)		458.241	1829.915
SGRDPNHFRPHGLPDK	(Y)		610.6455	1829.915
SGRDPNHFRPHGLPDK	(Y)		610.6473	1829.915
SGRDPNHFRPHGLPDK	(Y)		366.7888	1829.915
SGRDPNHFRPHGLPDK	(Y)		366.7904	1829.915
SGRDPNHFRPHGLPDK	(Y)		366.7905	1829.915
SGRDPnHFRPHGLPDK	(Y)	n:Deamida	366.9922	1829.915
SGRDPnHFRPHGLPDKY	(-)	n:Deamida	499.2503	1992.979
SGRDPNHFRPHGLPDKY	(-)		499.004	1992.979
SGRDPNHFRPHGLPDKY	(-)		664.9988	1992.979
SGRDPNHFRPHGLPDKY	(-)		499.0028	1992.979
SGRDPnHFRPHGLPDKY	(-)	n:Deamida	499.2542	1992.979
SGRDPNHFRPHGLPDKY	(-)		665.0001	1992.979
SGRDPNHFRPHGLPDKY	(-)		665.0002	1992.979
SGRDPNHFRPHGLPDKY	(-)		664.9989	1992.979
SGRDPNHFRPHGLPDKY	(-)		665.0002	1992.979
SGRDPNHFRPHGLPDKY	(-)		399.4038	1992.979
SGRDPNHFRPHGLPDKY	(-)		399.4042	1992.979
SGRDPnHFRPHGLPDKY	(-)	n:Deamida	399.6014	1992.979
SGRDPNHFRPHGLPDKY	(-)		499.0027	1992.979
SGRDPnHFRPHGLPDKY	(-)	n:Deamida	665.3246	1992.979
SGRDPNHFRPHGLPDKY	(-)		499.0023	1992.979
SGRDPNHFRPHGLPDKY	(-)		665.0026	1992.979
SGRDPNHFRPHGLPDKY	(-)		664.9994	1992.979
SGRDPNHFRPHGLPDKY	(-)		664.9994	1992.979
SGRDPNHFRPHGLPDKY	(-)		499.0032	1992.979
SGRDPnHFRPHGLPDKY	(-)	n:Deamida	499.2503	1992.979
SGRDPnHFRPHGLPDKY	(-)	n:Deamida	499.2555	1992.979
SGRDPNHFRPHGLPDKY	(-)		664.9989	1992.979
SGRDPNHFRPHGLPDKY	(-)		499.0026	1992.979
SGRDPnHFRPHGLPDKY	(-)	n:Deamida	665.3246	1992.979
SGRDPNHFRPHGLPDKY	(-)		665.0006	1992.979

SGRDPNHFRPHGLPDKY	(-)		665.0009	1992.979
SGRDPnHFRPHGLPDKY	(-)	n:Deamida	665.3263	1992.979
SGRDPnHFRPHGLPDKY	(-)	n:Deamida	499.2547	1992.979
SILVQALAVLQALYkCHDEWCSkSDTSLPLIGSILR	(V)	C:Carbamic	835.0453	4085.156
SKCPRLTEICVgILGnMACFQETCLSIgK	(N)	SKCPRLTEIC:Carbamic	700.1284	3372.624
SLFLGVSGDGWYSFFR	(E)		613.2981	1837.891
SLFLGVSGDGWYSFFR	(E)		613.2981	1837.891
SLGVFLNGHFQ	(N)		609.8223	1218.627
SLPLVGSLIQ	(V)		513.8041	1026.619
SLPLVGSLIQ	(V)		513.8041	1026.619
SLPLVGSLIQ	(V)		513.8038	1026.619
SLYIRERE	(M)		533.2863	1065.569
SNFIGADKY	(F)		507.7527	1014.489
SNFIGADKY	(F)		507.7515	1014.489
SNIFQALTKETVTKGLK	(E)		626.6931	1878.07
SNIFQALTKETVTKGLK	(E)		626.6936	1878.07
SNIFQALTKETVTKGLK	(E)		626.6936	1878.07
SNIFQALTKETVTKGLK	(E)		626.6936	1878.07
SNIFQALTKETVTKGLK	(E)		626.6931	1878.07
SNSDDEEQQTELDEEMENEICRVWDMsMEDVALFLQI	(L)	C:Carbamic	1425.836	5700.39
SPPPPSR	(D)		369.2014	737.394
SPVVEDFIKILREVDKVLADDLEKSFPSLK	(V)		1143.952	3429.888
SQRITDLFK	(F)		554.3049	1107.616
SQRVTDLFKYGDSGHGVEDSKADQAANEWGRSGKDP	(N)		977.7262	3907.823
SSQCFGSCPVYSkLPnKYEWLDVYMhILQLLTTVDDGIQA	(D)	C:Carbamic	819.1061	5683.737
SSQCFGSCPVYSkLPnKYEWLDVYMhILQLLTTVDDGIQA	(D)	SSQCFGSCF C:Carbamic	818.9715	5683.737
SSQCFGSCPVYSkLPnKYEWLDVYMhILQLLTTVDDGIQA	(D)	SSQCFGSCF C:Carbamic	818.9668	5683.737
SSQCFGSCPVYSkLPnKYEWLDVYMhILQLLTTVDDGIQA	(D)	SSQCFGSCF C:Carbamic	819.1027	5683.737
SSQCFGSCPVYSkLPnKYEWLDVYMhILQLLTTVDDGIQA	(D)	SSQCFGSCF C:Carbamic	818.9612	5683.737
SSQCFGSCPVYSkLPnKYEWLDVYmHILQLLTTVDDGIQA	(D)	C:Carbamic	827.4109	5683.737
SSSYGIQGAMSSGRNGVTER	(F)		682.0003	2043.951
SSSYGIQGAMSSGRNGVTER	(F)		681.9986	2043.951
STLVQAFAVLQALYRCQDQWkSk	(A)	C:Carbamic	707.3616	2740.424
SVGPSVDDSPPELPDFKIVPCILEAAKQVRSDNP	(E)	C:Carbamic	618.9844	3708.843
SWITSPSCENKEEEDSQLDITFCLLEAAK	(Q)	C:Carbamic	883.149	3529.599
TDLTQDDFHLKILK	(D)		843.9517	1686.906
TFLREAGQGTK	(D)		604.318	1207.643
TFQDVYFVSESFEDAKEKMREFTKTIRRPFGVKYNPYTR	(S)		962.8831	4810.409
TFQDVYFVSESFEDAKEKMREFTKTIRRPFGVKYNPYTR	(S)		962.8872	4810.409
TFQDVYFVSESFEDAKEKMREFTKTIRRPFGVKYNPYTR	(S)		962.8847	4810.409
TGFsIRPVAGYLSPR	(D)	TGFsIRPVA s:Phosphor	567.6175	1620.886
TKGLKEGQLSK	(Q)		396.9024	1188.695
TLADDLEKSF	(P)		569.7936	1138.563
TLADDLEKSFPSLK	(A)		521.9374	1563.826
TLAGNLEESFPSLK	(N)		502.6009	1505.785
TLAGNLEEsFPSLKR	(S)	s:Phosphor	581.294	1661.886
TLAGNLEESFPSLkRSFR	(E)	k:Acetyl	524.2698	2052.087

TLLASILSVLSAmFASETQQEYVnIGk	(N)	m:Oxidized	744.14	2913.528
TLLASILSVLSAmFASETQQEYVnIGkNRALVGLSLTHILQHI	(E)	C:Carbamic	881.618	5226.729
TMKLFTGLVFCSLVLGVSSQWYSFLGEEAAQ	(G)	C:Carbamic	835.6623	3339.679
TMKLFTGLVFCSLVLGVSSQWYSFLGEEAAQ	(G)	C:Carbamic	668.7326	3339.679
TMKLFTGLVFCSLVLGVSSQWYSFLGEEAAQ	(G)	C:Carbamic	835.6623	3339.679
TVIWTFtYK	(L)	TVIWTFtYK t:Phosphor	619.8071	1158.619
TVIWTFtYK	(L)	TVIWTFtYK t:Phosphor	619.8015	1158.619
TVIWTFtYK	(L)	TVIWTFtYK t:Phosphor	619.8073	1158.619
TVIWTFtYK	(L)	TVIWTFtYK t:Phosphor	619.8073	1158.619
TVIWTFtYK	(L)	TVIWTFtYK t:Phosphor	619.8071	1158.619
TVIWTFtYK	(L)	TVIWTFtYK t:Phosphor	619.8071	1158.619
TVIWTFtYKLLWS	(K)		829.4566	1657.899
TVLASAFSVLSAIYASQTEQEYLKIEKGsHNLAQACHK	(L)	TVLASAFSV C:Carbamic	1089.04	4193.134
TVLASIFSVLSAIYASQ	(A)		590.6523	1769.968
TVLASVFSVLSAIYASQAEQEYLKIEKGKYHFDLPLI	(D)		835.0603	4171.237
TVLASVFSVLSAIYASQAEQEYLKIEKGKYHFDLPLI	(D)		696.0529	4171.237
TVLAsVFSVLSAIYASQAEQEYLKIEKVDLPLIDSLIR	(V)	TVLAsVFSV s:Phosphor	861.26	4222.326
TVLAsVFSVLSAIYASQTEQEYLKIGK	(V)	TVLAsVFSV s:Phosphor	621.9181	2945.587
TVLASVYVLSAIYVS	(R)		836.4618	1671.92
TVLASVYVLSAIYVS	(R)		836.4603	1671.92
TVLASVYVLSIYASQAEQEYLKIEEGKYHLPLIDSLIRVLQ	(K)	C:Carbamic	828.5878	5793.987
TVLASVYVLSIYASQAEQEYLKIEEGKYHLPLIDSLIRVLQ	(K)	C:Carbamic	828.5878	5793.987
TVPWFPK	(K)		437.7372	874.482
TWDMIR	(A)	TWDMIR TWDMLR	411.2084	821.397
TWDMIR	(A)	TWDMIR TWDMLR	411.2036	821.397
TWDMIR	(A)	TWDMIR TWDMLR	411.2031	821.397
TWDMIR	(A)	TWDMIR TWDMLR	411.2042	821.397
TWGTVFRELNK	(L)		450.9036	1350.716
TWGTVFRELNK	(L)		450.9042	1350.716
TWGTVFRELNK	(L)		450.9033	1350.716
VDKVLADYLEENFPSLK	(E)		660.6757	1980.032
VDLPLIDSLIRVLQnmEQCQKKPEnSAESnTGETk	(K)	C:Carbamic	810.2007	3985.001
VDLPLIDSLIRVLQNMEEQCQkKPEnSAESnTGETK	(K)	VDLPLIDSLI C:Carbamic	1008.243	3985.001
VEQEYLK	(I)		454.7386	908.472
VEQEYLK	(I)		454.7387	908.472
VEQEYLkIEK	(S)	VEQEYLkIEl y:Phosphor	700.8482	1278.694
VGDLVDKLFDLDEELMkTWItDKPQDk	(R)	VGDLVDKLI k:Acetyl,t:F	1119.19	3191.618
VGDLVDKLFDLDEELMKTWITDKPQDKRGDESPTPL	(D)		833.2014	4162.054
VGDVVDK	(L)		366.1962	731.393
VGGLIK	(A)		293.6995	586.392
VGILGNMTCFQEICVSISSDKNLGEVLLHCLYSDPPTLLE ⁻	(I)	C:Carbamic	1224.366	4894.377
VISDAR	(E)		330.6875	660.367
VISDAR	(E)		330.6877	660.367
VISDAR	(E)		330.6872	660.367
VISDAR	(E)		330.6871	660.367
VISDAR	(E)		330.6877	660.367
VISDAR	(E)		330.6885	660.367

VISDAR	(E)		330.6877	660.367
VISDAR	(E)		330.6872	660.367
VISDAR	(E)		330.6876	660.367
VISDAR	(E)		330.6906	660.367
VISDAREAVQ	(K)	VISDAREAVQ VISDARE	544.2878	1087.574
VISDAREAVQKFTG	(H)		507.6119	1520.807
VISDAREDLQ	(R)		573.2915	1145.58
VISDAREKSQRITDLFKFG	(D)		1105.597	2210.193
VISDARENFQRFTDRFSF	(G)		745.6951	2235.094
VISDAREnIQRFTDPLFK	(G)	n:Deamida	717.3859	2149.14
VISDAREnIQRFTDPLFK	(G)	n:Deamida	717.3799	2149.14
VISDAREnIQRFTDPLFK	(G)	n:Deamida	717.3831	2149.14
VISDAREnIQRFTDPLFK	(G)	n:Deamida	717.3857	2149.14
VISDARER	(S)		473.2669	945.511
VISDGR	(E)		323.6787	646.352
VISDGR	(E)		323.6793	646.352
VISDGR	(E)		323.6795	646.352
VISDGR	(E)		323.6791	646.352
VISDGR	(E)		323.6787	646.352
VISDGR	(E)		323.6805	646.352
VISDGR	(E)		323.6778	646.352
VISDGR	(E)		323.6802	646.352
ViSNAREDIQQFLGHGAEDSLADQAAnEWGRSGk	(D)	s:Phosphor	1265.242	3669.764
VISNARENSQR	(V)		637.3275	1273.661
VISNARENSQR	(V)		637.3406	1273.661
VISNARETIQ	(G)		565.8156	1130.616
VISNARETIQGItdPLFKCmTR	(D)	VISNARETI(C:Carbamic	530.0562	2550.317
VkPFDPKITckQECLITTFQDVYFVSESFEDAK	(E)	C:Carbamic	1035.243	3969.929
VLADBLEKSFPSLK	(V)		521.2925	1561.847
VLADBLEKSFPSLK	(V)		781.4408	1561.847
VLADYLEEnFPsLkEkHVnLLHIESR	(K)	n:Deamida	815.6626	3093.637
VLADYLEENFPSLKEVALSACGfk	(G)	C:Carbamic	686.5859	2700.359
VLEDSKSNEKAEEWGRSGKDPDRFRPDGLPK	(K)		1181.606	3542.762
VLKDVSCCELLSNIFQDLtKEIVLQALK	(E)	C:Carbamic	533.6179	3116.728
VLQNIEH	(C)	VLQNIEH	426.7351	852.457
VLQNIEH	(C)		426.7337	852.457
VLQNIEH	(C)		426.7258	852.457
VLQNIEH	(C)		426.7367	852.457
VLQNIEH	(C)		426.7326	852.457
VLQNIEH	(C)		426.7342	852.457
VLQNIEH	(C)		426.7333	852.457
VLQNIEH	(C)		426.7305	852.457
VLQNIEH	(C)		426.7257	852.457
VLQNIEH	(C)		426.738	852.457
VLQNIEH	(C)		426.7286	852.457
VLQNIEHCQKKPENSVESNTEETKKSDLTQEDFHLKILKDI(L)	(L)	C:Carbamic	1430.333	7147.588
VLQNMEHCQkkPENSADSNAEETK	(K)	C:Carbamic	719.0865	2787.267

VLQNMEHCQkkPENSADSNAEETK	(K)		C:Carbamic	719.0802	2787.267
VLQNMEHCQkKPENSADSNAEETk	(K)	VLQNMEHk	C:Carbamic	719.0777	2787.267
VLQNmEQCQKKPENSASNTTEETKK	(T)		C:Carbamic	989.4798	2950.388
VLQnmEQCQKKPENSVESnTDETKK	(T)		C:Carbamic	994.7977	2964.404
VLQnmEQCQKKPENSVESnTDETKK	(T)		C:Carbamic	994.7978	2964.404
VLREVDETLADDLE	(E)			808.8893	1616.801
VLSFPGTWDmLRAYNDMREAnYIGADk	(Y)	VLSFPGTW	m:Oxidized	533.0774	3133.487
VQAAQGAGDMWRAYQDMKK	(S)			718.675	2154.022
VTDLFKFGDSGHGEADSRAD	(Q)			708.6697	2123.963
VTDLFKHGDSGH	(G)			656.8162	1312.628
VTDLFKHGDSGH	(G)			656.815	1312.628
VTDWLK	(H)			381.218	761.419
VWDMAMDKDVAGLLQAFK	(A)			680.0074	2038.014
VWDmsmDEDVALFLQEFKAPDIFmGVLAK	(S)		m:Oxidized	695.5305	3345.624
VWDmsmDEDVALFLQEFKAPDIFmGVLAK	(S)		m:Oxidized	869.1591	3345.624
VWDmsmDEDVALFLQEFNAPDIFmGILAK	(S)	VWDmsm	l m:Oxidized	695.5275	3345.588
WAAAVISNGR	(E)			522.7846	1044.559
WAAGVISDAREMVQGSSGRGHEDSA	(A)			858.4113	2573.18
WLTLKEAGQGTRDMWRAYSMDREANYKNSDKYFHAF	(K)			1217.79	6084.858
WTNPRKSLK	(S)			565.3288	1129.648
WVQFMKEAGQGSRDMWRAYSMDKKNWKNSDKYFH	(R)			733.6892	4397.059
YCGYREDNIPQLEDVSnFLKER	(T)		C:Carbamic	698.0797	2745.294
YDAAQRGPGGAWVAKLISDAREDIQQFLGHGAEDSLAD	(D)			1043.325	5212.522
YDAARRG	(P)	YDAARRG		404.7039	808.406
YDAARRG	(P)	YDAARRG		404.7035	808.406
YDAARRG	(P)	YDAARRG		404.7028	808.406
YDAARRG	(P)			404.7025	808.406
YDAARRG	(P)			404.7021	808.406
YDAARRG	(P)			404.7029	808.406
YDAARRG	(P)			404.7056	808.406
YDAARRG	(P)			404.7026	808.406
YDAARRG	(P)			404.7021	808.406
YDAARRGPGGAWAAKVISDGRENFQRFTDRFSFGGSGR	(G)			833.4145	4163.046
YEFNAPDIFMGVLAR	(T)			581.6233	1742.857
YFADLAMSYPKGDPIPKVEFTEEEIKTWGTVFRELNKLYPT	(S)		C:Carbamic	1625.064	6497.303
YFHARG	(N)			375.6926	750.368
YFHARG	(N)			375.6902	750.368
YFHARGNFDAARR	(G)			527.5887	1580.783
YFHARGNFDAARR	(G)			527.5893	1580.783
YFHARGNFDAARR	(G)			790.8825	1580.783
YFHARGNFDAARR	(G)			790.8796	1580.783
YFHARGNFDAARRPGGLWAAEVISDLREMVQKYSDSG	(W)			818.9668	5726.685
YFHARGNYDAAQRGPGGAWAAKVISDAREKSQRITDLF	(G)			900.4701	4498.292
YFHARGNYDAARR	(G)			798.9053	1596.778
YFHARGNYDAASRGAGGR	(V)			963.4618	1925.911
YFHARGNYDAASRGAGGR	(V)			963.462	1925.911
YFHARGNYDAASRGAGGR	(V)			963.4426	1925.911

YFHARGNYDAASRGAGGR	(V)		963.4506	1925.911
YFHARGNYDAASRGAGGR	(V)		963.463	1925.911
YFHARGnYDAASRGAGGR	(V)	n:Deamida	963.9628	1925.911
YFHARGnYDAASRGAGGR	(V)	n:Deamida	963.9646	1925.911
YFHARGnYDAASRGAGGR	(V)	n:Deamida	963.9628	1925.911
YFHARGNYDAASRGAGGR	(V)		963.4563	1925.911
YFHARGNYDAASRGAGGR	(V)		963.4536	1925.911
YFHARGNYDAASRGAGGR	(V)		963.4607	1925.911
YFHARGnYDAASRGAGGR	(V)	n:Deamida	963.959	1925.911
YFHARGnYDAASRGAGGR	(V)	n:Deamida	963.9561	1925.911
YFHARGNYDAASRGAGGR	(V)		963.4663	1925.911
YFHARGNYDAASRGAGGR	(V)		963.4658	1925.911
YFHARGnYDAATkGTGR	(R)	n:Deamida	964.4628	1884.91
yFQGLMNRYyFGIRDHGLESLQSTQk	(A)	y:Phosphor	819.3892	3151.542
yFQGLMNRYyFGIRDHGLESLQSTQk	(A)	y:Phosphor	819.3998	3151.542
YHLPLIDSLIRVLQNMEHCQKkPEnSVDSNTEETK	(K)	C:Carbamic	1404.01	4166.065
YIGADK	(Y)		333.678	666.346
YIGADK	(Y)		333.6777	666.346
YIGADK	(Y)		333.6774	666.346
YIGADK	(Y)		333.6769	666.346
YKNSDKYFHARGNYDAAQRGPGGVWAAEVISDARENIQ (L)			1096.285	4382.145
YLTRETCLAAANSLPSYkPSFQHLLAALSETDPKLADVMT (-)		C:Carbamic	1042.544	5124.57
YLTRETCLAAANSLPSYkPSFQHLLAALSETDPKLADVMT (-)		C:Carbamic	1042.531	5124.57
YLTRETCLAAANSLPSYkPSFQHLLAALSETDPKLADVMT (-)		C:Carbamic	1042.534	5124.57
YSDMKEANYIGADKYFHARGNYDAAQRGPGGAWAAK (V)			790.7733	3949.846
YSDMKEANYIGADKYFHARGNYDAAQRGPGGAWAAK (V)			790.7809	3949.846
YSDSGFDAEDsAADQKANHWGR	(S)	s:Phosphor	850.3484	2427.023

species	accession_1	accession_2	entry_name
9TELE	NO1 A0A1A8S3Z	A0A1A8S3Z	Serum amyloid A-like 1
9TELE	A0A1A7WC	A0A1A7WC	Serum amyloid A-like 1
MACNP	A0A515EIR	A0A515EIR	Serum amyloid A
TAKRU	H2U9W6	H2U9W6	Serum amyloid A-like 1
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	PIC A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
RABIT	P35543	P35543	Serum amyloid A-3 protein
LATCH	H3AUK4	H3AUK4	Serum amyloid A like 1
RAT	Q5M878	Q5M878	Serum amyloid A protein
RAT	Q5M878	Q5M878	Serum amyloid A protein
RAT	Q5M878	Q5M878	Serum amyloid A protein
NOTKU	A0A1A8KK	A0A1A8KK	Serum amyloid A protein
TAKRU	H2V509	H2V509	Serum amyloid A protein
TAKRU	H2V509	H2V509	Serum amyloid A protein
TAKRU	H2U9W6	H2U9W6	Serum amyloid A-like 1

HORSE A0A5F5Q4|A0A5F5Q4|Serum amyloid A like 1
HORSE A0A5F5Q4|A0A5F5Q4|Serum amyloid A like 1
RABIT A0A5F9DS(A0A5F9DS(Serum amyloid A like 1
PANTR|PAI A0A2I3SXC A0A2I3SXC Serum amyloid A like 1
CEREL B6D986 B6D986 Serum amyloid A protein
9TELE A0A1A7WC A0A1A7WC Serum amyloid A-like 1
SAIBB A0A2K6RY\A0A2K6RY\ Serum amyloid A like 1
9TELE A0A1A7WC A0A1A7WC Serum amyloid A-like 1
SAIBB A0A2K6RY\A0A2K6RY\ Serum amyloid A like 1
SAIBB|RHIF A0A2K6RY\A0A2K6RY\ Serum amyloid A like 1
MUSPF|BC M3YQK5 M3YQK5|E Serum amyloid A like 1
MUSPF|BC M3YQK5 M3YQK5|E Serum amyloid A like 1
MUSPF|BC M3YQK5 M3YQK5|E Serum amyloid A like 1
TAKRU H2U9W6 H2U9W6|f Serum amyloid A-like 1
TAKRU H2U9W6 H2U9W6|f Serum amyloid A-like 1
TAKRU H2U9W6 H2U9W6|f Serum amyloid A-like 1
TAKRU H2U9W6 H2U9W6|f Serum amyloid A-like 1
NOTKU A0A1A8KK:A0A1A8KK: Serum amyloid A protein
9TELE A0A1A7W9 A0A1A7W9 Serum amyloid A protein
9TELE A0A1A7W9 A0A1A7W9 Serum amyloid A protein
9TELE A0A1A7W9 A0A1A7W9 Serum amyloid A protein
9TELE A0A1A7W9 A0A1A7W9 Serum amyloid A protein
9TELE A0A1A7W9 A0A1A7W9 Serum amyloid A protein
9TELE A0A1A7W9 A0A1A7W9 Serum amyloid A protein
9TELE A0A1A7W9 A0A1A7W9 Serum amyloid A protein
9TELE A0A1A7W9 A0A1A7W9 Serum amyloid A protein
MONDO F7FFU5 F7FFU5 Serum amyloid A like 1
MONDO F7FFU5 F7FFU5 Serum amyloid A like 1
MONDO F7FFU5 F7FFU5 Serum amyloid A like 1
MONDO F7FFU5 F7FFU5 Serum amyloid A like 1
MONDO F7FFU5 F7FFU5 Serum amyloid A like 1
MONDO F7FFU5 F7FFU5 Serum amyloid A like 1
MONDO F7FFU5 F7FFU5 Serum amyloid A like 1
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MONDO F7FFU5 F7FFU5 Serum amyloid A like 1
MONDO F7FFU5 F7FFU5 Serum amyloid A like 1
MONDO F7FFU5 F7FFU5 Serum amyloid A like 1
MONDO F7FFU5 F7FFU5 Serum amyloid A like 1
MONDO F7FFU5 F7FFU5 Serum amyloid A like 1
MONDO F7FFU5 F7FFU5 Serum amyloid A like 1
MONDO F7FFU5 F7FFU5 Serum amyloid A like 1
HUMAN|BI A0A0D5ZZ:A0A0D5ZZ: Serum amyloid A protein
ORNAN F6QGS9 F6QGS9 Serum amyloid A like 1
ORNAN F6QGS9 F6QGS9 Serum amyloid A like 1
VULVU|PIC A0A3Q7RF:A0A3Q7RF: Serum amyloid A protein
VULVU|PIC A0A3Q7RF:A0A3Q7RF: Serum amyloid A protein
VULVU|PIC A0A3Q7RF:A0A3Q7RF: Serum amyloid A protein

HORSE	F6PJF6	F6PJF6	Serum amyloid A protein
HORSE	F6PJF6	F6PJF6	Serum amyloid A protein
FELCA	Q5XXU5	Q5XXU5	Serum amyloid A protein (Fragment)
HORSE	A0A5F5Q0I	A0A5F5Q0I	Serum amyloid A protein
MACMU	F6V9Q5	F6V9Q5	Constitutively expressed serum amyloid A protein
MACMU	F6V9Q5	F6V9Q5	Constitutively expressed serum amyloid A protein
SHEEP	P42819	P42819	Serum amyloid A protein
SHEEP	P42819	P42819	Serum amyloid A protein
MOUSE D/	Q3UWC2	Q3UWC2 C	Serum amyloid A protein
MOUSE	Q3UWC2	Q3UWC2	Serum amyloid A protein
MOUSE	Q3UWC2	Q3UWC2	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE FE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
HORSE	F7BBH8	F7BBH8 F7	Serum amyloid A protein
FELCA	Q5XXW0	Q5XXW0 C	Serum amyloid A protein (Fragment)

HORSE	F6ZPQ6	F6ZPQ6	F7 Serum amyloid A protein
HORSE	F6ZPQ6	F6ZPQ6	Serum amyloid A protein
HORSE	F6ZPQ6	F6ZPQ6	F7 Serum amyloid A protein
HORSE	F6ZPQ6	F6ZPQ6	F7 Serum amyloid A protein
HORSE	F6ZPQ6	F6ZPQ6	F7 Serum amyloid A protein
HORSE	F6ZPQ6	F6ZPQ6	F7 Serum amyloid A protein
HORSE	F7C0Y4	F7C0Y4	Serum amyloid A protein
HORSE	F7C0Y4	F7C0Y4	Serum amyloid A protein
HORSE	F7C0Y4	F7C0Y4	Serum amyloid A protein
HORSE	F7C0Y4	F7C0Y4	Serum amyloid A protein
HORSE	F7C0Y4	F7C0Y4	Serum amyloid A protein
HORSE	F7C0Y4	F7C0Y4	Serum amyloid A protein

CANLF	A0A5F4D1f	A0A5F4D1f	Serum amyloid A protein
RABIT	P22000	P22000	Serum amyloid A-2 protein
ORENI	I3JND5	I3JND5	Serum amyloid A-like 1
HORSE	A0A5F5Q0I	A0A5F5Q0I	Serum amyloid A protein
ORYLA	H2LN91	H2LN91	A(Serum amyloid A-like 1
HORSE	F7BBH8	F7BBH8	F6 Serum amyloid A protein
HORSE	F7BBH8	F7BBH8	F6 Serum amyloid A protein
HORSE	F7BBH8	F7BBH8	F6 Serum amyloid A protein
HORSE	F7BBH8	F7BBH8	F6 Serum amyloid A protein
HORSE	F7BBH8	F7BBH8	F6 Serum amyloid A protein
HORSE	F7BBH8	F7BBH8	F6 Serum amyloid A protein
HORSE	F7BBH8	F7BBH8	F6 Serum amyloid A protein
HORSE	F7BBH8	F7BBH8	F6 Serum amyloid A protein
HORSE	F7BBH8	F7BBH8	F6 Serum amyloid A protein
HORSE	F7BBH8	F7BBH8	F6 Serum amyloid A protein
HORSE	F7BBH8	F7BBH8	F6 Serum amyloid A protein
HORSE	F7BBH8	F7BBH8	F6 Serum amyloid A protein
HORSE	F7BBH8	F7BBH8	F6 Serum amyloid A protein
HORSE	F7BBH8	F7BBH8	F6 Serum amyloid A protein
HORSE	F7BBH8	F7BBH8	F6 Serum amyloid A protein
HORSE	F7BBH8	F7BBH8	F6 Serum amyloid A protein
HORSE	F7BBH8	F7BBH8	F6 Serum amyloid A protein
HORSE	F7BBH8	F7BBH8	F6 Serum amyloid A protein
ARAVE	A0A4Y2H1f	A0A4Y2H1f	Serum amyloid A protein
NOMLE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
RUPRU CA	E1UYU4	E1UYU4	B(Serum amyloid A protein
HORSE	F7BBH8	F7BBH8	F6 Serum amyloid A protein
FELCA	A0A337SUf	A0A337SUf	Serum amyloid A protein
FELCA	A0A337SUf	A0A337SUf	Serum amyloid A protein
TAKRU	H2V509	H2V509	Serum amyloid A protein
MONDO	F7FFU5	F7FFU5	Serum amyloid A like 1
MONDO	F7FFU5	F7FFU5	Serum amyloid A like 1
MONDO	F7FFU5	F7FFU5	Serum amyloid A like 1
MONDO	F7FFU5	F7FFU5	Serum amyloid A like 1
ORYLA	H2LN91	H2LN91	A(Serum amyloid A-like 1

MUSPF CA	M3YQK5	M3YQK5	A Serum amyloid A like 1
MUSPF CA	M3YQK5	M3YQK5	A Serum amyloid A like 1
MUSPF CA	M3YQK5	M3YQK5	A Serum amyloid A like 1
MUSPF CA	M3YQK5	M3YQK5	A Serum amyloid A like 1
MUSPF CA	M3YQK5	M3YQK5	A Serum amyloid A like 1
MUSPF CA	M3YQK5	M3YQK5	A Serum amyloid A like 1
MUSPF CA	M3YQK5	M3YQK5	A Serum amyloid A like 1
MUSPF CA	M3YQK5	M3YQK5	A Serum amyloid A like 1
MUSPF CA	M3YQK5	M3YQK5	A Serum amyloid A like 1
MUSPF CA	M3YQK5	M3YQK5	A Serum amyloid A like 1
MUSPF CA	M3YQK5	M3YQK5	A Serum amyloid A like 1
FELCA CAN	M3VUA7	M3VUA7	J Serum amyloid A like 1
FELCA CAN	M3VUA7	M3VUA7	J Serum amyloid A like 1
FELCA CAN	M3VUA7	M3VUA7	J Serum amyloid A like 1
FELCA CAN	M3VUA7	M3VUA7	J Serum amyloid A like 1
FELCA CAN	M3VUA7	M3VUA7	J Serum amyloid A like 1
FELCA CAN	M3VUA7	M3VUA7	J Serum amyloid A like 1
FELCA CAN	M3VUA7	M3VUA7	J Serum amyloid A like 1
FELCA CAN	M3VUA7	M3VUA7	J Serum amyloid A like 1
FELCA CAN	M3VUA7	M3VUA7	J Serum amyloid A like 1
FELCA CAN	M3VUA7	M3VUA7	J Serum amyloid A like 1
FELCA CAN	M3VUA7	M3VUA7	J Serum amyloid A like 1
FELCA CAN	M3VUA7	M3VUA7	J Serum amyloid A like 1
FELCA CAN	M3VUA7	M3VUA7	J Serum amyloid A like 1
FELCA CAN	M3VUA7	M3VUA7	J Serum amyloid A like 1
FELCA CAN	M3VUA7	M3VUA7	J Serum amyloid A like 1
PANTR HU	H2R5J4	H2R5J4	J3I Serum amyloid A like 1
ORNAN	F6QGS9	F6QGS9	Serum amyloid A like 1
PIG SAIBB	A0A5G2QN	A0A5G2QN	Serum amyloid A like 1
PIG	A0A480KN	A0A480KN	Serum amyloid A protein
SARHA	G3WV59	G3WV59	Serum amyloid A like 1
SARHA	G3WV59	G3WV59	Serum amyloid A like 1
PIG	F1S9B2	F1S9B2	Serum amyloid A like 1
PIG	F1S9B2	F1S9B2	Serum amyloid A like 1
PIG	F1S9B2	F1S9B2	Serum amyloid A like 1
PIG	F1S9B2	F1S9B2	Serum amyloid A like 1
PIG	F1S9B2	F1S9B2	Serum amyloid A like 1
NOMLE	G1S7R0	G1S7R0	Serum amyloid A protein
PANTA FEL	T1W3H8	T1W3H8	C Serum amyloid A protein
BOBOX	A0A4W2BS	A0A4W2BS	Serum amyloid A like 1
BOBOX	A0A4W2BS	A0A4W2BS	Serum amyloid A like 1
RABIT	P35543	P35543	Serum amyloid A-3 protein
RABIT	P35543	P35543	Serum amyloid A-3 protein
RABIT	P35543	P35543	Serum amyloid A-3 protein
PAPAN M/	A0A2I3MZ	A0A2I3MZ	Serum amyloid A like 1
PAPAN M/	A0A2I3MZ	A0A2I3MZ	Serum amyloid A like 1
RAT	Q5M878	Q5M878	Serum amyloid A protein
CEBCA AO	A0A2K5QF	A0A2K5QF	Serum amyloid A like 1
RHIRO PRC	A0A2K6Q6	A0A2K6Q6	Serum amyloid A like 1
SAIBB RHIF	A0A2K6RY	A0A2K6RY	Serum amyloid A like 1

SAIBB|RHIF A0A2K6RY\ A0A2K6RY\ Serum amyloid A like 1
SAIBB|RHIF A0A2K6RY\ A0A2K6RY\ Serum amyloid A like 1
RABIT P35543 P35543 Serum amyloid A-3 protein
BUBBU|BO D2U6Q0 D2U6Q0|V Serum amyloid A protein (Fragment)
MANLE|CE A0A2K5XIC A0A2K5XIC Serum amyloid A like 1
CAVPO H0V714 H0V714 Serum amyloid A like 1
CAVPO H0V714 H0V714 Serum amyloid A like 1
URSMA|UF A0A452VG A0A452VG Serum amyloid A like 1
URSMA|UF A0A452VG A0A452VG Serum amyloid A like 1
URSMA|UF A0A452VG A0A452VG Serum amyloid A like 1
URSMA|UF A0A452VG A0A452VG Serum amyloid A like 1
URSMA|UF A0A452VG A0A452VG Serum amyloid A like 1
PIG A0A5G2QN A0A5G2QN Serum amyloid A like 1
PIG A0A5G2QN A0A5G2QN Serum amyloid A like 1
PIG A0A5G2QN A0A5G2QN Serum amyloid A like 1
PIG A0A287AI4 A0A287AI4 Serum amyloid A like 1
PIG A0A287AI4 A0A287AI4 Serum amyloid A like 1
PIG A0A287AI4 A0A287AI4 Serum amyloid A like 1
PIG A0A287AI4 A0A287AI4 Serum amyloid A like 1
PIG A0A287AI4 A0A287AI4 Serum amyloid A like 1
PIG A0A287A4I A0A287A4I Serum amyloid A like 1
RABIT A0A5F9DS\ A0A5F9DS\ Serum amyloid A like 1
RABIT A0A5F9DS\ A0A5F9DS\ Serum amyloid A like 1
RABIT A0A5F9DS\ A0A5F9DS\ Serum amyloid A like 1
RABIT A0A5F9DS\ A0A5F9DS\ Serum amyloid A like 1
RABIT A0A5F9DS\ A0A5F9DS\ Serum amyloid A like 1
RABIT A0A5F9DS\ A0A5F9DS\ Serum amyloid A like 1
RABIT A0A5F9DS\ A0A5F9DS\ Serum amyloid A like 1
RABIT A0A5F9DS\ A0A5F9DS\ Serum amyloid A like 1
RABIT A0A5F9DS\ A0A5F9DS\ Serum amyloid A like 1
RABIT A0A5F9DS\ A0A5F9DS\ Serum amyloid A like 1
RABIT A0A5F9DS\ A0A5F9DS\ Serum amyloid A like 1
RABIT A0A5F9DS\ A0A5F9DS\ Serum amyloid A like 1
RABIT A0A5F9DS\ A0A5F9DS\ Serum amyloid A like 1
RABIT G1SHI3 G1SHI3 Serum amyloid A like 1
ICTTR I3M295 I3M295 Serum amyloid A like 1
MOUSE P04918 P04918 Serum amyloid A-3 protein
9TELE|NOT A0A1A8BD A0A1A8BD Serum amyloid A protein
SAIBB|RHIF A0A2K6RY\ A0A2K6RY\ Serum amyloid A like 1
SAIBB|RHIF A0A2K6RY\ A0A2K6RY\ Serum amyloid A like 1
RHIBE|PAP A0A2K6KSF A0A2K6KSF Serum amyloid A like 1
SAIBB A0A2K6RY\ A0A2K6RY\ Serum amyloid A like 1
SAIBB A0A2K6RY\ A0A2K6RY\ Serum amyloid A like 1
HORSE A0A5F5Q4I A0A5F5Q4I Serum amyloid A like 1
PROCO|ICT A0A2K6ETL A0A2K6ETL Serum amyloid A like 1
MYOLU G1PAL8 G1PAL8 Serum amyloid A like 1
MYOLU G1PAL8 G1PAL8 Serum amyloid A like 1
FELCA M3VUA7 M3VUA7 Serum amyloid A like 1

HORSE	F7BBH8	F7BBH8	F6 Serum amyloid A protein
PIG RABIT	F1S9B2	F1S9B2	A0 Serum amyloid A like 1
NEOVI	P18575	P18575	Serum amyloid A-1 protein
NEOVI	P18575	P18575	Serum amyloid A-1 protein
NEOVI	P18575	P18575	Serum amyloid A-1 protein
NEOVI	P18575	P18575	Serum amyloid A-1 protein
NEOVI	P18575	P18575	Serum amyloid A-1 protein
NEOVI	P18575	P18575	Serum amyloid A-1 protein
NEOVI	P18575	P18575	Serum amyloid A-1 protein
NEOVI	P18575	P18575	Serum amyloid A-1 protein
NEOVI	P18575	P18575	Serum amyloid A-1 protein
VULVU NE	A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU NE	A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU NE	A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU NE	A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU NE	A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU NE	A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU NE	A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU NE	A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU NE	A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU NE	A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU NE	A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU NE	A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU NE	A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU NE	A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU NE	A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU NE	A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU NE	A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU NE	A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU NE	A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
CANLF	P19708	P19708	Serum amyloid A protein
CANLF	P19708	P19708	Serum amyloid A protein
CANLF	A0A096P6	A0A096P6	Serum amyloid A protein
CANLF	A0A096P6	A0A096P6	Serum amyloid A protein
CANLF	A0A5F4BZ	A0A5F4BZ	Serum amyloid A protein
SAIBB	A0A2K6RY	A0A2K6RY	Serum amyloid A like 1
SAIBB	A0A2K6RY	A0A2K6RY	Serum amyloid A like 1
ORYLA	H2LN91	H2LN91	A Serum amyloid A-like 1
PANTR	H2Q392	H2Q392	Serum amyloid A protein
TAKRU	H2V509	H2V509	Serum amyloid A protein
PROCO	A0A2K6ETL	A0A2K6ETL	Serum amyloid A like 1
OTOGA	H0X4B8	H0X4B8	Serum amyloid A like 1
LATCH	H3AUK4	H3AUK4	Serum amyloid A like 1
LATCH	H3AUK4	H3AUK4	Serum amyloid A like 1
LATCH	H3AUK4	H3AUK4	Serum amyloid A like 1
URSMA UF	A0A452VG	A0A452VG	Serum amyloid A like 1
URSMA UF	A0A452VG	A0A452VG	Serum amyloid A like 1
MONDO	F7FFU5	F7FFU5	Serum amyloid A like 1
MYOLU	G1PAL8	G1PAL8	Serum amyloid A like 1
MYOLU	G1PAL8	G1PAL8	Serum amyloid A like 1

MYOLU	G1PAL8	G1PAL8	Serum amyloid A like 1
MYOLU	G1PAL8	G1PAL8	Serum amyloid A like 1
MYOLU	G1PAL8	G1PAL8	Serum amyloid A like 1
MYOLU	G1PAL8	G1PAL8	Serum amyloid A like 1
MYOLU	G1PAL8	G1PAL8	Serum amyloid A like 1
MYOLU	G1PAL8	G1PAL8	Serum amyloid A like 1
MYOLU	G1PAL8	G1PAL8	Serum amyloid A like 1
MYOLU	G1PAL8	G1PAL8	Serum amyloid A like 1
MYOLU	G1PAL8	G1PAL8	Serum amyloid A like 1
RABIT	A0A5F9DS	A0A5F9DS	Serum amyloid A like 1
NOMLE	G1S7Q7	G1S7Q7	Serum amyloid A like 1
NOMLE	G1S7Q7	G1S7Q7	Serum amyloid A like 1
LATCH	H3AUK4	H3AUK4	Serum amyloid A like 1
LATCH	H3AUK4	H3AUK4	Serum amyloid A like 1
LATCH	H3AUK4	H3AUK4	Serum amyloid A like 1
LATCH	H3AUK4	H3AUK4	Serum amyloid A like 1
NOTKU	A0A1A8KK	A0A1A8KK	Serum amyloid A protein
NOTKU	A0A1A8KK	A0A1A8KK	Serum amyloid A protein
NOTKU	A0A1A8KK	A0A1A8KK	Serum amyloid A protein
9TELE	A0A1A8G3	A0A1A8G3	Serum amyloid A-like 1
MYOLU	G1PAL8	G1PAL8	Serum amyloid A like 1
MYOLU	G1PAL8	G1PAL8	Serum amyloid A like 1
MYOLU	G1PAL8	G1PAL8	Serum amyloid A like 1
MYOLU	G1PAL8	G1PAL8	Serum amyloid A like 1
MYOLU	G1PAL8	G1PAL8	Serum amyloid A like 1
MYOLU	G1PAL8	G1PAL8	Serum amyloid A like 1
SARHA	G3WV59	G3WV59	Serum amyloid A like 1
PIG	F1S9B2	F1S9B2	Serum amyloid A like 1
PIG	F1S9B2	F1S9B2	Serum amyloid A like 1
PIG	F1S9B2	F1S9B2	Serum amyloid A like 1
PIG	F1S9B2	F1S9B2	Serum amyloid A like 1
MESAU	P20727	P20727	P2 Serum amyloid A-2 protein
CAPHI BOV	A0A452EM	A0A452EM	Serum amyloid A like 1
BOVIN	B8Y7I4	B8Y7I4	A0 Serum amyloid A protein (Fragment)
TAKRU	H2U9W6	H2U9W6	Serum amyloid A-like 1
TAKRU	H2U9W6	H2U9W6	Serum amyloid A-like 1
ORNAN	F6QGS9	F6QGS9	Serum amyloid A like 1
9TELE	A0A1A7WC	A0A1A7WC	Serum amyloid A-like 1
NOMLE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
PANTR NO	A0A2I3TSR	A0A2I3TSR	Serum amyloid A protein
NOMLE	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
PIG OTOG	A0A5G2QN	A0A5G2QN	Serum amyloid A like 1
URSMA UF	A0A452VG	A0A452VG	Serum amyloid A like 1
URSMA UF	A0A452VG	A0A452VG	Serum amyloid A like 1
URSMA UF	A0A452VG	A0A452VG	Serum amyloid A like 1
URSMA UF	A0A452VG	A0A452VG	Serum amyloid A like 1

HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
HORSE	P19857	P19857	Serum amyloid A protein
LATCH	H3AUK4	H3AUK4	Serum amyloid A like 1
PANTR PAI	A0A2I3TSR	A0A2I3TSR	Serum amyloid A protein
NOMLE M.	G1S7R0	G1S7R0 G.	Serum amyloid A protein
NOMLE M.	A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
MACMU	F7CLU1	F7CLU1 F6	Serum amyloid A protein
MACMU	F7CLU1	F7CLU1 F6	Serum amyloid A protein
MACMU	F7CLU1	F7CLU1 F6	Serum amyloid A protein
MACMU	F7CLU1	F7CLU1 F6	Serum amyloid A protein
MACMU	F7CLU1	F7CLU1 F6	Serum amyloid A protein
PANTR PAI	A0A2I3TSR	A0A2I3TSR	Serum amyloid A protein
MACNP	A0A515EIR	A0A515EIR	Serum amyloid A
MACNP	A0A515EIR	A0A515EIR	Serum amyloid A
VULVU	A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
VULVU	A0A3Q7RF	A0A3Q7RF	Serum amyloid A protein
9TELE	A0A1A7WC	A0A1A7WC	Serum amyloid A-like 1
9TELE	A0A1A8CL	A0A1A8CL	Serum amyloid A-like 1
MONDO	F7FFU5	F7FFU5	Serum amyloid A like 1
SARHA	G3WV59	G3WV59	Serum amyloid A like 1

CAVPO	H0V714	H0V714	Serum amyloid A like 1
MUSPF	M3YQK5	M3YQK5	Serum amyloid A like 1
MUSPF	M3YQK5	M3YQK5	Serum amyloid A like 1
MUSPF	M3YQK5	M3YQK5	Serum amyloid A like 1
MUSPF	M3YQK5	M3YQK5	Serum amyloid A like 1
MUSPF	M3YQK5	M3YQK5	Serum amyloid A like 1
MUSPF	M3YQK5	M3YQK5	Serum amyloid A like 1
MUSPF	M3YQK5	M3YQK5	Serum amyloid A like 1
MUSPF	M3YQK5	M3YQK5	Serum amyloid A like 1
MUSPF	M3YQK5	M3YQK5	Serum amyloid A like 1
URSMA UF	A0A452VG	A0A452VG	Serum amyloid A like 1
URSMA UF	A0A452VG	A0A452VG	Serum amyloid A like 1
URSMA UF	A0A452VG	A0A452VG	Serum amyloid A like 1
CAPHI	A0A452EM	A0A452EM	Serum amyloid A like 1
RABIT	A0A5F9DS	A0A5F9DS	Serum amyloid A like 1
PANTR NO	A0A2I3TSR	A0A2I3TSR	Serum amyloid A protein
FELCA	A0A337SU	A0A337SU	Serum amyloid A protein
CEBCA	A0A2K5QF	A0A2K5QF	Serum amyloid A like 1
MACEU	P53613	P53613	Serum amyloid A protein
MACEU	P53613	P53613	Serum amyloid A protein
MOUSE	A0A1B0GT	A0A1B0GT	Serum amyloid A-3 protein
MOUSE	A0A1B0GT	A0A1B0GT	Serum amyloid A-3 protein
MOUSE	A0A1B0GT	A0A1B0GT	Serum amyloid A-3 protein
MOUSE	A0A1B0GT	A0A1B0GT	Serum amyloid A-3 protein
MOUSE	A0A1B0GT	A0A1B0GT	Serum amyloid A-3 protein
MOUSE	A0A1B0GT	A0A1B0GT	Serum amyloid A-3 protein
HORSE	F6PJF6	F6PJF6	Serum amyloid A protein
CAPHI	Q0PG40	Q0PG40	Serum amyloid A protein
RABIT	A0A5F9DS	A0A5F9DS	Serum amyloid A like 1
NOMLE	G1S7Q7	G1S7Q7	Serum amyloid A like 1
NOMLE	G1S7Q7	G1S7Q7	Serum amyloid A like 1
NOMLE	G1S7Q7	G1S7Q7	Serum amyloid A like 1
NOMLE	G1S7Q7	G1S7Q7	Serum amyloid A like 1
NOMLE	G1S7Q7	G1S7Q7	Serum amyloid A like 1
PROCO	A0A2K6ETL	A0A2K6ETL	Serum amyloid A like 1
PROCO	A0A2K6ETL	A0A2K6ETL	Serum amyloid A like 1
PROCO	A0A2K6ETL	A0A2K6ETL	Serum amyloid A like 1
PROCO	A0A2K6ETL	A0A2K6ETL	Serum amyloid A like 1
PROCO	A0A2K6ETL	A0A2K6ETL	Serum amyloid A like 1
PROCO	A0A2K6ETL	A0A2K6ETL	Serum amyloid A like 1
MACMU	A0A1D5QY	A0A1D5QY	Serum amyloid A like 1
RABIT	G1SHI3	G1SHI3	Serum amyloid A like 1
9TELE	A0A1A7WC	A0A1A7WC	Serum amyloid A-like 1
9TELE	A0A1A7WC	A0A1A7WC	Serum amyloid A-like 1
HORSE	A0A5F5Q0I	A0A5F5Q0I	Serum amyloid A protein
HORSE	A0A5F5Q0I	A0A5F5Q0I	Serum amyloid A protein
HORSE	A0A5F5Q0I	A0A5F5Q0I	Serum amyloid A protein

HORSE	A0A5F5Q0I	A0A5F5Q0I	Serum amyloid A protein
HORSE	A0A5F5Q0I	A0A5F5Q0I	Serum amyloid A protein
HORSE	A0A5F5Q0I	A0A5F5Q0I	Serum amyloid A protein
HORSE	A0A5F5Q0I	A0A5F5Q0I	Serum amyloid A protein
HORSE	A0A5F5Q0I	A0A5F5Q0I	Serum amyloid A protein
RABIT	P35543	P35543	Serum amyloid A-3 protein
RABIT	P35543	P35543	Serum amyloid A-3 protein
RABIT	P35543	P35543	Serum amyloid A-3 protein
HORSE	F6ZL17	F6ZL17 F7I	Serum amyloid A protein
HORSE	F6ZL17	F6ZL17 F7I	Serum amyloid A protein
HORSE	F6ZL17	F6ZL17 F7I	Serum amyloid A protein
HORSE	F6ZL17	F6ZL17 F7I	Serum amyloid A protein
CAVPO	H0V714	H0V714	Serum amyloid A like 1
PIG	A0A5G2QN	A0A5G2QN	Serum amyloid A like 1
OTOGA	H0X4B8	H0X4B8	Serum amyloid A like 1
URSMA UF	A0A452VG	A0A452VG	Serum amyloid A like 1
PIG	Q2HXZ9	Q2HXZ9	Serum amyloid A protein
HUMAN	A0A0D5ZZZ	A0A0D5ZZZ	Serum amyloid A protein
9TELE	A0A1A8S3Z	A0A1A8S3Z	Serum amyloid A-like 1
9TELE	A0A1A8S3Z	A0A1A8S3Z	Serum amyloid A-like 1
9TELE	A0A1A8S3Z	A0A1A8S3Z	Serum amyloid A-like 1
9TELE	A0A1A8S3Z	A0A1A8S3Z	Serum amyloid A-like 1
9TELE	A0A1A8S3Z	A0A1A8S3Z	Serum amyloid A-like 1
TAKRU OR	H2U9W6	H2U9W6 F	Serum amyloid A-like 1
TAKRU OR	H2U9W6	H2U9W6 F	Serum amyloid A-like 1
TAKRU OR	H2U9W6	H2U9W6 F	Serum amyloid A-like 1
TAKRU OR	H2U9W6	H2U9W6 F	Serum amyloid A-like 1
TAKRU OR	H2U9W6	H2U9W6 F	Serum amyloid A-like 1
COLLI	A0A2I0MH	A0A2I0MH	Serum amyloid A-like 1
COLLI	A0A2I0MH	A0A2I0MH	Serum amyloid A-like 1
COLLI	A0A2I0MH	A0A2I0MH	Serum amyloid A-like 1
PIG	F1S9B3	F1S9B3	Serum amyloid A like 1
PIG	F1S9B3	F1S9B3	Serum amyloid A like 1
PIG	F1S9B3	F1S9B3	Serum amyloid A like 1
PIG	F1S9B3	F1S9B3	Serum amyloid A like 1
PIG	F1S9B3	F1S9B3	Serum amyloid A like 1
PIG	F1S9B3	F1S9B3	Serum amyloid A like 1
PIG	F1S9B3	F1S9B3	Serum amyloid A like 1
PIG	F1S9B3	F1S9B3	Serum amyloid A like 1
PIG	F1S9B3	F1S9B3	Serum amyloid A like 1
PIG	F1S9B3	F1S9B3	Serum amyloid A like 1
MACNP	A0A515EIR	A0A515EIR	Serum amyloid A
MACNP	A0A515EIR	A0A515EIR	Serum amyloid A
MACNP	A0A515EIR	A0A515EIR	Serum amyloid A
MACNP	A0A515EIR	A0A515EIR	Serum amyloid A
MACNP	A0A515EIR	A0A515EIR	Serum amyloid A

MACNP	A0A515EIR	A0A515EIR	Serum amyloid A
ORYLA	H2LN91	H2LN91 A	Serum amyloid A-like 1
SARHA	G3WV59	G3WV59	Serum amyloid A like 1
MESAU	P20727	P20727	Serum amyloid A-2 protein
CALJA	F6ZH70	F6ZH70 U	Serum amyloid A protein
CALJA	F6ZH70	F6ZH70 U	Serum amyloid A protein
CALJA	F6ZH70	F6ZH70 U	Serum amyloid A protein
CALJA	F6ZH70	F6ZH70 U	Serum amyloid A protein
CALJA	F6ZH70	F6ZH70 U	Serum amyloid A protein
CALJA	F6ZH70	F6ZH70 U	Serum amyloid A protein
CALJA	F6ZH70	F6ZH70 U	Serum amyloid A protein
CALJA	F6ZH70	F6ZH70 U	Serum amyloid A protein
CALJA	F6ZH70	F6ZH70 U	Serum amyloid A protein
CALJA	F6ZH70	F6ZH70 U	Serum amyloid A protein
CALJA	F6ZH70	F6ZH70 U	Serum amyloid A protein
CALJA	F6ZH70	F6ZH70 U	Serum amyloid A protein
CALJA	F6ZH70	F6ZH70 U	Serum amyloid A protein
CALJA	F6ZH70	F6ZH70 U	Serum amyloid A protein
CALJA	F6ZH70	F6ZH70 U	Serum amyloid A protein
CALJA	F6ZH70	F6ZH70 U	Serum amyloid A protein
CALJA	F6ZH70	F6ZH70 U	Serum amyloid A protein
CALJA	F6ZH70	F6ZH70 U	Serum amyloid A protein
CALJA	F6ZH70	F6ZH70 U	Serum amyloid A protein
CALJA	F6ZH70	F6ZH70 U	Serum amyloid A protein
HORSE	F6ZL17	F6ZL17 F7	Serum amyloid A protein
HORSE	F6ZL17	F6ZL17 F7	Serum amyloid A protein
AOTNA	A0A2K5F0E	A0A2K5F0E	Serum amyloid A like 1
SARHA	G3WV59	G3WV59	Serum amyloid A like 1
PIG RABIT	F1S9B2	F1S9B2 A0	Serum amyloid A like 1
PANTR	A0A2I3SXC	A0A2I3SXC	Serum amyloid A like 1
PAPAN M/	A0A096MZ	A0A096MZ	Serum amyloid A like 1
PAPAN M/	A0A096MZ	A0A096MZ	Serum amyloid A like 1
PAPAN M/	A0A096MZ	A0A096MZ	Serum amyloid A like 1
URSMA UF	A0A452VG	A0A452VG	Serum amyloid A like 1
MOUSE	Q3UWC2	Q3UWC2	Serum amyloid A protein
MONDO	F7FFU5	F7FFU5	Serum amyloid A like 1
MONDO	F7FFU5	F7FFU5	Serum amyloid A like 1
SARHA	G3WV59	G3WV59	Serum amyloid A like 1
BUBBU	A0A0N6YQ	A0A0N6YQ	Serum amyloid A protein
BUBBU	A0A076JSH	A0A076JSH	Serum amyloid A protein
BUBBU	A0A076JSH	A0A076JSH	Serum amyloid A protein
9TELE	A0A0S7LG	A0A0S7LG	Serum amyloid A protein
9TELE	A0A0S7LG	A0A0S7LG	Serum amyloid A protein
9TELE	A0A0S7LG	A0A0S7LG	Serum amyloid A protein
DANRE	Q642J9	Q642J9	Serum amyloid A protein
CALJA	F6ZH70	F6ZH70 U	Serum amyloid A protein
NOMLE	G1S7R2	G1S7R2	Serum amyloid A protein
MOUSE	P97375	P97375 P0	Serum amyloid A protein
MACNP	A0A515EIR	A0A515EIR	Serum amyloid A
MACNP	A0A515EIR	A0A515EIR	Serum amyloid A

HORSE	F7BBH8	F7BBH8 F6	Serum amyloid A protein
HORSE	F7BBH8	F7BBH8 F6	Serum amyloid A protein
HORSE	F7BBH8	F7BBH8 F6	Serum amyloid A protein
HORSE	F7BBH8	F7BBH8 F6	Serum amyloid A protein
HORSE	F7BBH8	F7BBH8 F6	Serum amyloid A protein
HORSE	F7BBH8	F7BBH8 F6	Serum amyloid A protein
HORSE	F7BBH8	F7BBH8 F6	Serum amyloid A protein
HORSE	F7BBH8	F7BBH8 F6	Serum amyloid A protein
HORSE	F7BBH8	F7BBH8 F6	Serum amyloid A protein
HORSE	F7BBH8	F7BBH8 F6	Serum amyloid A protein
HORSE	F7BBH8	F7BBH8 F6	Serum amyloid A protein
HORSE	F7BBH8	F7BBH8 F6	Serum amyloid A protein
HORSE	F7BBH8	F7BBH8 F6	Serum amyloid A protein
HORSE	F7BBH8	F7BBH8 F6	Serum amyloid A protein
HORSE	F7BBH8	F7BBH8 F6	Serum amyloid A protein
HORSE	F7BBH8	F7BBH8 F6	Serum amyloid A protein
HORSE	F7BBH8	F7BBH8 F6	Serum amyloid A protein
HORSE	F7BBH8	F7BBH8 F6	Serum amyloid A protein
HORSE	F7BBH8	F7BBH8 F6	Serum amyloid A protein
RHIBE	A0A2K6KSF	A0A2K6KSF	Serum amyloid A like 1
RHIBE	A0A2K6KSF	A0A2K6KSF	Serum amyloid A like 1
URSMA UF	A0A452VG	A0A452VG	Serum amyloid A like 1
URSMA UF	A0A452VG	A0A452VG	Serum amyloid A like 1
URSMA UF	A0A452VG	A0A452VG	Serum amyloid A like 1
URSMA UF	A0A452VG	A0A452VG	Serum amyloid A like 1
MONDO	F7FFU5	F7FFU5	Serum amyloid A like 1
MONDO	F7FFU5	F7FFU5	Serum amyloid A like 1
SARHA	G3WV59	G3WV59	Serum amyloid A like 1
ORNAN	F6QGS9	F6QGS9	Serum amyloid A like 1
CAVPO	H0V714	H0V714	Serum amyloid A like 1
MYOLU	G1PAL8	G1PAL8	Serum amyloid A like 1
MACFA	A0A2K5U4	A0A2K5U4	Serum amyloid A like 1
MACFA	A0A2K5U4	A0A2K5U4	Serum amyloid A like 1
RHIRO RHI	A0A2K6Q6	A0A2K6Q6	Serum amyloid A like 1
RHIRO RHI	A0A2K6Q6	A0A2K6Q6	Serum amyloid A like 1
RHIRO RHI	A0A2K6Q6	A0A2K6Q6	Serum amyloid A like 1
ICTTR	I3M295	I3M295	Serum amyloid A like 1
9TELE NO1	A0A1A8S3z	A0A1A8S3z	Serum amyloid A-like 1
9TELE	A0A1A7WC	A0A1A7WC	Serum amyloid A-like 1
MYOLU	G1PAL8	G1PAL8	Serum amyloid A like 1
MYOLU	G1PAL8	G1PAL8	Serum amyloid A like 1
MYOLU	G1PAL8	G1PAL8	Serum amyloid A like 1
MYOLU	G1PAL8	G1PAL8	Serum amyloid A like 1
NOMLE HC	G1S7R2	G1S7R2 F7	Serum amyloid A protein
NOMLE HC	G1S7R2	G1S7R2 F7	Serum amyloid A protein
NOMLE HC	G1S7R2	G1S7R2 F7	Serum amyloid A protein
NOMLE HC	G1S7R2	G1S7R2 F7	Serum amyloid A protein

NOMLE	HC	G1S7R2	G1S7R2	F7	Serum amyloid A protein
NOMLE	HC	G1S7R2	G1S7R2	F7	Serum amyloid A protein
NOMLE	HC	G1S7R2	G1S7R2	F7	Serum amyloid A protein
NOMLE	HC	G1S7R2	G1S7R2	F7	Serum amyloid A protein
NOMLE	HC	G1S7R2	G1S7R2	F7	Serum amyloid A protein
NOMLE	HC	G1S7R2	G1S7R2	F7	Serum amyloid A protein
NOMLE	HC	G1S7R2	G1S7R2	F7	Serum amyloid A protein
NOMLE	HC	G1S7R2	G1S7R2	F7	Serum amyloid A protein
NOMLE	HC	G1S7R2	G1S7R2	F7	Serum amyloid A protein
NOMLE	FE	G1S7R2	G1S7R2	Q	Serum amyloid A protein
MESAU	HC	P19453	P19453	F7	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
MOUSE	M	P04918	P04918	Q	Serum amyloid A-3 protein
PIG		F1S9B2	F1S9B2		Serum amyloid A like 1
MACNE		A0A2K6B0	A0A2K6B0		Serum amyloid A like 1
MACMU		F6V9Q5	F6V9Q5		Constitutively expressed serum amyloid A protein
MACMU		F6V9Q5	F6V9Q5		Constitutively expressed serum amyloid A protein
RABIT		A0A5F9DS	A0A5F9DS		Serum amyloid A like 1
FELCA		Q1T770	Q1T770	Q	Serum amyloid A protein
FELCA		M3VUA7	M3VUA7		Serum amyloid A like 1
NOMLE	FE	G1S7R2	G1S7R2	Q	Serum amyloid A protein
9TELE	NOT	A0A1A8CL	A0A1A8CL		Serum amyloid A-like 1
MYOLU		G1PAL8	G1PAL8		Serum amyloid A like 1
MYOLU		G1PAL8	G1PAL8		Serum amyloid A like 1
RHIRO		A0A2K6Q6	A0A2K6Q6		Serum amyloid A like 1

HORSE	F7BJA9	F7BJA9	Serum amyloid A protein
HORSE	F7BJA9	F7BJA9	Serum amyloid A protein
HORSE	F7BJA9	F7BJA9	Serum amyloid A protein
ORENI	I3JND6	I3JND6 I3J	Serum amyloid A-like 1
LATCH	H3AUK4	H3AUK4	Serum amyloid A like 1
MOUSE	P31532	P31532	Serum amyloid A-4 protein
MOUSE	P31532	P31532	Serum amyloid A-4 protein
9TELE	A0A1A8CLC	A0A1A8CLC	Serum amyloid A-like 1
ORNAN	F6QGS9	F6QGS9	Serum amyloid A like 1
ORNAN	F6QGS9	F6QGS9	Serum amyloid A like 1
ORNAN	F6QGS9	F6QGS9	Serum amyloid A like 1
CAPHI	A0A452EM	A0A452EM	Serum amyloid A like 1
9TELE	A0A1A7WC	A0A1A7WC	Serum amyloid A protein
9TELE	A0A1A7WC	A0A1A7WC	Serum amyloid A protein
MYOLU	G1PAL8	G1PAL8	Serum amyloid A like 1
MYOLU	G1PAL8	G1PAL8	Serum amyloid A like 1
MYOLU	G1PAL8	G1PAL8	Serum amyloid A like 1
MYOLU	G1PAL8	G1PAL8	Serum amyloid A like 1
MYOLU	G1PAL8	G1PAL8	Serum amyloid A like 1
MACNE M	A0A2K6B0	A0A2K6B0	Serum amyloid A like 1
ICTTR HOR	I3M295	I3M295 AC	Serum amyloid A like 1
MACMU	A0A1D5QY	A0A1D5QY	Serum amyloid A like 1
CANLF	A0A5F4D1	A0A5F4D1	Serum amyloid A protein
NEOVI	P02739	P02739	Serum amyloid A-2 protein
PAPAN M	A0A2I3MZ	A0A2I3MZ	Serum amyloid A like 1
PAPAN M	A0A2I3MZ	A0A2I3MZ	Serum amyloid A like 1
PAPAN M	A0A2I3MZ	A0A2I3MZ	Serum amyloid A like 1
PAPAN M	A0A2I3MZ	A0A2I3MZ	Serum amyloid A like 1
PAPAN M	A0A2I3MZ	A0A2I3MZ	Serum amyloid A like 1
PAPAN M	A0A2I3MZ	A0A2I3MZ	Serum amyloid A like 1
HORSE	F6PJF6	F6PJF6	Serum amyloid A protein
HORSE	F6PJF6	F6PJF6	Serum amyloid A protein
ORYLA	H2LN91	H2LN91 AC	Serum amyloid A-like 1
COLLI	A0A2I0MH	A0A2I0MH	Serum amyloid A-like 1
9TELE	A0A1A7WC	A0A1A7WC	Serum amyloid A-like 1
SAIBB RHIF	A0A2K6RY	A0A2K6RY	Serum amyloid A like 1
RUPRU	E1UYU4	E1UYU4	Serum amyloid A protein
PIG	F1S9B2	F1S9B2	Serum amyloid A like 1
PIG	F1S9B2	F1S9B2	Serum amyloid A like 1
PIG	F1S9B2	F1S9B2	Serum amyloid A like 1
PIG RABIT	F1S9B2	F1S9B2 A0	Serum amyloid A like 1
MYOLU	G1PAL8	G1PAL8	Serum amyloid A like 1
MUSPF	M3YQK5	M3YQK5	Serum amyloid A like 1
MUSPF	M3YQK5	M3YQK5	Serum amyloid A like 1
PIG SHEEP	A0A5G2QN	A0A5G2QN	Serum amyloid A like 1
PIG	A0A287AI4	A0A287AI4	Serum amyloid A like 1
PIG	A0A287AI4	A0A287AI4	Serum amyloid A like 1

VULVU|PIC A0A3Q7RF:A0A3Q7RF:Serum amyloid A protein
VULVU|PIC A0A3Q7RF:A0A3Q7RF:Serum amyloid A protein
VULVU|PIC A0A3Q7RF:A0A3Q7RF:Serum amyloid A protein
VULVU|PIC A0A3Q7RF:A0A3Q7RF:Serum amyloid A protein
MOUSE|M P04918 P04918|P1Serum amyloid A-3 protein
MOUSE P04918 P04918 Serum amyloid A-3 protein
RABIT P53614 P53614 Serum amyloid A-1 protein
CANLF A0A5F4D1:A0A5F4D1:Serum amyloid A protein
HORSE P19857 P19857 Serum amyloid A protein
BUBBU|BO A0A076JSH A0A076JSHSerum amyloid A protein
BUBBU|BO A0A076JSH A0A076JSHSerum amyloid A protein
BUBBU|BO A0A076JSH A0A076JSHSerum amyloid A protein
BUBBU|BO A0A076JSH A0A076JSHSerum amyloid A protein
NEOVI P18575 P18575|P0Serum amyloid A-1 protein
HORSE|DA F6ZPQ6 F6ZPQ6|F7Serum amyloid A protein
HORSE|DA F6ZPQ6 F6ZPQ6|F7Serum amyloid A protein
HORSE|DA F6ZPQ6 F6ZPQ6|F7Serum amyloid A protein
HORSE|DA F6ZPQ6 F6ZPQ6|F7Serum amyloid A protein
HORSE|DA F6ZPQ6 F6ZPQ6|F7Serum amyloid A protein
HORSE|DA F6ZPQ6 F6ZPQ6|F7Serum amyloid A protein
HORSE|DA F6ZPQ6 F6ZPQ6|F7Serum amyloid A protein
HORSE|DA F6ZPQ6 F6ZPQ6|F7Serum amyloid A protein
HORSE|DA F6ZPQ6 F6ZPQ6|F7Serum amyloid A protein
CALJA F6ZH70 F6ZH70 Serum amyloid A protein
FELCA A0A337SU:A0A337SU:Serum amyloid A protein
FELCA A0A337SU:A0A337SU:Serum amyloid A protein
RUPRU|CA E1UYU4 E1UYU4|B:Serum amyloid A protein
BOVIN Q32PB7 Q32PB7 Serum amyloid A protein
PIG F1S9B2 F1S9B2 Serum amyloid A like 1
MACMU A0A1D5QY A0A1D5QY Serum amyloid A like 1
MACMU A0A1D5QY A0A1D5QY Serum amyloid A like 1
RABIT A0A5F9DS:A0A5F9DS:Serum amyloid A like 1
RABIT G1SHI3 G1SHI3 Serum amyloid A like 1
HUMAN P35542 P35542 Serum amyloid A-4 protein
SARHA G3WV59 G3WV59 Serum amyloid A like 1
CAPHI A0A452EM A0A452EM Serum amyloid A like 1
CAPHI A0A452EM A0A452EM Serum amyloid A like 1
CAPHI A0A452EM A0A452EM Serum amyloid A like 1
CAPHI A0A452EM A0A452EM Serum amyloid A like 1
CAPHI A0A452EM A0A452EM Serum amyloid A like 1
CAPHI A0A452EM A0A452EM Serum amyloid A like 1
CAPHI A0A452EM A0A452EM Serum amyloid A like 1
CAPHI A0A452EM A0A452EM Serum amyloid A like 1
CAPHI A0A452EM A0A452EM Serum amyloid A like 1
CAPHI A0A452EM A0A452EM Serum amyloid A like 1
CAPHI A0A452EM A0A452EM Serum amyloid A like 1
CAPHI A0A452EM A0A452EM Serum amyloid A like 1
CAPHI A0A452EM A0A452EM Serum amyloid A like 1
URSMA|UF A0A452VG A0A452VG Serum amyloid A like 1

URSMA|UF A0A452VG A0A452VG Serum amyloid A like 1
 URSMA|UF A0A452VG A0A452VG Serum amyloid A like 1
 PANTR|PAI A0A2I3SXC A0A2I3SXC Serum amyloid A like 1
 SAIBB A0A2K6RY\ A0A2K6RY\ Serum amyloid A like 1
 SAIBB A0A2K6RY\ A0A2K6RY\ Serum amyloid A like 1
 HORSE A0A5F5Q4| A0A5F5Q4| Serum amyloid A like 1
 HORSE F6PJF6 F6PJF6 Serum amyloid A protein
 9TELE A0A0S7LG; A0A0S7LG; Serum amyloid A protein
 HORSE F7C0Y4 F7C0Y4 Serum amyloid A protein
 PIG A0A480KN' A0A480KN' Serum amyloid A protein
 PIG A0A480KN' A0A480KN' Serum amyloid A protein
 PIG F1S9C0 F1S9C0 Serum amyloid A protein
 TAKRU H2U9W6 H2U9W6|† Serum amyloid A-like 1
 RABIT|HOF A0A5F9DS(A0A5F9DS(Serum amyloid A like 1
 RABIT|HOF A0A5F9DS(A0A5F9DS(Serum amyloid A like 1
 OTOGA|RA H0X4B8 H0X4B8|A(Serum amyloid A like 1
 SALSA B9EPA2 B9EPA2 Serum amyloid A protein
 9TELE A0A098GJ3 A0A098GJ3 Serum amyloid A protein
 CANLF J9NVE9 J9NVE9 Serum amyloid A protein
 MACFA A0A2K5U4| A0A2K5U4| Serum amyloid A like 1
 MOUSE P04918 P04918 Serum amyloid A-3 protein
 PIG F1S9B2 F1S9B2 Serum amyloid A like 1
 CALJA U3FFT2 U3FFT2 Serum amyloid A protein
 PANTA T1W3H8 T1W3H8 Serum amyloid A protein
 PANTA T1W3H8 T1W3H8 Serum amyloid A protein
 PANTA T1W3H8 T1W3H8 Serum amyloid A protein
 PANTA T1W3H8 T1W3H8 Serum amyloid A protein
 PANTA T1W3H8 T1W3H8 Serum amyloid A protein
 PANTA T1W3H8 T1W3H8 Serum amyloid A protein
 PANTA T1W3H8 T1W3H8 Serum amyloid A protein
 PANTA T1W3H8 T1W3H8 Serum amyloid A protein
 PANTA T1W3H8 T1W3H8 Serum amyloid A protein
 PANTA T1W3H8 T1W3H8 Serum amyloid A protein
 HORSE F6PJF6 F6PJF6|F6z Serum amyloid A protein
 SARHA G3WV59 G3WV59 Serum amyloid A like 1
 RABIT A0A5F9DS(A0A5F9DS(Serum amyloid A like 1
 VULVU|TA| A0A3Q7RF; A0A3Q7RF; Serum amyloid A protein
 VULVU|TA| A0A3Q7RF; A0A3Q7RF; Serum amyloid A protein
 9TELE|NO1 A0A1A8PR' A0A1A8PR' Serum amyloid A protein
 9TELE|NO1 A0A1A8PR' A0A1A8PR' Serum amyloid A protein
 9TELE|NO1 A0A1A8PR' A0A1A8PR' Serum amyloid A protein
 9TELE|NO1 A0A1A8PR' A0A1A8PR' Serum amyloid A protein
 9TELE A0A1A8FV; A0A1A8FV; Serum amyloid A protein
 CANLF A0A5F4D1(A0A5F4D1(Serum amyloid A protein
 SALSA|ON(B9EPA2 B9EPA2|A(Serum amyloid A protein
 TAKRU H2V509 H2V509 Serum amyloid A protein
 TAKRU H2V509 H2V509 Serum amyloid A protein
 TAKRU H2V509 H2V509 Serum amyloid A protein

TAKRU	H2V509	H2V509	Serum amyloid A protein
TAKRU	H2V509	H2V509	Serum amyloid A protein
TAKRU	H2V509	H2V509	Serum amyloid A protein
TAKRU	H2V509	H2V509	Serum amyloid A protein
TAKRU	H2V509	H2V509	Serum amyloid A protein
TAKRU	H2V509	H2V509	Serum amyloid A protein
TAKRU	H2V509	H2V509	Serum amyloid A protein
TAKRU	H2V509	H2V509	Serum amyloid A protein
TAKRU	H2V509	H2V509	Serum amyloid A protein
TAKRU	H2V509	H2V509	Serum amyloid A protein
TAKRU	H2V509	H2V509	Serum amyloid A protein
TAKRU	H2V509	H2V509	Serum amyloid A protein
TAKRU	H2V509	H2V509	Serum amyloid A protein
TAKRU	H2V509	H2V509	Serum amyloid A protein
BUBBU	F6K454	F6K454	Serum amyloid A protein (Fragment)
RAT	Q5M878	Q5M878	Serum amyloid A protein
RAT	Q5M878	Q5M878	Serum amyloid A protein
FELCA	M3VUA7	M3VUA7	Serum amyloid A like 1
NOMLE	FE A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE	FE A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE	FE A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
NOMLE	FE A0A2I3HAC	A0A2I3HAC	Serum amyloid A protein
MACMU	F6V9P6	F6V9P6	Serum amyloid A protein
ORYLA	H2LN91	H2LN91 A	Serum amyloid A-like 1
ORYLA	H2LN91	H2LN91 A	Serum amyloid A-like 1
ORYLA	H2LN91	H2LN91 A	Serum amyloid A-like 1
HORSE	F7C0Y4	F7C0Y4	Serum amyloid A protein
HORSE	F7C0Y4	F7C0Y4	Serum amyloid A protein
9TELE	A0A1A8FV!	A0A1A8FV!	Serum amyloid A protein