

Supplementary table 1

Protein	Sequence	P-value	Xcorr	dCn
RIR2_DROME	FSLKS*PSKK	0.9917	2.039	0.291
UPTR:Q9W3R9_DROME	KRS*PISIEIK	1	2.649	0.3
UPTR:Q9W3R9_DROME	KRSPIS*IEIK	0.9655	2.039	0.082
UPTR:Q8MYV4_DROME	ASS*GDEKEPFAK	0.9807	2.61	0.142
UPTR:Q5UHE2_DROME	AAS*PEPMK	0.9395	1.794	0.155
UPTR:Q9VAY1_DROME	RVS*PVPAK	0.9962	2.231	0.193
UPTR:Q7KJV6_DROME	LSVQS*PPK	0.994	2.174	0.241
UPTR:Q8T3Q6_DROME	KLS*PQPPVVDKK	0.9943	2.093	0.262
HP1_DROME	RKS*EEPTAPSGNK	0.9805	2.374	0.169
UPTR:Q9VLK2_DROME	LSKPAS*PPK	0.9783	1.589	0.296
UPTR:Q6AWF3_DROME	RGS*ESGSTADAHLR	0.9184	2.806	0.067
UPTR:Q6AWQ1_DROME	KRES*PIGR	0.995	1.753	0.275
RIR2_DROME	KMS*IGHEANGQLAK	0.948	2.445	0.125
UPTR:Q8MYY9_DROME	RRPS*EDEEEQTK	0.9976	2.498	0.265
GYS_DROME	VES*GADLKDYFDR	1	3.36	0.408
UPTR:Q8IHF0_DROME	RQDS*PVKR	0.9989	2.836	0.216
GROU_DROME	TRS*PLDIENDSKR	0.9922	3.697	0.112
UPTR:Q7KRZ4_DROME	TRS*PLDIENDSK	0.9896	2.235	0.141
UPTR:Q6NPA6_DROME	RS*TTLYEK	0.9633	1.612	0.13
UPTR:Q9VZQ1_DROME	SKS*PDTEDRQPSAK	0.9857	2.187	0.249
UPTR:Q9VZQ1_DROME	SKS*PDTEDR	0.9847	1.962	0.18
UPTR:Q6NN85_DROME	RPPS*PDAIR	0.9313	1.562	0.215
UPTR:Q9VQK7_DROME	AHGS*EDEQVAEKEK	0.9819	1.903	0.229
UPTR:Q9VQK7_DROME	AHGS*EDEQVAEK	1	2.748	0.456
UPTR:Q86LF5_DROME	SKS*PTPLPGK	0.9439	2.081	0.23
UPTR:Q9VBZ5_DROME	AKVS*PTGPVR	0.9979	2.051	0.314
UPTR:Q6AWQ1_DROME	RQS*PQQNR	0.9799	1.902	0.161
UPTR:Q9Y145_DROME	HAS*PLPAAPR	0.998	1.978	0.432
UPTR:Q7KN56_DROME	TNIIFGS*PKR	0.9121	1.476	0.148
UPTR:Q9VWH6_DROME	TTs*LNQLKK	0.9723	1.492	0.198
YC17_DROME	WRDES*DDEEGDQK	0.9941	2.971	0.18
VAV_DROME	SHS*DEAIYK	0.993	1.938	0.29
UPTR:Q7Z2C9_DROME	KFS*GGDQDEATPNKK	1	2.884	0.294
GP:AY122261_1	LKNQDS*DDEDVEAR	0.9917	3.056	0.159
UPTR:Q9VNA1_DROME	FES*VDKLSR	0.9971	2.132	0.254
UPTR:Q9VU43_DROME	KTGS*VEPAPAK	0.9937	2.366	0.156
UPTR:Q9VU43_DROME	TGS*VEPAPAK	0.9944	2.478	0.219
UPTR:Q8INM3_DROME	AVRS*PAVEQK	0.9955	2.035	0.241
UPTR:Q9Y162_DROME	SDS*DDEDGDDPEKKK	0.995	2.799	0.211
UPTR:Q7KRZ4_DROME	NSVS*PADREK	0.9692	1.733	0.214
UPTR:Q9V695_DROME	KSTS*PTELSR	0.907	1.908	0.035
UPTR:Q9NJH7_DROME	AGKNDDS*DEEEVPAK	1	3.905	0.312
UPTR:Q9VYV4_DROME	NAGGVGVGVGEKS*PDLKK	0.9761	1.706	0.247
UPTR:Q94885_DROME	KES*TETGSER	0.9716	1.813	0.193
UPTR:Q9W3W1_DROME	SQVDEKPQPS*PVPLRR	1	2.792	0.357
UPTR:Q9W3W1_DROME	SQVDEKPQPS*PVPLR	0.9987	2.829	0.38
UPTR:Q9VP57_DROME	HFEVHQSPS*ASTVSPK	0.9012	3.276	0.013
UPTR:Q9VP57_DROME	HFEVHQSPSASTVS*PK	0.9801	3.777	0.07
UPTR:O16040_DROME	TADS*PAKEPQEICEVK	0.9129	3.622	0.402
UPTR:Q9W2V7_DROME	RADRS*DDEGDALPNSK	1	3.508	0.397
UPTR:Q8SWR4_DROME	DQS*PVPEGSAR	0.9955	2.01	0.339
UPTR:Q9V859_DROME	ASAFQFS*DDEEEVKR	0.9582	2.144	0.204
UPTR:Q8MR49_DROME	AS*AFQFSDDEEEVKR	0.9552	3.014	0.021
UPTR:Q8MR49_DROME	ASAFQFS*DDEEEV	0.9972	2.573	0.321
UPTR:Q9VZ00_DROME	HAVKPAALSPSPSS*PSAR	0.9623	4.02	0.017
UPTR:Q9VZ00_DROME	HAVKPAALSPSPS*SPSAR	0.9515	3.931	0.007
SSRP_DROME	NYKPEAGGDS*DNEKGK	1	2.653	0.394
UPTR:Q9V3H9_DROME	KAKS*PIIFNR	0.9967	2.037	0.271

Protein	Sequence	P-value	Xcorr	dCn
GP:AE003832_37	KAGDAANKDEDS*DNETH	0.937	2.78	0.095
GP:AE003832_37	AGDAANKDEDS*DNETH	0.9689	3.252	0.095
HMGD_DROME	SKKEESDEDDDDDES*E	0.9993	3.1	0.325
HMGD_DROME	SKKEES*DEDDDDDESE	1	4.232	0.296
HMGD_DROME	KEESDEDDDDDES*E	1	4.01	0.541
HMGD_DROME	KEES*DEDDDDDESE	1	3.599	0.488
UPTR:Q8MRH4_DROME	ATVSTAAPHIVRDPS*PAR	1	3.098	0.408
UPTR:Q9VNA1_DROME	RAS*QDVSSLR	0.9986	2.135	0.37
UPTR:Q9VAE9_DROME	RKS*AGDEDVLK	0.9817	1.746	0.182
UPTR:Q9NHN6_DROME	RFS*DDIADQR	0.9978	2.262	0.271
UPTR:Q9V3V0_DROME	NGSGAVDS*PPPPK	0.9892	2.309	0.211
UPTR:Q8IH82_DROME	KTGNLLASS*QPK	0.9617	2.118	0.11
RS3A_DROME	VFEVS*LADLQK	0.9976	2.395	0.337
UPTR:Q9UB07_DROME	HSS*PTAVAVTPAK	0.9952	3.359	0.147
UPTR:Q9VGZ9_DROME	DLNDS*PKVEQK	0.9993	3.016	0.296
UPTR:Q9VW6_DROME	KLS*PSESPESSK	0.9085	1.816	0.047
DKC1_DROME	KPAAQEVS*PTNGSSEPSKR	0.9804	2.796	0.151
UPTR:Q9W2U7_DROME	LAFS*DDESTPEEHQGQGK	0.9688	2.114	0.17
UPTR:Q9V624_DROME	EAEATS*PSENTR	0.9248	1.773	0.125
UPTR:Q8MR20_DROME	RSS*DSDLSVTPK	0.9265	1.424	0.183
UPTR:Q9W2J6_DROME	KTDKEEETGS*S	0.9544	2.239	0.007
UPTR:Q9VAE9_DROME	LAGTGSNS*LGSSTR	0.9916	2.56	0.222
UPTR:Q9VY91_DROME	FVS*EGDGGHVKPTTFTMRD	0.996	3.579	0.183
UPTR:Q867Y1_DROME	RAPS*PPPAKPAEPPKPAEPR	0.9956	3.3	0.198
UPTR:Q867Y1_DROME	APS*PPPAKPAEPPKPAEPR	0.9983	2.085	0.404
UPTR:Q9VFF3_DROME	VQQALGES*DDEVVEVPIER	0.9948	2.295	0.251
UPTR:Q8IGE9_DROME	S*ISLKEEDTDVEQHQNNR	0.9872	3.81	0
UPTR:Q9VT61_DROME	ADDAS*DDEDVKVK	0.9976	1.946	0.348
HSP27_DROME	RAS*GGPNALLPAVGK	1	3.335	0.438
UPTR:Q8MPP1_DROME	SVS*PTTAATSSSPVK	0.9771	2.69	0.095
UPTR:Q24478_DROME	EAVTAS*EGEDDVHLEADNIR	0.9568	1.992	0.169
UPTR:O17045_DROME	NVGIFIKDDS*DEEDVDDKK	0.9978	2.489	0.295
UPTR:Q6AWP8_DROME	AASDASEALGSGSALS*PTAAKPIK	0.9383	3.497	0.038
GP:M26400_1	KIDAGLS*ASQQNLVDNHSIAK	0.9594	4.819	0.413
GP:M26400_1	KIDAGLSAS*QQNLVDNHSIAK	0.9732	4.747	0.463
GP:M26400_1	IDAGLSAS*QQNLVDNHSIAK	0.9516	2.892	0.082
UPTR:Q9VBP9_DROME	RTS*TTVLDSQAFK	0.9922	2.776	0.092
UPTR:Q9V5A0_DROME	KLS*EEYTSSSAQK	0.9972	2.023	0.361
UPTR:Q9V468_DROME	EDLAAGDAPPS*PTTK	0.9875	3.486	0.056
UPTR:Q8MZ42_DROME	NVAENLAGSSSS*PSR	0.9862	3.05	0.096
UPTR:Q8T080_DROME	SNS*QEADSEELLR	0.9721	2.832	0.04
UPTR:Q6NP07_DROME	NLAEEEEAGTTHQNNVSTS*PK	0.9458	3.884	0.015
GP:AE003480_69	SELDDLDS*NQVAEEAPSAIVR	0.9258	3.007	0.052
UPTR:Q9VUY9_DROME	ALGGIVLTAS*HNPGGPENDFGIK	0.9294	3.546	0.025
UPTR:Q9XYZ7_DROME	TSLFSCADSKDS*PK	1	3.494	0.36
UPTR:Q96829_DROME	DAAES*PAAVDASASAATDDVADKK	0.9554	1.937	0.194
UPTR:Q9W019_DROME	NPEHAAS*DDEVANK	1	3.537	0.522
UPTR:Q5BII8_DROME	TGPAPFKS*PAQSGGSK	0.9262	1.39	0.246
UPTR:O16048_DROME	S*QSSENILNEKDR	0.964	2.456	0.147
UPTR:Q9VUZ8_DROME	RAAIDS*DDDEDYGC	1	3.752	0.437
UPTR:Q9VBX3_DROME	KKESNS*EDELEYDPSLYPQR	0.9556	3.993	0.032
UPTR:Q6NLK4_DROME	KKES*NSEDELEYDPSLYPQR	0.968	3.977	0.069
UPTR:Q9VHC0_DROME	AQS*LAGEGEKEKDNK	0.9915	1.62	0.364
UPTR:Q9VHC0_DROME	AQS*LAGEGEKEK	0.9793	1.832	0.158
UPTR:Q9V426_DROME	KKENDS*EEELEYDPALYPQR	1	4.185	0.402
UPTR:Q9V426_DROME	KENDS*EEELEYDPALYPQR	0.9606	2.342	0.172
UPTR:Q86B44_DROME	SDLMLESGCPELS*PR	0.9971	2.503	0.332
SRR55_DROME	NGNAS*PDRNNNESMDD	1	3.179	0.467
UPTR:Q9VXE6_DROME	ELPEES*EEEEEEDESSAGALR	1	4.598	0.482
GP:AF006529_1	EKEVS*DDEADDEKK	0.994	1.625	0.33
UPTR:Q9V6S4_DROME	VFGSLKPNSNQGDS*DGE	0.9964	2.983	0.243
UPTR:Q8INW7_DROME	SPTAGHDFNGSSTTPGYANQGS*LPR	0.9969	2.804	0.248

Protein	Sequence	P-value	Xcorr	dCn
UPTR:Q9V534_DROME	LQCLAGVMVTAS*HNPK	0.9943	4.013	0.082
UPTR:Q8ML25_DROME	LQS*GGEGVGITSEQLAK	1	3.643	0.492
UPTR:Q9VXK5_DROME	DVLQNIQS*DDDEETYDLNNLAK	1	5.017	0.375
UPTR:Q9VYV4_DROME	VLDGDDTNNDGVGVLDLDES*QGAGGR	0.9507	2.219	0.196
UPTR:Q9VMJ7_DROME	IVEDNFS*NDEDEPR	1	3.387	0.436
UPTR:Q5BHY9_DROME	NS*PATPVYQETAPGPR	0.985	2.438	0.172
MODU_DROME	VQEETVPVQSPSKK	0.9928	2.903	0.099
MODU_DROME	SEGADEVDES*DDDEEAPVEKPVSK	1	3.413	0.326
UPTR:Q9VSH4_DROME	KS*PEPVVAEAAEAPSSK	1	3.739	0.544
UPTR:Q24496_DROME	TPFASTPNDS*PDVILK	0.9924	2.577	0.218
UPTR:P91675_DROME	TATVGADS*DEEDIEPPQPDAGDLTR	0.9396	4.196	0.004
UPTR:Q9V3V0_DROME	YEDEDDDRVRGS*PR	0.9749	2.016	0.153
ARS2_DROME	KPVRPVNS*DGENWDDDAENSAPK	1	3.485	0.437
UPTR:Q9VI58_DROME	KTS*LPGSTAPNIAAPVTK	0.9952	3.36	0.083
UPTR:Q8SX18_DROME	GGGGGS*GSNLNEQTAEDGQAQQQQQPR	0.9196	3.875	0.004
UPTR:Q8SX18_DROME	GGGGGSGS*NLN EQTAEDGQAQQQQQPR	0.9794	3.651	0.001
ATU_DROME	KAPAAADIFGDADDIS*DDEDEAGPAAR	0.9962	2.451	0.28
MCM2_DROME	AAGIHRDRDLFGQGS*DDEDDVGPR	0.9966	2.545	0.292
MCM2_DROME	DLFGQGS*DDEDDVGPR	1	3.733	0.5
MCM2_DROME	DDRLLGFGQGS*DDEDDVGPR	1	4.751	0.525
GP:S80255_1	AVRPSDNISLPPTS*PGNISLPATSPAR	0.9386	3.453	0.056
UPTR:Q6AWQ1_DROME	SS*VEYAGPAVN TIDL CR	0.9613	3.04	0
UPTR:Q9VU43_DROME	S*SVEYAGPAVN TIDL CR	0.9374	2.802	0
UPTR:Q9I7T7_DROME	SVATSTS*TENL SAAATASK	0.9892	4.212	0.074
UPTR:Q8IGZ9_DROME	SGSVSSASSSVSSS*TENLK	0.9941	4.236	0.059
UPTR:Q86BS3_DROME	VENSEAPAPVS*PAPVPQK	1	3.132	0.493
UPTR:Q9VVG9_DROME	IEVK S*DDDIDEVPVEK	0.9978	2.33	0.299
UPTR:Q9UB07_DROME	YALDTNDIGQPES*DEELCDEATRPR	0.9987	3.387	0.256
UPTR:Q8IGG3_DROME	SGS*VSSFPDALDENNTSSGLNSPTDSL PK	0.9578	4.342	0.017
UPTR:Q9V4M0_DROME	ESS*SDDQQQAFYAGGS DR	0.9768	3.429	0.003
UPTR:Q9V4M0_DROME	ESSS*DDDQQQAFYAGGS DR	0.9796	3.761	0.005
UPTR:Q9V544_DROME	VSVLDEDL DDELPS*DEEKADETNRPK	0.907	2.98	0.085
UPTR:Q8MQK4_DROME	TT S*IGNQTTTANPSECII R	0.9063	2.441	0
UPTR:Q9VN21_DROME	TT S*TQDNEQPQGETAQK	0.9919	4.533	0.001
UPTR:Q8MYV4_DROME	ESES AAGTPVNA DQPGS*PNAK	1	3.239	0.422
SQD_DROME	DVTADGPGS*ENG DAGAAG STNGSSDNQSAASGQR	0.9979	4.622	0.167
UPTR:Q9VU84_DROME	INVFNQNQPQDAPVPS*PPR	0.9987	3.373	0.322
UPTR:Q9VBX3_DROME	TT GETSPQA EKEDS*ANEQSADPAVAAEE DESK	0.9954	5.046	0.121
UPTR:Q9VBX3_DROME	TT GETS*PQA EKEDSANEQSADPAVAAEE DESK	0.95	3.621	0.021
UPTR:O16043_DROME	KESSEAVLP AVENGSEE VTNGDS*T DAPAIEAVK	0.9022	4.28	0.138
UPTR:Q9V468_DROME	RRS*PER	0.9186	1.539	0.059
UPTR:Q8MQS4_DROME	SSS*LDLNK	0.9461	1.852	0.135
UPTR:Q9VL57_DROME	SAS*GADVTEK	0.9933	2.029	0.287
UPTR:Q8SZS8_DROME	SKS*PVPVTVK	0.9838	1.719	0.255
UPTR:Q9VWS3_DROME	SSGS*SLNIQR	0.9318	1.588	0.181
UPTR:Q9VHR6_DROME	GRGS*VESLNR	0.9342	1.494	0.22
UPTR:Q9VLD6_DROME	AFS*ADRTPLK	0.9936	1.954	0.239
UPTR:Q6XHX7_DROYA	APS*ADNVNVAR	0.9674	1.571	0.288
UPTR:Q8IGE9_DROME	RTTKS*EGDQSGVEAGAK	0.9956	3.171	0.159
UPTR:Q8IGE9_DROME	SEG DQS*GVEAGAK	0.9963	3.092	0.209
UPTR:Q9VN21_DROME	TTKS*EGDQSGVEAGAK	0.9906	3.016	0.164
UPTR:Q9V4Z4_DROME	VRQAAGS*DDES	0.9971	2.017	0.289
UPTR:Q9VK59_DROME	NTS*PDGGNF SR	0.9801	2.276	0.169
UPTR:Q960C4_DROME	RRGS*PSFLDR	0.9572	1.521	0.178
UPTR:Q960C4_DROME	RGS*PSFLDR	0.9542	1.622	0.209
UPTR:Q9V6Q6_DROME	LES*PERLDTKPAELLK	0.9957	2.07	0.253
UPTR:Q8IMW2_DROME	RRNS*NEQPPP PPPPEVK	0.9992	3.39	0.235
UPTR:Q9W261_DROME	SAS*PLSTPALNR	0.922	1.826	0.143
ARS2_DROME	KELAEDSKDS*DSKP EDK	0.9712	2.953	0.086
NCD_DROME	SRS*ACDINELR	0.996	2.387	0.189
UPTR:Q9VZ00_DROME	VSTS*PPPTIAASR	0.9472	1.613	0.214
UPTR:Q8MSU7_DROME	IPS*PSRPSIQANSFQDPR	0.9897	3.628	0.1

Protein	Sequence	P-value	Xcorr	dCn
UPTR:Q24147_DROME	SHS*TGSPEKDER	0.9337	2.203	0.001
UPTR:Q9I7K6_DROME	KKPEDPSSEAEALCS*PAKR	0.9739	2.165	0.153
UPTR:Q9I7K6_DROME	KKPEDPSSEAEALCS*PAK	1	3.945	0.353
UPTR:Q9W179_DROME	LSNFRGS*APDLSR	0.901	1.814	0.048
UPTR:Q9W1H5_DROME	DNHES*RLSPFQK	0.9573	1.139	0.338
UPTR:Q8IME2_DROME	WVAEGS*PTHSTPVR	0.9749	2.978	0.051
UPTR:Q8MR29_DROME	VEPEDDS*DEELVR	0.9517	1.647	0.214
UPTR:Q8MZC0_DROME	SNTGS*DDEDGAPVLSK	0.9929	2.631	0.221
GP:AE003493_34	RQS*LELTPEQLER	0.9973	1.69	0.379
UPTR:Q9VJ87_DROME	TQDS*DEFNLEGPGSK	0.9946	3.404	0.15
UPTR:O46093_DROME	SDPLLGQDSVGVS*PIR	0.999	2.642	0.409
UPTR:Q8MQK8_DROME	LIFEDVPIQKES*DGEDPEEKPEEK	0.938	2.082	0.167
UPTR:Q9VHC8_DROME	NNS*QQSTGTVASTGTPSK	0.9879	2.429	0.202
UPTR:Q8MSN4_DROME	ILPDDGSAS*PIKNNVDSK	0.9248	1.434	0.229
UPTR:Q9VAW4_DROME	KDTS*PSASIEGAGSSGNEAK	0.9898	3.815	0.001
UPTR:Q9VAW4_DROME	DTSPS*ASIEGAGSSGNEAK	0.9414	2.563	0.053
UPTR:Q9VAW4_DROME	DTS*PSASIEGAGSSGNEAK	0.9578	2.969	0.001
UPTR:Q9VT61_DROME	DKDADGGDES*DDDDDDEEDDKEDEK	1	4.524	0.458
UPTR:Q9VXF9_DROME	SANRPVGGNPAISTLDFSNIAVPGTSSGGS*PPSR	0.9497	2.816	0.099
UPTR:Q9XZ21_DROME	RSS*PEDDKLRL	0.9859	2.592	0.12
UPTR:Q9VUL1_DROME	GCRLS*PR	0.9596	1.757	0.152
UPTR:Q9VAW5_DROME	SGS*LGNKPQVANR	0.9513	2.205	0.161
UPTR:Q9VYQ8_DROME	NS*PPQLPK	0.9616	1.304	0.346
UPTR:Q86BR5_DROME	RPPS*PPPR	0.9653	2.192	0.106
UPTR:Q9VLT5_DROME	SSNFGDHANAS*PPR	0.9953	1.888	0.276
UPTR:Q9VSW1_DROME	APS*DSKEFHEVTK	0.9971	2.146	0.329
UPTR:Q8MRS4_DROME	RLS*LADASK	0.991	1.957	0.237
GP:U01842_1	SLTPSKTS*PR	0.9353	1.896	0.097
UPTR:Q86BM5_DROME	SSS*PPPPLPK	0.9795	1.844	0.253
UPTR:Q8MRM6_DROME	SQS*PPRTEQVVMTPR	0.9848	2.635	0.149
UPTR:Q9GQN4_DROME	KRPLDS*DPENEQTKR	0.9608	2.071	0.14
UPTR:Q8MRH4_DROME	SS*SPAPVPVAVAR	0.913	2.523	0.003
UPTR:Q86R99_DROME	RTQS*FENDQK	0.9952	1.817	0.318
UPTR:Q9V5T3_DROME	GTDS*DGEPSAAQK	0.9314	2.074	0.101
UPTR:Q7KMK8_DROME	ENAPVAKS*PEKK	0.9803	1.689	0.233
UPTR:Q9W4I2_DROME	RVS*ENQEIEDR	0.9987	2.22	0.403
UPTR:Q8MRH0_DROME	RSS*VGIGVEQHTVDVGQGAER	0.9497	2.429	0.13
UPTR:Q8MR13_DROME	KENS*SDSLASGSQK	0.9721	2.174	0.116
UPTR:Q24036_DROME	EGGEQEKS*NEQEGTEGDKIEK	0.9185	1.983	0.202
UPTR:Q9W5W9_DROME	LLGSIS*PEPSTPAPR	0.9818	1.849	0.356
UPTR:Q9VKD8_DROME	TLGES*DEETDNVSK	0.9051	1.886	0.144
UPTR:Q86BS3_DROME	SDTAAPHS*PLPASSQVSPSSRPSR	0.9741	1.978	0.204
ECM29_DROME	ELRKES*DDEDEPNTSQELSADER	1	3.037	0.412
GP:AY069224_1	KES*DDEDEPNTSQELSADER	0.9962	3.096	0.205
UPTR:Q9VYV4_DROME	NTATES*ETENENTNPAAALTPLQSGEAK	0.9166	2.944	0.044
HP1_DROME	KIDNPESSAKVS*DAEEEEEEYAVEK	0.9847	3.49	0.103
HP1_DROME	IDNPRESSAKVS*DAEEEEEEYAVEK	0.9857	2.831	0.148
UPTR:Q9NJH7_DROME	QAAVAENAGEDEAS*DDEEGGSTVK	0.9072	1.362	0.348
UPTR:Q9V608_DROME	KHVS*LDVK	0.9625	1.572	0.134
UPTR:Q9VKJ9_DROME	KAPS*PPKPK	0.9975	1.581	0.402
UPTR:Q9VC60_DROME	DFDQS*PTR	0.9714	1.768	0.187
UPTR:Q8SWR4_DROME	LRS*PEQEDQK	0.9927	2.027	0.181
UPTR:Q8MKN2_DROME	SRS*PGGQSAASGGK	0.9767	1.991	0.143
41_DROME	LLQDPLLS*PTTR	0.9614	1.86	0.174
GP:L08825_1	SGYKDVFDFGDS*DNENEPDAYLAR	0.9959	3.019	0.226
GP:L08825_1	DVDFGDS*DNENEPDAYLAR	1	3.624	0.42
UPTR:Q9W4L2_DROME	TS*PIQVNNGAALACPLVR	0.9683	3.239	0.511
UPTR:Q9W584_DROME	SLS*NVNPLLCTTPQK	0.9176	2.591	0.364
UPTR:Q9W0B0_DROME	FKS*PAHS*PEAPPKK	1	2.618	0.324
HMGD_DROME	SKKEES*DEDDDDDES*E	0.9769	3.011	0.112
HMGD_DROME	S*KKEESDEDDDDDES*E	0.9252	2.773	0.048
HMGD_DROME	KEES*DEDDDDDES*E	0.9985	2.15	0.359

Protein	Sequence	P-value	Xcorr	dCn
HMGD_DROME	KKEES*DEDDDDES*E	1	3.805	0.472
GP:AF119716_1	MLQKS*DDS*ADEKEAPVSSK	0.9971	2.334	0.32
GP:AE003480_69	AVDLVDDS*NDVDNS*IEAEEEKPR	1	2.997	0.305
UPTR:Q5U167_DROME	ILDPSHNDS*DNDS*DFNEDVECASR	0.9715	3.187	0.1
UPTR:Q9XZ21_DROME	AQS*PSIEINAQQLS*PTHNATEVNVPK	0.9119	2.203	0.166
GP:AE003627_46	KPEANDDDDVDLFGS*DS*EEEDGEAR	0.9903	2.948	0.212
UPTR:Q6NLK4_DROME	TTGETS*PQAEKEDS*ANEQSADPAVAEEDESK	0.9797	4.973	0.044
UPTR:Q9VN21_DROME	TTKS*EGDQS*GVEAGAK	0.9283	1.489	0.159
UPTR:Q86BM5_DROME	SSS*PPPLPKS*PPPSR	0.9514	2.156	0.134
UPTR:Q9VJK6_DROME	QS*PVLNLSKGSGNTDHGGSNCAGS*ER	0.9369	1.522	0.195
UPTR:Q960C4_DROME	LRAQS*DDGS*DAETGVGDGALEEFQQSR	0.9342	2.439	0.125
HMGZ_DROME	KKES*S*EEEEEDES*E	0.9861	1.999	0.202
UPTR:Q6IKY8_DROME	CTHGQNPIAVS*IS*HFAY*PLGQLK	0.955	2.167	0.14
UPTR:Q9VK58_DROME	TINQIFKSGHMGLEKNTFS*HY*R	0.9175	2.958	0.096
UPTR:O16043_DROME	ADEAVAT*PEKK	0.9989	2.518	0.312
PSA3_DROME	KAGDAANKDEDSDNET*H	0.9256	2.124	0.045
C190_DROME	APSSFGST*GSVSK	0.9236	2.456	0.002
UPTR:Q8IGE9_DROME	SISLKEEDT*DVEQHQNNR	0.9892	3.174	0.152
UPTR:Q9VN21_DROME	TTSQT*DNEQPQGETAQKR	0.9045	2.114	0.002
UPTR:Q8IGE9_DROME	TT*SQTDNEQPQGETAQKR	0.9697	3.224	0.001
RFC1_DROME	T*ASSEDDVVAATPEPIAK	0.9512	2.604	0.05
UPTR:Q6XHQ8_DROYA	AAAADAAGDAADNGT*SKDGEDAADAAAAAPAK	0.935	3.301	0.025
UPTR:Q9VAW4_DROME	KDT*SPSASIEGAGSSGNEAK	0.9864	3.357	0.004
UPTR:O16043_DROME	ESSEAVLPENGSEEVTNGDST*DAPAIEAVKR	0.9046	3.338	0.078
UPTR:Q86PC7_DROME	AAEAVT*PPPSKK	0.976	2.448	0.097
UPTR:Q95T28_DROME	KEEQET*DDEDKGSSGK	0.9921	2.037	0.251
UPTR:Q70HU3_DROME	TSAT*SPTDKDAPLAPLK	0.9145	2.062	0
UPTR:Q9VYV4_DROME	VLDGDDT*NDGVGVDLDDES*QGAGGR	1	3.873	0.374
UPTR:Q7KRQ4_DROME	TDLEQENIKDRT*PS*PSNQNEDPTQK	0.9526	3.706	0.071
UPTR:Q9V3W7_DROME	RGT*PT*YSPVR	0.942	1.824	0.053
GP:AE003425_1	QLLHGEPNVSY*ICSR	0.9586	3.987	0.172
UPTR:Q59E39_DROME	IYHY*IQR	0.9613	1.714	0.19
UPTR:Q9VW47_DROME	EEDQVEPRPPY*EPKQDKDT*VR	0.9385	2.317	0.182

Supplementary Table 2

* * *

MMDGYAQEWPRLTHTDNGLAMDQLGGDLPLDVGFEQTRAR**SNTWPCPRPENFVEPTDELDs**
ARSNTWPCPRPENFVEPTDELDs

ASNQQLAPGDSQQAIQNANAAK
GDSQQAIQNANAACK
GDSQQAIQNANAAK
PGDSQQAIQNANAACK

ASNQQLAPGDSQQAIQNANAAK
TKA**SNQQLAPGDSQQAIQNANAAKKNSSRRNAWGNLSYADLITHAIGSATDKRLTLSQIYEW**
TK
TKASNQQLAPGDSQQAIQNANAACK
PGDSQQAIQNANAACK
PGDSQQAIQNANAACK
ASNQQLAPGDSQQAIQNANAACK

**

MVQNVPYFKDKGDSNSSAGWKNSIRHNLSLHNRFMRVQNEGTGKSSWWMLNPEAKPGKSVRR
SSWWMLNPEAKPGK

RAASMETSRYEK **SGGGFQ**
RAA**SMETSRYEKRRGRAKKRVEALRQAGVVGLNDATPS**PSSVSEG**LDFPESPLHSGGGFQ**
RAASMETSRYEK **SGGGFQ**
AASMETSRYEK

* * *

LSPDFR **ASSNASSCGRLSPIR**
L**SPDFRQRASSNASSCGRLS**PIRAQDLEPDWGFVVDYQNTTMTQAHQAQALEELTGTMAELT
LSPDFR **ASSNASSCGRLSPIR**
ASSNASSCGRLSPIR

LCNQQQQGFSAAASGLPSQPPPPYQPPQHQQAQQQQQQSPYALNGPASGYNTLQPQSQCLL
HRSLNCSCMHNARDGLSPNSVTTMSPAYPNSEPSSDSLNTYSNVLDGPADTAALMVQQQQ
QQQQQQQLSASLEGQCLEVNNEAQPIDEFNLENFPVGNLECNVEELLQQEMSYGGLLDINI
PLATVNTNLVNSSSGPLSISNISNLSNISSNSGSSLNLQQLQQLQQQQQQQAQQQQQQAQ
QQQQHQHQHQQQLLLNNNNNNSSSLELATQTATTNLNARVQYSQPSVVTSPPSWVH

Supplementary Table 3

MS Level	Protein	Sequence	Peptide probability	dCn
MS3	UPTR:O96829_DROME	AAES*PAAVDASASAATDDVADKK	0.9986	0.469
MS2	UPTR:Q6NMV3_DROME	AAFLQHLPDAL\$PTTLQK	0.9931	0.117
MS3	UPTR:Q6NMV3_DROME	AAFLQHLPDAL\$PTTLQK	0.9642	0.127
MS3	UPTR:Q86B44_DROME	AAGLGALDSPYLIDS*DDEDEQK	0.9096	0.204
MS2	MCM2_DROME	AAMT\$*PVGDFEPFENEDEILGDQTVR	0.9994	0.203
MS3	MCM2_DROME	AAMT\$*PVGDFEPFENEDEILGDQTVR	0.9128	0.249
MS2	MCM2_DROME	AAMT\$*SPVGDFEPFENEDEILGDQTVR	0.9033	0.001
MS3	MCM2_DROME	AAMT\$*SPVGDFEPFENEDEILGDQTVR	0.9052	0.001
MS2	MCM2_DROME	AAMTS\$*PVGDFEPFENEDEILGDQTVR	0.9378	0.029
MS3	MCM2_DROME	AAMTS\$*PVGDFEPFENEDEILGDQTVR	0.9388	0.029
MS2	UPTR:Q9W352_DROME	AAS*PEIFLNPELQGIR	1	0.485
MS3	UPTR:Q9W352_DROME	AAS*PEIFLNPELQGIR	1	0.431
MS2	UPTR:Q6AWP8_DROME	AASDASEALGSGSALS*PTAAK	0.9398	0.191
MS3	UPTR:Q6AWP8_DROME	AASDASEALGSGSALS*PTAAK	0.9502	0.106
MS2	UPTR:Q6AWP8_DROME	AASDASEALGSGSALS*PTAAKPK	0.9903	0.122
MS3	UPTR:Q6AWP8_DROME	AASDASEALGSGSALS*PTAAKPK	0.9957	0.133
MS2	CAS_DROME	AAT*PAPS*AGATAGNLSAAQVK	0.9555	0.148
MS2	UPTR:Q9V369_DROME	AATTFTFGKPSAPIGASVS*PLAK	0.9988	0.172
MS3	UPTR:Q9V369_DROME	AATTFTFGKPSAPIGASVS*PLAK	0.9998	0.134
MS2	UPTR:Q9VT61_DROME	ADDAS*DDEDVK	0.9277	0.051
MS3	UPTR:Q9VT61_DROME	ADDAS*DDEDVK	0.9642	0.126
MS2	UPTR:Q9VT61_DROME	ADDAS*DDEDVKVK	0.9901	0.147
MS3	UPTR:Q9VT61_DROME	ADDAS*DDEDVKVK	0.9619	0.193
MS2	UPTR:O16043_DROME	ADEAVAT*PEKK	0.9581	0.08
MS3	UPTR:O16043_DROME	ADEAVAT*PEKK	0.925	0.118
MS2	UPTR:Q961K0_DROME	ADSGPFLFTPPIHFNS*VDRR	0.9818	0.131
MS3	UPTR:Q961K0_DROME	ADSGPFLFTPPIHFNS*VDRR	0.9815	0.131
MS2	UPTR:Q7KRW8_DROME	AELPEDAEVIS*EDEL PASNNNNNTATEPK	0.9774	0.131
MS3	UPTR:Q7KRW8_DROME	AELPEDAEVIS*EDEL PASNNNNNTATEPK	0.9723	0.131
MS2	UPTR:Q8I1G5_DROER	AENQNS*AMDMDEDDPVPEITSAHFEEAMK	0.992	0.231
MS3	UPTR:Q8I1G5_DROER	AENQNS*AMDMDEDDPVPEITSAHFEEAMK	0.9112	0.093
MS2	SEPT1_DROME	AERDS*SSQVVSNSVLGEK	0.9991	0.097
MS3	SEPT1_DROME	AERDS*SSQVVSNSVLGEK	0.9269	0.097
MS2	UPTR:Q8MRH0_DROME	AES*TIESLPVIAGNER	0.988	0.081
MS3	UPTR:Q8MRH0_DROME	AES*TIESLPVIAGNER	0.9643	0.341
MS2	UPTR:Q8MRH0_DROME	AEST*IESLPVIAGNER	0.9754	0.052
MS3	UPTR:Q8MRH0_DROME	AEST*IESLPVIAGNER	0.92	0.053
MS2	GP:U07652_1	AEVAET*PS*VEAQEEVAQPAEAQVLEAK	0.995	0.294
MS3	GP:U07652_1	AEVAET*PS*VEAQEEVAQPAEAQVLEAK	0.9939	0.369
MS2	UPTR:Q8MYR6_DROME	AFEDDDNS*DEDDL DLLQTPK	0.9651	0.396
MS3	UPTR:Q8MYR6_DROME	AFEDDDNS*DEDDL DLLQTPK	0.963	0.396
MS2	UPTR:Q8IRM4_DROME	AFEDPDVT*HVEGEVDPVR	0.9822	0.141
MS3	UPTR:Q8IRM4_DROME	AFEDPDVT*HVEGEVDPVR	0.9817	0.141
MS2	UPTR:Q95ST5_DROME	AFLAQTAY*TELLAL\$*R	0.9598	0.23
MS3	UPTR:Q9Y130_DROME	AFLAQTAY*TELLAL\$*R	0.9471	0.229
MS2	UPTR:Q9VP57_DROME	AGDES*GEQNAEADIESLFEK	0.997	0.472
MS3	UPTR:Q9VP57_DROME	AGDES*GEQNAEADIESLFEK	0.999	0.475
MS2	UPTR:Q9VP57_DROME	AGDESGEQNAEADIES*LFEK	0.9027	0.146
MS3	UPTR:Q9VP57_DROME	AGDESGEQNAEADIES*LFEK	0.9999	0.457
MS2	UPTR:Q9VWS3_DROME	AGEADPGVIS*EDEDEFVFDNL SHK	0.9987	0.23
MS3	UPTR:Q9VWS3_DROME	AGEADPGVIS*EDEDEFVFDNL SHK	0.9987	0.23
MS2	UPTR:Q9NJH7_DROME	AGKNDDS*DEEEVVPAK	0.9102	0.131
MS3	UPTR:Q9NJH7_DROME	AGKNDDS*DEEEVVPAK	0.9494	0.162
MS2	UPTR:Q9VQK7_DROME	AHGS*EDEQVAEK	0.9991	0.358
MS3	UPTR:Q9VQK7_DROME	AHGS*EDEQVAEK	1	0.448
MS2	UPTR:O96046_DROME	AISAFNQMQS*PVSETPPAR	0.9949	0.21
MS3	UPTR:O96046_DROME	AISAFNQMQS*PVSETPPAR	0.9946	0.212
MS2	UPTR:Q7KHA1_DROSI	ALGGIVLT*ASHNPGGPENDFGIK	0.982	0.004
MS3	UPTR:Q7KHA1_DROSI	ALGGIVLT*ASHNPGGPENDFGIK	0.9586	0.012

MS Level	Protein	Sequence	Peptide probability	dCn
MS2	UPTR:Q7KHA1_DROSI	ALGGIVLTAS*HNPGGPENDFGIK	0.9017	0.149
MS3	UPTR:Q7KHA1_DROSI	ALGGIVLTAS*HNPGGPENDFGIK	0.9696	0.059
MS2	UPTR:Q6NP07_DROME	ALLTETEAQVS*PK	0.9983	0.407
MS3	UPTR:Q6NP07_DROME	ALLTETEAQVS*PK	0.9681	0.441
MS2	ECM29_DROME	ALPDNS*MEVDEVPEPELK	0.9998	0.344
MS3	ECM29_DROME	ALPDNS*MEVDEVPEPELK	0.9998	0.344
MS2	GYS_DROME	ALQAVYPDYVDELSLYGS*K	0.9566	0.074
MS2	UPTR:Q9GU72_DROME	ALS*GEDFPALGSEALER	0.9976	0.3
MS3	UPTR:Q9GU72_DROME	ALS*GEDFPALGSEALER	0.9976	0.281
MS2	MCM2_DROME	AMT*S*PVGDFEPFENEDEILGDQTVR	0.9674	0.251
MS3	MCM2_DROME	AMT*S*PVGDFEPFENEDEILGDQTVR	0.9944	0.307
MS2	UPTR:Q86DR2_DROME	ANE PANAPEDS*EDEK	0.998	0.258
MS3	UPTR:Q86DR2_DROME	ANE PANAPEDS*EDEK	0.9981	0.258
MS3	G3P2_DROME	ANGPLKGILGY*T*DEEVVSTDFLSDTHSSVFDAK	0.9927	0.253
MS2	IMA_DROME	ANS*INTQDSR	0.9406	0.329
MS3	IMA_DROME	ANS*INTQDSR	0.998	0.245
MS2	UPTR:Q9VVI9_DROME	APEAPSREPGADS*IVPGK	0.988	0.146
MS3	UPTR:Q9VVI9_DROME	APEAPSREPGADS*IVPGK	0.9973	0.278
MS2	UPTR:Q9VB74_DROME	APEGS*FINDPAEPSFR	0.902	0.171
MS2	UPTR:Q8MMD2_DROME	APS*GEGFGDGGFVANFPK	0.9963	0.309
MS3	UPTR:Q8MMD2_DROME	APS*GEGFGDGGFVANFPK	0.9958	0.327
MS2	UPTR:Q95RV6_DROME	APS*VSPANFEDDQMLFR	0.911	0.164
MS3	UPTR:Q9VV52_DROME	APS*VSPANFEDDQMLFR	0.9405	0.245
MS2	UPTR:Q8SWX2_DROME	AQS*PEPLFGLLSCGADLIR	0.9997	0.329
MS3	UPTR:Q8SWX2_DROME	AQS*PEPLFGLLSCGADLIR	1	0.481
MS2	MA205_DROME	ARNS*TLMGGEVAPSNECVPTPNGQINAEEVVK	0.9497	0.028
MS3	MA205_DROME	ARNS*TLMGGEVAPSNECVPTPNGQINAEEVVK	0.9105	0.344
MS2	UPTR:O16125_DROME	ARS*VEALLCEK	0.9984	0.291
MS3	UPTR:O16125_DROME	ARS*VEALLCEK	0.989	0.239
MS3	UPTR:Q8IRB9_DROME	AS*IAGTGMSLEEINK	0.999	0.367
MS2	UPTR:Q9V9C7_DROME	AS*IVDQLSR	0.9322	0.118
MS3	UPTR:Q6XIQ8_DROYA	AS*IVDQLSR	0.9453	0.156
MS2	UPTR:Q86NY3_DROME	AS*SEKDEEEAEDPEK	0.9571	0.48
MS3	UPTR:Q86NY3_DROME	AS*SEKDEEEAEDPEK	0.9289	0.462
MS2	UPTR:Q9VNS2_DROME	AS*SVNFSAPDLDVESVK	0.9766	0.405
MS3	UPTR:Q9VNS2_DROME	AS*SVNFSAPDLDVESVK	0.9779	0.408
MS2	UPTR:Q8MR49_DROME	ASAFQFS*DDEEEVKR	0.9696	0.224
MS3	UPTR:Q8MR49_DROME	ASAFQFS*DDEEEVKR	0.9679	0.224
MS2	UPTR:O16043_DROME	ASEPTVS*FAADKDEK	0.9819	0.161
MS3	UPTR:O16043_DROME	ASEPTVS*FAADKDEK	0.9602	0.147
MS2	UPTR:Q95TU5_DROME	ASIVQQPDGQS*PIAAIPQLQIQPSPQHSR	0.9999	0.246
MS3	UPTR:Q95TU5_DROME	ASIVQQPDGQS*PIAAIPQLQIQPSPQHSR	0.9998	0.213
MS2	UPTR:Q9VVA0_DROME	ASLQLPS*PIITR	0.9997	0.383
MS3	UPTR:Q9VVA0_DROME	ASLQLPS*PIITR	0.9998	0.383
MS2	UPTR:Q81D7_DROVI	ASNIVANAS*AAAAAAGADT*PATLADTTMPTLNK	0.9971	0.173
MS2	UPTR:Q86NY3_DROME	ASS*EKDEEEAEDPEK	0.9104	0.038
MS3	UPTR:Q86NY3_DROME	ASS*EKDEEEAEDPEK	0.9082	0.038
MS2	UPTR:Q9VNS2_DROME	ASS*VNFSAPDLDVESVK	0.9939	0.056
MS3	UPTR:Q9VNS2_DROME	ASS*VNFSAPDLDVESVK	0.9294	0.012
MS2	UPTR:Q9U4I2_DROME	AT*ITPVVKSSSGSSK	0.9069	0.191
MS2	MLRN_DROME	AT*SNVFAMFDQAQIAEFK	0.9515	0.415
MS3	UPTR:Q9N618_DROSI	AT*SNVFAMFDQAQIAEFK	0.9639	0.019
MS2	UPTR:O96046_DROME	ATAPPPDVVPQIEVETVDT*PPR	0.9732	0.122
MS3	UPTR:O96046_DROME	ATAPPPDVVPQIEVETVDT*PPR	0.995	0.116
MS2	UPTR:Q9N618_DROSI	ATS*NVFAMFDQAQIAEFK	0.9072	0.005
MS3	MLRN_DROME	ATS*NVFAMFDQAQIAEFK	0.9926	0.007
MS2	UPTR:Q9VYV4_DROME	AVDAVS*PVAAGADSAPAIGQK	1	0.436
MS3	UPTR:Q9VYV4_DROME	AVDAVS*PVAAGADSAPAIGQK	1	0.464
MS2	GP:S80255_1	AVRPSDNISLPPTS*PGNISLPATSPAR	0.9842	0.169
MS3	GP:S80255_1	AVRPSDNISLPPTS*PGNISLPATSPAR	0.9934	0.179
MS3	UPTR:Q7KVW2_DROME	CAVGY*VTPAGLQQLIEELPASKGNR	0.9564	0.238

MS Level	Protein	Sequence	Peptide probability	dCn
MS2	UPTR:Q5BHU7_DROME	CLAGVMVTAS*HNPK	0.9558	0.141
MS3	UPTR:Q8SZP3_DROME	CLELLQELET*R	0.9774	0.076
MS2	UPTR:Q9V6Z5_DROME	CSNCNQVSYCS*VQHQK	0.9854	0.175
MS3	UPTR:Q9V6Z5_DROME	CSNCNQVSYCS*VQHQK	0.996	0.217
MS2	UPTR:Q8IFW6_DROME	DAAES*PAAVDASASAATDDVADK	0.9991	0.291
MS3	UPTR:Q8IFW6_DROME	DAAES*PAAVDASASAATDDVADK	0.994	0.295
MS2	UPTR:O96829_DROME	DAAES*PAAVDASASAATDDVADKK	0.9819	0.163
MS3	UPTR:O96829_DROME	DAAES*PAAVDASASAATDDVADKK	1	0.354
MS2	UPTR:Q8T8R1_DROME	DCS*LGGGGGPGGVGGGGGGGGGMR	0.9984	0.603
MS3	UPTR:Q8T8R1_DROME	DCS*LGGGGGPGGVGGGGGGGGGMR	0.9984	0.622
MS2	UPTR:Q9W2U4_DROME	DDPAAMEIDDT*S*QEVM	0.9544	0.266
MS3	UPTR:Q9W2U4_DROME	DDPAAMEIDDT*S*QEVM	0.9328	0.252
MS2	MCM2_DROME	DDRDLGFGQS*DDEDVGPR	0.9631	0.335
MS3	MCM2_DROME	DDRDLGFGQS*DDEDVGPR	0.9762	0.373
MS2	UPTR:Q6VNW7_DROST	DEADDET*KEGDDK	0.9772	0.232
MS3	UPTR:Q6VNW7_DROST	DEADDET*KEGDDK	0.9781	0.232
MS3	UPTR:Q86NW2_DROME	DENS*PS*AVY*EDCDPVCAGVLQATKK	0.9336	0.184
MS2	MODU_DROME	DES*DDDEEAPVEKPVSK	0.9926	0.373
MS3	MODU_DROME	DES*DDDEEAPVEKPVSK	0.9847	0.316
MS2	UPTR:Q8MQX4_DROME	DFS*PVIGQNVR	0.931	0.133
MS3	UPTR:Q8MQX4_DROME	DFS*PVIGQNVR	0.9443	0.148
MS2	MCM2_DROME	DLGFGQS*DDEDVGPR	1	0.452
MS3	MCM2_DROME	DLGFGQS*DDEDVGPR	1	0.37
MS2	UPTR:Q9VB98_DROME	DLIY*AILKHLEGPR	0.9876	0.242
MS3	UPTR:Q9VB98_DROME	DLIY*AILKHLEGPR	0.9882	0.242
MS2	UPTR:Q8IGH2_DROME	DPPEGDVIRPS*NVEPIDVKPTVTADVR	0.9915	0.102
MS3	UPTR:Q8IGH2_DROME	DPPEGDVIRPS*NVEPIDVKPTVTADVR	0.9815	0.102
MS2	UPTR:Q8IHA4_DROME	DRLDLENGDEEALFAAVERPS*TEQDQR	1	0.406
MS2	UPTR:Q8IRB9_DROME	DRNS*IGFAFGSSTPR	0.9779	0.284
MS3	UPTR:Q8IRB9_DROME	DRNS*IGFAFGSSTPR	0.935	0.246
MS2	SSRP_DROME	DVDFGDS*DNENEPMAYLAR	0.9374	0.135
MS3	SSRP_DROME	DVDFGDS*DNENEPMAYLAR	0.9993	0.509
MS2	MA205_DROME	DVLDHGPETS*VDMELPLDQVPNDADIMK	0.9468	0.059
MS3	MA205_DROME	DVLDHGPETS*VDMELPLDQVPNDADIMK	0.9065	0.062
MS2	UPTR:Q9VXK5_DROME	DVLQNIQS*DDDEETYDLNNLAK	0.9983	0.482
MS3	UPTR:Q9VXK5_DROME	DVLQNIQS*DDDEETYDLNNLAK	0.998	0.369
MS2	UPTR:Q86BM5_DROME	EAAAGEDIT*PLADESIK	0.9999	0.34
MS3	UPTR:Q86BM5_DROME	EAAAGEDIT*PLADESIK	0.9994	0.287
MS2	UPTR:Q86BM5_DROME	EAAAGEDITPLADES*IK	0.9999	0.394
MS3	UPTR:Q9U7E6_DROME	EAAAGEDITPLADES*IK	0.9998	0.472
MS2	UPTR:Q9U7E6_DROME	EAAAGEDITPLADES*IKSK	0.9251	0.087
MS3	UPTR:Q86BM5_DROME	EAAAGEDITPLADES*IKSK	0.967	0.083
MS2	UPTR:Q24478_DROME	EAELENDQEEFIKEDS*PIPHS*DSVAELR	0.908	0.189
MS2	UPTR:Q24478_DROME	EAELENDQEEFIKEDS*PIPHSDSVAELR	0.9502	0.113
MS3	UPTR:Q24478_DROME	EAELENDQEEFIKEDS*PIPHSDSVAELR	0.9595	0.157
MS2	UPTR:Q7YZA2_DROME	EAS*EPIIEGPLTVSVLR	0.9986	0.303
MS3	UPTR:Q7YZA2_DROME	EAS*EPIIEGPLTVSVLR	0.9985	0.316
MS2	UPTR:Q9V468_DROME	EDLAAGDAPPS*PTTK	0.9711	0.04
MS3	UPTR:Q9V468_DROME	EDLAAGDAPPS*PTTK	0.9708	0.038
MS2	UPTR:Q9V468_DROME	EDLAAGDAPPSPTT*K	0.9948	0.022
MS3	UPTR:Q9V468_DROME	EDLAAGDAPPSPTT*K	0.9205	0.032
MS2	UPTR:Q7KW04_DROME	EDS*EEEQQPER	0.9898	0.166
MS3	UPTR:Q7KW04_DROME	EDS*EEEQQPER	0.9991	0.34
MS3	KI10A_DROME	EEMLSCS*FNSPNGK	0.9112	0.078
MS2	UPTR:Q8MZ42_DROME	EEPES*PNSTVGAQLDALFAK	0.9649	0.011
MS3	UPTR:Q8MZ42_DROME	EEPES*PNSTVGAQLDALFAK	0.9622	0.011
MS2	UPTR:Q8MZ42_DROME	EEPESPNSGT*VGAQLDALFAK	0.9404	0.009
MS3	UPTR:Q8MZ42_DROME	EEPESPNSGT*VGAQLDALFAK	0.9368	0.009
MS2	UPTR:Q7KR73_DROME	EEQLS*PLDEVQIIDDK	0.9999	0.348
MS3	UPTR:Q7KR73_DROME	EEQLS*PLDEVQIIDDK	0.9993	0.241
MS2	VINC_DROME	EGLAPVRPPPET*DDEDEGVFR	0.9981	0.445

MS Level	Protein	Sequence	Peptide probability	dCn
MS3	VINC_DROME	EGLAPVRPPPPET*DDEDEGVFR	0.9973	0.445
MS2	UPTR:Q7YZ99_DROME	EGSEPLVAALADS*SLVDAIVSK	0.9731	0.064
MS3	UPTR:Q960C4_DROME	EGSEPLVAALADS*SLVDAIVSK	0.9864	0.067
MS2	HSP83_DROAV	EKEVS*DDEADDDK	0.9811	0.183
MS2	HSP83_DROME	EKEVS*DDEADDEK	0.9924	0.224
MS3	GP:AF006529_1	EKEVS*DDEADDEK	0.9983	0.281
MS2	UPTR:Q9VBU7_DROME	EKPAVAVVTASAS*APTSVQTAALGFGK	0.9919	0.078
MS3	UPTR:Q9VBU7_DROME	EKPAVAVVTASAS*APTSVQTAALGFGK	0.9094	0.084
MS2	GP:AE003515_37	ELDIDS*EGESDPLWLR	0.9747	0.041
MS3	GP:AE003515_37	ELDIDS*EGESDPLWLR	0.9055	0.328
MS3	GP:AF245280_1	ELGLS*LS*PNEIGCTIADLIQGQYPEI	0.9998	0.255
MS2	UPTR:Q9VXE6_DROME	ELPEES*EEEEEEDESSAGALR	0.9997	0.444
MS3	UPTR:Q9VXE6_DROME	ELPEES*EEEEEEDESSAGALR	0.998	0.302
MS3	UPTR:Q8MSV9_DROME	ELS*LDLNPLQPR	0.9592	0.207
MS2	UPTR:O16043_DROME	ENGAADSS*ATEPTDAVGEK	0.9821	0.077
MS3	UPTR:O16043_DROME	ENGAADSS*ATEPTDAVGEK	0.9974	0.074
MS2	UPTR:Q9W002_DROME	ENS*DFFPLAK	0.9649	0.198
MS3	UPTR:Q9W002_DROME	ENS*DFFPLAK	0.9987	0.257
MS3	UPTR:Q94885_DROME	ENTTFHS*PQR	0.9934	0.19
MS2	UPTR:Q8IN86_DROME	EQIQDVEDQDVS*	0.9789	0.152
MS3	1433E_DROME	EQIQDVEDQDVS*	0.9876	0.153
MS2	UPTR:Q9W4C1_DROME	ERVS*QELIDCDIDFVEDTTSK	0.9604	0.257
MS3	UPTR:Q9W4C1_DROME	ERVS*QELIDCDIDFVEDTTSK	0.9528	0.257
MS2	GYS_DROME	ES*GADLKDYFDR	0.9744	0.292
MS3	GP:AE003707_12	ES*GADLKDYFDR	0.9404	0.307
MS2	UPTR:Q6NLK4_DROME	ES*NSEDELEYDPSLYPQR	0.9933	0.357
MS3	UPTR:Q6NLK4_DROME	ES*NSEDELEYDPSLYPQR	0.9781	0.001
MS2	UPTR:Q8MYV4_DROME	ESESAAGTPVNADQPGS*PNAK	0.9999	0.498
MS3	UPTR:Q8MYV4_DROME	ESESAAGTPVNADQPGS*PNAK	0.9998	0.378
MS2	UPTR:Q6NLK4_DROME	ESNS*EDELEYDPSLYPQR	0.9929	0.005
MS3	UPTR:Q6NLK4_DROME	ESNS*EDELEYDPSLYPQR	0.9913	0.326
MS2	UPTR:O16043_DROME	ESSEAVLPAVENG*S*EVTNGDSTDAPAIKEAVK	0.9806	0.107
MS3	UPTR:O16043_DROME	ESSEAVLPAVENG*S*EVTNGDSTDAPAIKEAVK	0.9127	0.052
MS2	UPTR:O16043_DROME	ESSEAVLPAVENGSEEVTNGDS*TDAPIAEAVK	0.9776	0.026
MS3	UPTR:O16043_DROME	ESSEAVLPAVENGSEEVTNGDS*TDAPIAEAVK	0.9775	0.026
MS2	UPTR:Q9U7E6_DROME	ETEEHS*ENDKDLTTEK	0.9925	0.206
MS3	UPTR:Q86BM5_DROME	ETEEHS*ENDKDLTTEK	0.9529	0.236
MS2	UPTR:Q9W3R9_DROME	ETHTDDAS*NGLAPATALQEDLVK	0.9033	0.182
MS3	UPTR:Q9W3R9_DROME	ETHTDDAS*NGLAPATALQEDLVK	0.919	0.054
MS2	UPTR:Q9V3W9_DROME	ETRPLSS*DELIGELAQASLQSR	0.9429	0.035
MS3	UPTR:Q9V3W9_DROME	ETRPLSS*DELIGELAQASLQSR	0.9422	0.035
MS2	UPTR:Q8MLS9_DROME	EVS*EEAEFDDDPLGDAGAAR	0.9949	0.372
MS3	UPTR:Q8MLS9_DROME	EVS*EEAEFDDDPLGDAGAAR	0.9989	0.297
MS2	GP:AE003552_29	EVT*IEQTGEPAK	0.9187	0.194
MS3	GP:AE003552_29	EVT*IEQTGEPAK	0.9285	0.194
MS3	PSMF1_DROME	EVTTQTTNS*PRPIGSDPDPLR	0.9179	0.191
MS2	YC17_DROME	FDDFNVDDEEEDS*DDNIPSLSQNDEDDEEGGEGDKEK	0.9776	0.16
MS3	YC17_DROME	FDDFNVDDEEEDS*DDNIPSLSQNDEDDEEGGEGDKEK	0.9964	0.243
MS2	UPTR:Q23980_DROME	FESNRPV*LPQDSISFSR	0.9978	0.199
MS3	UPTR:Q23980_DROME	FESNRPV*LPQDSISFSR	0.9511	0.111
MS2	UPTR:Q24035_DROME	FGS*ASEETILK	0.9417	0.185
MS3	UPTR:Q24035_DROME	FGS*ASEETILK	0.9791	0.188
MS2	UPTR:Q7KR73_DROME	FS*PSTSGPELEFR	0.9988	0.239
MS3	UPTR:O96936_DROME	FS*PSTSGPELEFR	0.9971	0.323
MS2	UPTR:Q8IGK8_DROME	FTTLIS*QVADLTEEK	0.9242	0.108
MS3	UPTR:Q8IGK8_DROME	FTTLIS*QVADLTEEK	0.9846	0.112
MS2	UPTR:Q9W300_DROME	FVLFFKPVFGDALVVKGSEDPT*T*TTTVR	0.9503	0.257
MS2	UPTR:Q9VY91_DROME	FVS*EGDGGHVVKPTTF	0.9816	0.328
MS2	UPTR:Q9VY91_DROME	FVS*EGDGGHVVKPTTF	0.9289	0.056
MS2	UPTR:Q8MSV2_DROME	GAASWTPQGY*APAAAAAAAAVAQQAAAY*R	0.9312	0.023
MS2	UPTR:Q8IGZ9_DROME	GEPTRPIT*PGK	0.9936	0.352

MS Level	Protein	Sequence	Peptide probability	dCn
MS3	UPTR:Q8IGZ9_DROME	GEPTRPIT*PGK	0.9738	0.315
MS2	UPTR:Q8SXG3_DROME	GGAGAGAGASSGSGSIADFTAS*QSSAIVSGLEPK	0.9643	0.104
MS3	UPTR:Q8SXG3_DROME	GGAGAGAGASSGSGSIADFTAS*QSSAIVSGLEPK	0.9821	0.045
MS2	UPTR:Q8MT90_DROME	GGALPGEENLPT*SEMDLLAK	0.9433	0.095
MS3	UPTR:Q8MT90_DROME	GGALPGEENLPT*SEMDLLAK	0.9609	0.101
MS2	PSMF1_DROME	GGS*FIPSAFEPR	0.9345	0.223
MS3	UPTR:Q86B44_DROME	GLGALDSPYLIDS*DDEDEQK	0.9895	0.363
MS3	UPTR:O61683_DROPS	GLHGFHVHEFGDKT*NGCMSS*GPHF	0.995	0.353
MS3	UPTR:Q7KNC5_DROME	GLRPGS*PKPGHIER	0.9171	0.232
MS2	UPTR:Q8INM3_DROME	GLS*NSTEELHPAPPQIDAIPKFDELESK	0.9142	0.018
MS3	UPTR:Q8INM3_DROME	GLS*NSTEELHPAPPQIDAIPKFDELESK	0.9474	0.007
MS2	UPTR:Q8INM3_DROME	GLSNS*TEELHPAPPQIDAIPKFDELESK	0.9557	0.029
MS3	UPTR:Q8INM3_DROME	GLSNS*TEELHPAPPQIDAIPKFDELESK	0.9941	0.083
MS2	UPTR:Q8INM3_DROME	GLSNST*EELHPAPPQIDAIPKFDELESK	0.9673	0.001
MS2	UPTR:Q5LK13_DROME	GLVNTKLS*LDIQQK	0.9746	0.224
MS3	UPTR:Q5LK13_DROME	GLVNTKLS*LDIQQK	0.9396	0.252
MS3	UPTR:Q59E35_DROME	GPS*PNTHTTGGVTNS*AS*LV	0.9792	0.281
MS2	UPTR:Q7KR73_DROME	GRS*FDSEPATVEDK	0.9856	0.13
MS3	UPTR:Q7KR73_DROME	GRS*FDSEPATVEDK	0.9854	0.19
MS3	UPTR:Q7KUX7_DROME	GVGGSGAGS*GGGMNRRGY*NDRP	0.991	0.275
MS2	UPTR:Q9VNH2_DROME	GVS*PELIAQLGKPPR	0.9907	0.159
MS3	UPTR:Q9VNH2_DROME	GVS*PELIAQLGKPPR	0.9897	0.277
MS3	UPTR:Q9W1J0_DROME	GTLP GAS*T*GILFYLT*PDWK	0.9702	0.148
MS2	CPD1_DROME	HEDNDQQDDENS*GEEEHSSPEK	0.9987	0.427
MS3	GP:AY094819_1	HEDNDQQDDENS*GEEEHSSPEK	0.961	0.268
MS2	UPTR:Q9VY47_DROME	HEQSQAFNAETTVNDVAGS*LR	0.9563	0.123
MS3	UPTR:Q9VW47_DROME	HNEFDDS*NVDDDDLDKLVQNIK	0.9967	0.257
MS2	UPTR:Q8ML25_DROME	HNS*GLEGIVIDSGNSVAEEK	0.9976	0.228
MS3	UPTR:Q8ML25_DROME	HNS*GLEGIVIDSGNSVAEEK	0.9787	0.206
MS2	UPTR:Q4V5R8_DROME	HS*NIS*FPYGPISPLQAAQIR	0.9164	0.159
MS3	UPTR:Q4V5R8_DROME	HS*NIS*FPYGPISPLQAAQIR	0.917	0.159
MS2	GP:M26400_1	IDAGLSAS*QQNLVDNHSIAK	0.9938	0.097
MS3	GP:M26400_1	IDAGLSAS*QQNLVDNHSIAK	0.9932	0.097
MS2	UPTR:Q7KRQ9_DROME	IDEPLHS*PGLNGDLDLPVFR	0.9965	0.332
MS3	UPTR:Q7KRQ9_DROME	IDEPLHS*PGLNGDLDLPVFR	0.9985	0.282
MS2	GP:AF396455_1	IDLPGSEAIAS*PK	0.9332	0
MS3	BTHD_DROME	IDLPGSEAIAS*PK	0.9417	0.24
MS2	UPTR:Q6XJ26_DROYA	IDNPES*S*VKGS*DGEeeeeYAVEK	0.985	0.13
MS3	UPTR:Q6XJ26_DROYA	IDNPES*S*VKGS*DGEeeeeYAVEK	0.9376	0.133
MS2	HP1_DROME	IDNPESSAKVS*DAEEEEEEYAVEK	0.9289	0.043
MS3	GP:M14131_1	IDNPESSAKVS*DAEEEEEEYAVEK	0.9366	0.058
MS2	UPTR:Q8IME2_DROME	IEDPLQFVPAGT*NPR	0.9741	0.121
MS2	UPTR:Q9VVG9_DROME	IEVKS*DDDIDEVVPVEK	0.9981	0.183
MS3	UPTR:Q9VVG9_DROME	IEVKS*DDDIDEVVPVEK	0.9994	0.264
MS2	AP1_DROME	IFAPLVINS*PDLSK	0.9833	0.154
MS3	GP:Y12573_1	IFAPLVINS*PDLSK	0.9587	0.156
MS2	UPTR:Q7KT11_DROME	IFSAGLDVTDPPEPLS*PK	0.9677	0.177
MS2	GPN:X62637_1	IFVGLLTTEIS*DEEIK	0.9206	0.156
MS3	SQD_DROME	IFVGLLTTEIS*DEEIK	0.9086	0.036
MS2	LASP1_DROME	IGS*VSDIDPANGIYGSLTAAEQAHQQQK	0.9839	0.202
MS3	GP:AE003526_24	IGS*VSDIDPANGIYGSLTAAEQAHQQQK	0.9825	0.131
MS2	UPTR:Q9U8B5_DROME	IHDNES*DGEQQHVDEGLVR	0.9998	0.357
MS3	UPTR:Q9U8B5_DROME	IHDNES*DGEQQHVDEGLVR	0.9987	0.353
MS2	UPTR:Q86BB5_DROME	IIELSLS*PPIPTH RPK	0.9278	0.059
MS3	UPTR:Q86BB5_DROME	IIELSLS*PPIPTH RPK	0.9267	0.059
MS2	UPTR:Q94885_DROME	IILNDFS*LTTLK	0.9834	0.143
MS3	UPTR:Q94885_DROME	IILNDFS*LTTLK	0.9244	0.114
MS2	UNK_DROME	IISPGFGDGLSIS*PSVR	0.9942	0.111
MS3	UNK_DROME	IISPGFGDGLSIS*PSVR	0.9952	0.108
MS2	UPTR:Q9VWD4_DROME	IKFS*DAEEEEASKPVQK	0.927	0.292
MS3	UPTR:Q9VWD4_DROME	IKFS*DAEEEEASKPVQK	0.9153	0.371

MS Level	Protein	Sequence	Peptide probability	dCn
MS2	UPTR:Q8MRM6_DROME	ILEETSAPPSSRPLS*LEESQFESPPLTQEK	0.9708	0.104
MS3	UPTR:Q8MRM6_DROME	ILEETSAPPSSRPLS*LEESQFESPPLTQEK	0.9955	0.133
MS2	UPTR:Q8MRM6_DROME	ILEETSAPPSSRPLSLEES*QFESPPLTQEK	0.9754	0.184
MS3	UPTR:Q8MRM6_DROME	ILEETSAPPSSRPLSLEES*QFESPPLTQEK	0.9016	0.137
MS2	GP:AY122137_1	ILGQPCS*VESVTNGK	0.9452	0.206
MS3	GP:AY122137_1	ILGQPCS*VESVTNGK	0.9281	0.113
MS2	UPTR:Q9VU84_DROME	INVFNQNQPQDAPVPS*PPR	1	0.448
MS3	UPTR:Q9VU84_DROME	INVFNQNQPQDAPVPS*PPR	0.9913	0.244
MS2	UPTR:O76755_DROME	IPES*PCDQIDEPK	0.9998	0.26
MS3	UPTR:O76755_DROME	IPES*PCDQIDEPK	0.9998	0.254
MS2	UPTR:Q9VWS3_DROME	IPLSQVDEQPAAGS*LER	1	0.369
MS3	UPTR:Q9VWS3_DROME	IPLSQVDEQPAAGS*LER	0.9998	0.377
MS2	UPTR:Q8MSU7_DROME	IPSPSRP\$IQANSFQDPR	0.9887	0.101
MS3	UPTR:Q8MSU7_DROME	IPSPSRP\$IQANSFQDPR	0.983	0.086
MS2	UPTR:Q9V3W9_DROME	IPSTLDNVDLFS*PDLEVATSAQR	0.9981	0.209
MS3	UPTR:Q9XZE0_DROME	IPSTLDNVDLFS*PDLEVATSAQR	0.998	0.214
MS2	MLC2_DROME	IQLS*QVGECLR	0.9986	0.218
MS3	MLC2_DROME	IQLS*QVGECLR	0.9746	0.173
MS2	GP:U23420_1	IS*ILGLAANSAGVTR	0.9975	0.281
MS3	GP:U23420_1	IS*ILGLAANSAGVTR	0.9993	0.311
MS2	UPTR:O16125_DROME	IS*TAGAAAAAAPSPPAPK	0.986	0.036
MS3	UPTR:O16125_DROME	IS*TAGAAAAAAPSPPAPK	0.9846	0.038
MS2	UPTR:Q9W1K9_DROME	ISEEQQADVLAS*PR	1	0.382
MS3	UPTR:Q9W1K9_DROME	ISEEQQADVLAS*PR	1	0.391
MS2	UPTR:Q8T9E1_DROME	ISETS*LFAELVK	0.9886	0.134
MS3	UPTR:Q8T9E1_DROME	ISETS*LFAELVK	0.9686	0.101
MS2	UPTR:Q9W4X7_DROME	ISNLSES*MTEADLEELVK	0.942	0.114
MS3	UPTR:Q9W4X7_DROME	ISNLSES*MTEADLEELVK	0.9542	0.122
MS2	UPTR:Q86NR5_DROME	ISS*PTNQLAQWFSPPELLAK	0.9875	0.008
MS3	UPTR:Q86NR5_DROME	ISS*PTNQLAQWFSPPELLAK	0.9586	0.115
MS3	UPTR:Q86NR5_DROME	ISSPT*NQLAQWFSPPELLAK	0.9099	0.084
MS2	UPTR:Q9VMJ7_DROME	IVEDNFS*NDEDEPR	0.999	0.267
MS3	UPTR:Q9VMJ7_DROME	IVEDNFS*NDEDEPR	0.9986	0.194
MS2	UPTR:O46090_DROME	IVSDLTTGDPEDS*ECEDLLPQQPLSIPK	0.9349	0.211
MS3	UPTR:O46090_DROME	IVSDLTTGDPEDS*ECEDLLPQQPLSIPK	0.9944	0.211
MS2	GP:AY058497_1	IY*ATPIAK	0.9088	0.166
MS3	GP:AY058497_1	IY*ATPIAK	0.996	0.289
MS2	ATU_DROME	KAPAAADIFGDADDIS*DDEDEAGPAAR	0.9562	0.076
MS3	ATU_DROME	KAPAAADIFGDADDIS*DDEDEAGPAAR	0.9996	0.228
MS2	IF2B_DROME	KEDPQDEAS*AEGGAAAEEEDNLDESFGK	0.995	0.273
MS3	IF2B_DROME	KEDPQDEAS*AEGGAAAEEEDNLDESFGK	0.9993	0.277
MS2	HMGD_DROME	KEES*DED-DDDES*E	1	0.408
MS3	HMGD_DROME	KEES*DED-DDDES*E	0.9995	0.288
MS2	HMGD_DROME	KEES*DED-DDDESE	1	0.416
MS3	HMGD_DROME	KEES*DED-DDDESE	0.9943	0.244
MS2	UPTR:Q9V426_DROME	KENDS*EEELEYDPALYPQR	1	0.266
MS3	UPTR:Q9V426_DROME	KENDS*EEELEYDPALYPQR	0.9958	0.161
MS2	GP:AY069224_1	KES*DDEDEPNTSQELSADER	0.9359	0.181
MS3	GP:AY069224_1	KES*DDEDEPNTSQELSADER	0.9245	0.181
MS2	UPTR:Q8ML61_DROME	KES*LLHSVGGNLLIPSFQR	0.9223	0.089
MS3	UPTR:Q8ML61_DROME	KES*LLHSVGGNLLIPSFQR	0.9083	0.089
MS2	UPTR:Q6NLK4_DROME	KES*NSEDELEYDPSLYPQR	0.9903	0.117
MS3	UPTR:Q6NLK4_DROME	KES*NSEDELEYDPSLYPQR	0.9716	0.118
MS2	UPTR:O16043_DROME	KESSEAVLPNAVENGSEEVTNGDST*DAPAIEAVK	0.9834	0.009
MS3	UPTR:O16043_DROME	KESSEAVLPNAVENGSEEVTNGDST*DAPAIEAVK	0.9731	0.046
MS2	UPTR:Q9VVR0_DROME	KIEEAELPS*DGPL	0.9996	0.309
MS3	UPTR:Q9VVR0_DROME	KIEEAELPS*DGPL	0.999	0.309
MS2	UPTR:Q8I0K6_DROME	KIS*LPVADPFLEK	0.9415	0.137
MS3	UPTR:Q8I0K6_DROME	KIS*LPVADPFLEK	0.9973	0.33
MS2	UPTR:Q9NAX2_DROME	KLDLSLMFNQS*DDETEQR	0.9653	0.087
MS3	UPTR:Q9NAX2_DROME	KLDLSLMFNQS*DDETEQR	0.9602	0.094

MS Level	Protein	Sequence	Peptide probability	dCn
MS2	UPTR:Q7KRF7_DROME	KLS*NTSVGSYVPVEPAVAVR	0.9339	0.141
MS3	UPTR:Q8T0T0_DROME	KLS*NTSVGSYVPVEPAVAVR	0.9215	0.149
MS2	UPTR:Q7KR54_DROME	KLS*VNTIPGIEEVNIIK	0.9933	0.296
MS3	UPTR:Q7KR54_DROME	KLS*VNTIPGIEEVNIIK	0.9177	0.288
MS2	UPTR:Q9I7K6_DROME	KPEDPSSEAEALCS*PAK	0.9809	0.303
MS3	UPTR:Q9I7K6_DROME	KPEDPSSEAEALCS*PAK	0.9835	0.3
MS2	UPTR:Q9I7K6_DROME	KPEDPSSEAEALCS*PAKR	0.9985	0.222
MS3	UPTR:Q9I7K6_DROME	KPEDPSSEAEALCS*PAKR	0.9975	0.316
MS2	UPTR:Q8T4A1_DROME	KPGMASSAS*SSNLTLTGDPDSNDNQINGNAAEQEDLAQR	0.9627	0.041
MS3	UPTR:Q8T4A1_DROME	KPGMASSAS*SSNLTLTGDPDSNDNQINGNAAEQEDLAQR	0.9388	0.003
MS2	UPTR:Q9NL57_DROME	KPLGPNNSNQASMTGAAASGS*LPRPR	0.9755	0.207
MS2	UPTR:Q9VLK2_DROME	KPLILAPPES*PVPPK	0.9995	0.31
MS3	UPTR:Q9VLK2_DROME	KPLILAPPES*PVPPK	0.9995	0.323
MS2	UPTR:Q9VV79_DROME	KPLS*PLADHPQITISR	0.9853	0.117
MS3	UPTR:Q9VV79_DROME	KPLS*PLADHPQITISR	0.9987	0.199
MS2	UPTR:Q9NFR7_DROME	KPLVQQNS*LFVDPTNLPGLK	0.9294	0.086
MS3	UPTR:Q9NFR7_DROME	KPLVQQNS*LFVDPTNLPGLK	0.9995	0.216
MS2	UPTR:Q6NLK7_DROME	KPS*VSPSPGR	0.9805	0.267
MS3	UPTR:Q6NLK7_DROME	KPS*VSPSPGR	0.9174	0.222
MS2	GP:AE003784_30	KPVRPVNS*DGENWDDDDAENSAPK	0.9997	0.44
MS3	ARS2_DROME	KPVRPVNS*DGENWDDDDAENSAPK	0.9998	0.29
MS2	UPTR:Q9VCC0_DROME	KQEES*DEEFFDLDDIK	0.974	0.209
MS3	UPTR:Q9VCC0_DROME	KQEES*DEEFFDLDDIK	0.9515	0.254
MS2	UPTR:Q6XJ14_DROYA	KQGGLGS*MDIPLLADK	0.9993	0.318
MS3	UPTR:Q6XJ14_DROYA	KQGGLGS*MDIPLLADK	0.9946	0.315
MS2	UPTR:Q9VSH4_DROME	KS*PEPVVAEAAEAPSSK	1	0.396
MS3	UPTR:Q9VSH4_DROME	KS*PEPVVAEAAEAPSSK	1	0.414
MS2	UPTR:Q9VP17_DROME	KSS*SDTVIEPLIK	0.9906	0.085
MS3	UPTR:Q9VP17_DROME	KSS*SDTVIEPLIK	0.9401	0.08
MS2	SU11_DROME	KT*LTTVQGLSAEYDLK	0.9973	0.186
MS3	SU11_DROME	KT*LTTVQGLSAEYDLK	0.9958	0.209
MS2	UPTR:Q9VUB8_DROME	KTS*IIQPCNK	0.9061	0.221
MS3	UPTR:Q9VUB8_DROME	KTS*IIQPCNK	0.9955	0.18
MS2	UPTR:Q9VI58_DROME	KTS*LPGSTAPNIAAPVTK	0.9566	0.325
MS3	UPTR:Q9VI58_DROME	KTS*LPGSTAPNIAAPVTK	0.9512	0.32
MS2	UPTR:Q8IGS1_DROME	LADFGVAGQLTNT*TSK	0.9971	0.054
MS3	UPTR:Q8IGS1_DROME	LADFGVAGQLTNT*TSK	0.9972	0.061
MS2	UPTR:Q9W2U7_DROME	LAFLS*DDESTPEEHQQGK	0.9626	0.143
MS3	UPTR:Q9W2U7_DROME	LAFLS*DDESTPEEHQQGK	0.9971	0.188
MS2	UPTR:Q9W000_DROME	LAGAASLPEAGDQGT*LDK	0.994	0.187
MS3	UPTR:Q9W000_DROME	LAGAASLPEAGDQGT*LDK	0.9947	0.187
MS2	UPTR:Q9VU43_DROME	LALLLP GAS*GAGVINEDLEK	0.9922	0.285
MS3	UPTR:Q9VU43_DROME	LALLLP GAS*GAGVINEDLEK	0.9926	0.285
MS2	GP:AJ272505_1	LAPADTT*AVSTAQIELK	0.9932	0.057
MS3	SH3BG_DROME	LAPADTT*AVSTAQIELK	0.9969	0.061
MS2	UPTR:Q9VBU7_DROME	LAS*GEGQGNVLGSIFR	0.9951	0.42
MS3	UPTR:Q9VBU7_DROME	LAS*GEGQGNVLGSIFR	0.999	0.485
MS2	GP:AF017647_1	LAS*MDVDPLSLEEAVQEPNAQGR	0.946	0.134
MS3	GP:AF017647_1	LAS*MDVDPLSLEEAVQEPNAQGR	0.9948	0.234
MS2	UPTR:Q8IGX8_DROME	LAS*VDDIPK	0.987	0.193
MS3	MODU_DROME	LAS*VDDIPK	0.9883	0.195
MS2	UPTR:O61444_DROME	LCDFGISGQLVDS*IAK	0.9951	0.381
MS3	UPTR:O61444_DROME	LCDFGISGQLVDS*IAK	0.9994	0.379
MS2	UPTR:Q7K2Q3_DROME	LDS*MLDTPKPR	0.9088	0.135
MS3	UPTR:Q7K2Q3_DROME	LDS*MLDTPKPR	0.9096	0.13
MS2	UPTR:Q6NPA6_DROME	LDT*FCGSPPYAAPELFQGK	0.9737	0.149
MS3	UPTR:Q6NPA6_DROME	LDT*FCGSPPYAAPELFQGK	0.9995	0.326
MS2	UPTR:Q8MYR3_DROME	LEEQTEADS*PPPILTSAMATK	0.9957	0.394
MS2	TCTP_DROME	LEGANAS*EEEADEGTDITSESQGDVVLNHR	0.9992	0.184
MS3	TCTP_DROME	LEGANAS*EEEADEGTDITSESQGDVVLNHR	0.9994	0.245
MS2	UPTR:Q9VNA2_DROME	LEGLRPGS*PKPGHIER	1	0.308

MS Level	Protein	Sequence	Peptide probability	dCn
MS3	UPTR:Q7KNC5_DROME	LEGLRPGS*PKPGHIER	1	0.279
MS2	UPTR:Q8IQT4_DROME	LELS*EDDLPVAR	0.9955	0.246
MS3	UPTR:Q8IQT4_DROME	LELS*EDDLPVAR	0.9101	0.112
MS2	UPTR:Q8IGK0_DROME	LEPGTLELS*PK	0.9158	0.179
MS3	UPTR:Q8IGK0_DROME	LEPGTLELS*PK	0.928	0.179
MS3	UPTR:Q8INM3_DROME	LES*FEEDVEDHGNEEEENEEEHEEDK	0.9035	0.245
MS2	UPTR:Q9V6Q6_DROME	LES*PERLDTKPAELLK	0.9948	0.218
MS3	UPTR:Q9V6Q6_DROME	LES*PERLDTKPAELLK	0.9441	0.216
MS3	UPTR:Q7KRQ4_DROME	LFATGS*NDMTELNQSSK	0.9984	0.314
MS2	UPTR:Q960K6_DROME	LFDDS*DDDDDDLFAR	0.9977	0.175
MS3	UPTR:Q960K6_DROME	LFDDS*DDDDDDLFAR	0.9994	0.283
MS2	UPTR:Q8IGZ9_DROME	LGEPTRPIT*PGK	0.9882	0.417
MS3	UPTR:Q8IGZ9_DROME	LGEPTRPIT*PGK	0.949	0.44
MS2	MCM2_DROME	LGFGQS*DDEDDVGPR	0.9932	0.316
MS3	MCM2_DROME	LGFGQS*DDEDDVGPR	0.9845	0.283
MS2	UPTR:Q9VC17_DROME	LGGAVLRPAVLANSSGSNNSTS*PSAGEDSALLNNPFLR	0.994	0.02
MS3	UPTR:Q9VC17_DROME	LGGAVLRPAVLANSSGSNNSTS*PSAGEDSALLNNPFLR	0.9961	0.03
MS2	CDC37_DROME	LGPGGLDPADVFE*LPDELK	0.9999	0.367
MS3	CDC37_DROME	LGPGGLDPADVFE*LPDELK	0.9999	0.393
MS2	UPTR:Q8SX68_DROME	LGS*ITGSSAIAAAATAATTAAAGTAK	0.9967	0.035
MS3	UPTR:Q8SX68_DROME	LGS*ITGSSAIAAAATAATTAAAGTAK	0.9872	0.035
MS2	UPTR:Q9V4M0_DROME	LGS*PVANLVTEAPTPVALSPGEAANQEASAR	0.994	0.08
MS3	UPTR:Q9V4M0_DROME	LGS*PVANLVTEAPTPVALSPGEAANQEASAR	0.9928	0.08
MS2	UPTR:Q9V4M0_DROME	LGSPVANLVTEAPTPVALS*PGEAANQEASAR	0.9906	0.141
MS3	UPTR:Q9V4M0_DROME	LGSPVANLVTEAPTPVALS*PGEAANQEASAR	0.9901	0.215
MS2	GP:Z46894_1	LHDIDS*EDDEDQQMTIENLLNSK	0.9955	0.411
MS3	GP:Z46894_1	LHDIDS*EDDEDQQMTIENLLNSK	0.994	0.359
MS2	UPTR:Q8I092_DROME	LIDAEDIPMPNS*PPAEPSFDEETK	0.9988	0.387
MS3	UPTR:Q9V468_DROME	LIDAEDIPMPNS*PPAEPSFDEETK	0.9677	0.159
MS2	UPTR:Q7KSN8_DROME	LIFEDVPIQKES*DGEDPEEKPEEK	0.9401	0.327
MS3	UPTR:Q8MQK8_DROME	LIFEDVPIQKES*DGEDPEEKPEEK	0.9804	0.299
MS2	UPTR:Q95TR2_DROME	LIFS*GDEDEEEQDVPTR	0.999	0.381
MS3	UPTR:Q95TR2_DROME	LIFS*GDEDEEEQDVPTR	0.9992	0.327
MS2	UPTR:Q7KR73_DROME	LIS*PDECQVIVDGEQQSQTVSTLLK	0.9991	0.32
MS3	UPTR:Q7KR73_DROME	LIS*PDECQVIVDGEQQSQTVSTLLK	0.9902	0.329
MS2	UPTR:Q6AWK1_DROME	LKEFPIQQY*IPLDSHIQF	0.9289	0.202
MS3	UPTR:Q6AWK1_DROME	LKEFPIQQY*IPLDSHIQF	0.9974	0.206
MS2	UPTR:Q9VVA0_DROME	LLAAKPPVHHNSHSPNASLQLPS*PIIIR	0.9881	0.097
MS3	UPTR:Q9VVA0_DROME	LLAAKPPVHHNSHSPNASLQLPS*PIIIR	0.9814	0.102
MS2	UPTR:O44368_DROME	LLDLPTTLETADQACS*PIIHSLSICIPQR	0.994	0.294
MS3	UPTR:O44368_DROME	LLDLPTTLETADQACS*PIIHSLSICIPQR	0.9933	0.294
MS2	UPTR:Q9VHC8_DROME	LLGDENDDELLKS*PVSTPTTVAPIPDLLAEEK	0.9953	0.15
MS3	UPTR:Q9VHC8_DROME	LLGDENDDELLKS*PVSTPTTVAPIPDLLAEEK	0.9557	0.2
MS2	UPTR:Q9NFR7_DROME	LLGMPDSEPS*PTEEEAR	0.9214	0.042
MS2	UPTR:Q9W5W9_DROME	LLGSIS*PEPSTPAPR	0.9974	0.188
MS3	UPTR:Q9W5W9_DROME	LLGSIS*PEPSTPAPR	0.9692	0.36
MS2	UPTR:Q95TF8_DROME	LLGTIGS*ESETNTAK	0.9982	0.139
MS3	UPTR:Q95TF8_DROME	LLGTIGS*ESETNTAK	0.982	0.114
MS3	UPTR:Q9V3H3_DROME	LLIDTNTTASTHSAS*PSSFLPIVPPR	0.9297	0.086
MS2	MA205_DROME	LLPDTT*DEQLLTSALEEK	0.9047	0.019
MS3	MA205_DROME	LLPDTT*DEQLLTSALEEK	0.9033	0.019
MS2	MA205_DROME	LLPDTTDEQLLTS*ALEEK	0.9006	0.358
MS3	MA205_DROME	LLPDTTDEQLLTS*ALEEK	0.9648	0.06
MS2	UPTR:Q9VW85_DROME	LLPSVS*TEETSESGVAPGK	0.9973	0.041
MS3	UPTR:Q9VW85_DROME	LLPSVS*TEETSESGVAPGK	0.9898	0.041
MS2	UPTR:Q9VW85_DROME	LLPSVST*EETSESGVAPGK	0.9973	0.121
MS3	UPTR:Q9VW85_DROME	LLPSVST*EETSESGVAPGK	0.9841	0.082
MS2	41_DROME	LLQDPLLS*PTTR	0.9886	0.061
MS3	GP:L27467_1	LLQDPLLS*PTTR	0.9768	0.18
MS2	MA205_DROME	LLVPGSSSS*TTTTSSLR	0.9307	0.115
MS3	MA205_DROME	LLVPGSSSS*TTTTSSLR	0.9408	0.115

MS Level	Protein	Sequence	Peptide probability	dCn
MS2	UPTR:Q6AWF3_DROME	LNEELASHQQQQNQQLRPIS*PDIR	0.9975	0.302
MS3	UPTR:Q6AWF3_DROME	LNEELASHQQQQNQQLRPIS*PDIR	0.9664	0.136
MS2	UPTR:Q86BS3_DROME	LNNTDSSLEGSGLNDS*MDLEDLEEDLPSHTVK	0.973	0.127
MS3	UPTR:Q86BS3_DROME	LNNTDSSLEGSGLNDS*MDLEDLEEDLPSHTVK	0.9671	0.125
MS2	UPTR:Q9NJH5_DROME	LNRPPEAIS*PVSPPLGNGTVVLEEQTLSAK	0.9882	0.351
MS3	UPTR:Q9NJH5_DROME	LNRPPEAIS*PVSPPLGNGTVVLEEQTLSAK	0.9862	0.09
MS2	UPTR:Q9NJH5_DROME	LNRPPEAISPVS*PLGNGTVVLEEQTLSAK	0.9274	0.034
MS3	UPTR:Q9NJH5_DROME	LNRPPEAISPVS*PLGNGTVVLEEQTLSAK	0.9411	0.016
MS2	UPTR:Q9VNA2_DROME	LNS*SFIYPGQQLLVPDK	0.9384	0.033
MS2	UPTR:Q9V3H3_DROME	LNS*VTTGNGLNGNTDLFGSDPFELNNGPNIK	0.9729	0.028
MS3	UPTR:Q9V3H3_DROME	LNS*VTTGNGLNGNTDLFGSDPFELNNGPNIK	0.9497	0.13
MS2	UPTR:Q9V3H3_DROME	LNSVTGNGLNGNT*DLFGSDPFELNNGPNIK	0.9203	0.201
MS2	UPTR:Q9VTU3_DROME	LPGPAINPIVDNSDEPQPS*LSDLHDFEPK	0.9617	0.024
MS3	UPTR:Q9VTU3_DROME	LPGPAINPIVDNSDEPQPS*LSDLHDFEPK	0.9729	0.008
MS2	UPTR:Q9VTU3_DROME	LPGPAINPIVDNSDEPQPSLS*DLHDFEPK	0.968	0.34
MS3	UPTR:Q9VTU3_DROME	LPGPAINPIVDNSDEPQPSLS*DLHDFEPK	0.9896	0.023
MS2	UPTR:Q9W3H5_DROME	LPPLAHS*ISIDPSR	0.9731	0.095
MS3	UPTR:Q9W3H5_DROME	LPPLAHS*ISIDPSR	0.9695	0.342
MS2	UPTR:Q9W3H5_DROME	LPPLAHSIS*IDPSR	0.9996	0.283
MS3	UPTR:Q9W3H5_DROME	LPPLAHSIS*IDPSR	0.9977	0.186
MS2	UPTR:Q5BHU7_DROME	LQCLAGVMVTAS*HNPK	0.9854	0.038
MS3	UPTR:Q5BHU7_DROME	LQCLAGVMVTAS*HNPK	0.9632	0.027
MS3	UPTR:Q86NT2_DROME	LQGVLCAS*EER	0.9756	0.1
MS2	UPTR:Q9VYL6_DROME	LQHAES*LEDLASSGVAK	0.9992	0.335
MS3	UPTR:Q95S42_DROME	LQHAES*LEDLASSGVAK	0.9859	0.204
MS2	UPTR:Q6IHD1_DROME	LQIVEGGDS*AGEGGFGGGEVLAENV	0.9859	0.341
MS2	UPTR:Q8ML25_DROME	LQS*GGEGVGITSEQLAK	0.9997	0.387
MS3	UPTR:Q8ML25_DROME	LQS*GGEGVGITSEQLAK	0.9981	0.201
MS2	UPTR:Q9Y128_DROME	LQSQIS*QTLVNVPHAEVAEGEEAR	0.9211	0.063
MS2	UPTR:Q8MQL2_DROPS	LQY*FDLDVTNKPPLLNR	0.9792	0.067
MS3	UPTR:Q8MQL2_DROPS	LQY*FDLDVTNKPPLLNR	0.9703	0.067
MS2	GCP2_DROME	LS*LTQSQDFPTSTPVNCK	0.989	0.05
MS3	GCP2_DROME	LS*LTQSQDFPTSTPVNCK	0.9845	0.012
MS2	UPTR:Q7KQ11_DROME	LS*SAPTPTPSNPFAVLSSLIKD	0.9702	0.034
MS3	UPTR:Q7KQ11_DROME	LS*SAPTPTPSNPFAVLSSLIKD	0.9685	0.034
MS2	UPTR:Q6NP55_DROME	LS*VSTIPENPFEDQSSTIAR	0.9312	0.063
MS3	UPTR:Q6NP55_DROME	LS*VSTIPENPFEDQSSTIAR	0.9076	0.079
MS2	UPTR:Q4V5P0_DROME	LS*VVVKPMSSFPRK	0.9152	0.298
MS2	UPTR:Q8SX2_DROME	LSQVSSVSS*MELHK	0.9887	0.155
MS2	UPTR:Q7KQ11_DROME	LSS*APTPTPSNPFAVLSSLIKD	0.9022	0.005
MS3	UPTR:Q7KQ11_DROME	LSS*APTPTPSNPFAVLSSLIKD	0.9397	0
MS2	UPTR:Q86B44_DROME	LSTANEQQVAAGLGALDSPYLIDS*DDEDEQK	0.9989	0.093
MS3	UPTR:Q86B44_DROME	LSTANEQQVAAGLGALDSPYLIDS*DDEDEQK	0.9985	0.084
MS2	UPTR:O16125_DROME	LT*SIIDDTTERPPPDLVK	0.9084	0.018
MS2	UPTR:Q9VE73_DROME	LT*SLTEDVAAVPEDAPFR	0.9196	0
MS3	UPTR:Q9VE73_DROME	LT*SLTEDVAAVPEDAPFR	0.9282	0
MS2	ABL_DROME	LTIY*ATPIAK	0.9878	0.086
MS3	ABL_DROME	LTIY*ATPIAK	0.9806	0.094
MS2	UPTR:Q9VE73_DROME	LTS*LTEDVAAVPEDAPFR	0.9738	0.001
MS3	UPTR:Q9VE73_DROME	LTS*LTEDVAAVPEDAPFR	0.9919	0.034
MS2	UPTR:Q7YU85_DROME	LTTAVS*HDLADGLAASK	0.9762	0.242
MS3	UPTR:Q9VA36_DROME	LTTAVS*HDLADGLAASK	0.9949	0.178
MS3	TYSY_DROME	MALPPCHCLAQFY*VS*EK	0.9145	0.076
MS2	UPTR:Q9V8K6_DROME	MDVDEEDS*AAPK	0.9821	0.204
MS3	UPTR:Q9V8K6_DROME	MDVDEEDS*AAPK	0.9851	0.232
MS3	UPTR:Q9VD32_DROME	MGVT*CLY*VLVLVANVLANGIVVQQALIR	0.9585	0.298
MS3	UPTR:Q8SXG3_DROME	MNDS*FGDFNATQTAPTGAASNQK	0.9978	0.31
MS2	UPTR:Q9V346_DROME	MS*SPDGLDQAAEESLGNFVR	0.9896	0.019
MS3	UPTR:Q9V346_DROME	MS*SPDGLDQAAEESLGNFVR	0.9839	0.426
MS3	UPTR:Q9V346_DROME	MSS*PDGLDQAAEESLGNFVR	0.9787	0.002
MS3	UPTR:Q6XHM1_DROYA	MSYKIEPLPDS*Y*AGLGEGPHWDVAR	0.9845	0.156

MS Level	Protein	Sequence	Peptide probability	dCn
MS2	UPTR:Q9VYV4_DROME	NAGGVGVGVGEKS*PDLK	0.9999	0.299
MS3	UPTR:Q9VYV4_DROME	NAGGVGVGVGEKS*PDLK	0.999	0.351
MS2	UPTR:Q9VHU6_DROME	NANDLPDS*FFDLTVNDLK	0.995	0.193
MS3	UPTR:Q9VHU6_DROME	NANDLPDS*FFDLTVNDLK	0.9763	0.279
MS2	UPTR:Q9NJH7_DROME	NDDSDDEEVVPAK	0.9931	0.135
MS3	UPTR:Q9NJH7_DROME	NDDSDDEEVVPAK	0.9929	0.129
MS2	UPTR:Q9NFT0_DROME	NDNDETDS*PHEAAEIEEPDEEVDEADQETK	0.9251	0.426
MS3	UPTR:Q9NFT0_DROME	NDNDETDS*PHEAAEIEEPDEEVDEADQETK	0.9165	0.41
MS2	UPTR:Q8IMB7_DROME	NEEQAAANFLSSSS*FDD	0.9802	0.193
MS3	UPTR:Q8IMB7_DROME	NEEQAAANFLSSSS*FDD	0.9782	0.191
MS3	UPTR:Q9VZI1_DROME	NFS*DEQLR	0.9195	0.011
MS2	PR2_DROME	NFTHEELQS*IPDIQSLIGK	1	0.414
MS3	PR2_DROME	NFTHEELQS*IPDIQSLIGK	1	0.414
MS2	UPTR:Q9U3W1_DROME	NGVQNLSTLDDDEERFEDADE	0.9991	0.268
MS3	UPTR:Q9U3W1_DROME	NGVQNLSTLDDDEERFEDADE	0.9821	0.296
MS2	CDC37_DROME	NIEIS*DDEDDTHPNIDTPSLFR	0.9857	0.185
MS3	CDC37_DROME	NIEIS*DDEDDTHPNIDTPSLFR	0.9996	0.26
MS2	UPTR:Q7K765_DROME	NKQEALNNATAS*DTELELGDK	0.9794	0.133
MS2	UPTR:Q8MQN9_DROME	NLISLTGS*PGGAEK	0.995	0.214
MS3	UPTR:Q8MQN9_DROME	NLISLTGS*PGGAEK	0.9856	0.192
MS2	GP:AY122261_1	NQDS*DDEDVEAR	0.9543	0.116
MS3	GP:AY122261_1	NQDS*DDEDVEAR	0.9495	0.172
MS2	UPTR:Q9VGR7_DROME	NQRES*NFGSLMDR	0.9934	0.268
MS3	UPTR:Q9VGR7_DROME	NQRES*NFGSLMDR	0.9889	0.221
MS2	UPTR:Q86B74_DROME	NS*DSGAGTDALADALR	0.9743	0.267
MS3	UPTR:Q9VAT0_DROME	NS*DSGAGTDALADALR	0.992	0.132
MS2	UPTR:Q6NP19_DROME	NS*GGAITHSSEVLQSTAISDRPK	0.9884	0.166
MS3	UPTR:Q6NP19_DROME	NS*GGAITHSSEVLQSTAISDRPK	0.9998	0.429
MS2	UPTR:Q9I7D3_DROME	NS*LEEGLDK	0.9969	0.252
MS3	UPTR:Q9I7D3_DROME	NS*LEEGLDK	0.9413	0.152
MS3	UPTR:Q8MQV7_DROME	NTDEGAHVDDILDS*DDEVEMDPLR	0.9915	0.218
MS2	UPTR:Q9VD68_DROME	NTGKNIS*NVLVELLYG	0.9075	0.266
MS3	UPTR:Q9VD68_DROME	NTGKNIS*NVLVELLYG	0.9944	0.266
MS2	UPTR:Q86NT4_DROME	NTSS*SGGGGASALQTPENVSPVR	0.9997	0.014
MS3	UPTR:Q7KR74_DROME	NTSS*SGGGGASALQTPENVSPVR	0.9979	0.019
MS2	SSRP_DROME	NYKPEAGGDS*DNEK	0.9622	0.234
MS2	UPTR:Q24036_DROME	PAEETPAVAAAEEKS*EEPEK	0.9959	0.413
MS3	UPTR:Q24036_DROME	PAEETPAVAAAEEKS*EEPEK	0.9998	0.449
MS3	UPTR:Q86BS3_DROME	PAPVS*PAPVPQK	0.9734	0.386
MS2	UPTR:Q8IRB9_DROME	PAS*IAGTGMSELINK	0.9783	0.218
MS2	GP:AY069224_1	PDNS*MEVDEVPEPELK	0.9975	0.351
MS3	GP:AY069224_1	PDNS*MEVDEVPEPELK	0.9981	0.353
MS2	UPTR:Q8IRM4_DROME	PDVT*HVEGEVDPVR	0.9964	0.364
MS3	UPTR:Q8IRM4_DROME	PDVT*HVEGEVDPVR	0.991	0.348
MS2	UPTR:Q8MR29_DROME	PEDDS*DEELVR	0.9869	0.268
MS3	UPTR:Q8MR29_DROME	PEDDS*DEELVR	0.9974	0.369
MS3	UPTR:Q7PLX1_DROME	PGGDDSDDELQTAVPPSHDIYR	0.9961	0.267
MS2	UPTR:Q8IGK0_DROME	PGTLELS*PK	0.9989	0.34
MS3	UPTR:Q8IGK0_DROME	PGTLELS*PK	0.9292	0.269
MS2	UPTR:Q24050_DROME	PLDGGLPAGAS*PK	0.9921	0.361
MS3	UPTR:Q24050_DROME	PLDGGLPAGAS*PK	0.9876	0.368
MS2	UPTR:Q9VNH5_DROME	PPEGFS*DEEPEER	0.9757	0.365
MS3	UPTR:Q9VNH5_DROME	PPEGFS*DEEPEER	0.9182	0.353
MS3	UPTR:Q8MT44_DROME	PPGS*AAAY*LY*QQNAAAAAAFPQLISLHQIR	0.9128	0.187
MS2	UPTR:Q9VA36_DROME	PSNFVQHIEPS*PVASK	0.995	0.278
MS3	UPTR:Q9VA36_DROME	PSNFVQHIEPS*PVASK	0.9988	0.334
MS3	UPTR:Q8MLD9_DROME	PSTVAVLLS*DLNQGITSVLSHSEDPDVVSLSGTAAQQV	0.995	0.29
MS2	UPTR:Q8INW7_DROME	QAAGASTGLS*ELDSLQLDLQK	0.9595	0.076
MS2	UPTR:Q24478_DROME	QDS*PSQPTIIVK	0.973	0.184
MS3	UPTR:Q24478_DROME	QDS*PSQPTIIVK	0.9775	0.183
MS2	UPTR:Q9VJH2_DROME	QEPEGLNEDFAPES*PATK	0.9693	0.136

MS Level	Protein	Sequence	Peptide probability	dCn
MS3	UPTR:Q9VJH2_DROME	QEPEGLNEDFAPES*PATK	0.9226	0.166
MS2	UPTR:Q24478_DROME	QEPTS*PFEQLR	0.9781	0.242
MS3	UPTR:Q24478_DROME	QEPTS*PFEQLR	0.9808	0.245
MS2	UPTR:Q9VXK5_DROME	QGLGLS*DDDNEGNAK	0.9987	0.277
MS3	UPTR:Q9VXK5_DROME	QGLGLS*DDDNEGNAK	0.9993	0.389
MS2	ARS2_DROME	QGPQS*PKLDEDEGNENTEPK	0.9662	0.24
MS3	GP:AE003784_30	QGPQS*PKLDEDEGNENTEPK	0.983	0.241
MS2	UPTR:Q9VUM1_DROME	QIS*GTASSVAFTPLQGLEIVNPQAAER	0.9384	0.011
MS3	UPTR:Q9VUM1_DROME	QIS*GTASSVAFTPLQGLEIVNPQAAER	0.9057	0.018
MS2	UPTR:Q9VUM1_DROME	QISGT*ASSVAFTPLQGLEIVNPQAAER	0.9062	0.017
MS2	UPTR:Q9VUM1_DROME	QISGTASS*VAFTPLQGLEIVNPQAAER	0.9273	0.044
MS3	UPTR:Q9VUM1_DROME	QISGTASS*VAFTPLQGLEIVNPQAAER	0.9226	0.044
MS2	UPTR:Q7KVY5_DROME	QLLHGEPNVSY*ICSR	0.9939	0.09
MS3	UPTR:Q7KVY5_DROME	QLLHGEPNVSY*ICSR	0.9968	0.088
MS2	UPTR:Q9VY91_DROME	QNS*GSGGSANQTNGNGAAGAGGAHGASVMPGLINR	0.9955	0.108
MS3	UPTR:Q9VY91_DROME	QNS*GSGGSANQTNGNGAAGAGGAHGASVMPGLINR	0.9948	0.108
MS2	UPTR:Q9NI59_DROBU	QNVVLVT*INY*RLGALGFLS*LK	0.9729	0.183
MS2	UPTR:Q9VZD8_DROME	QPEEGAGGDAGEDDPKPAAGGT*SDDDDLEAAAAK	0.9483	0.394
MS3	UPTR:Q9VZD8_DROME	QPEEGAGGDAGEDDPKPAAGGT*SDDDDLEAAAAK	0.97	0.45
MS2	UPTR:Q9VZD8_DROME	QPEEGAGGDAGEDDPKPAAGGT*SDDDDLEAAAAK	0.9603	0.009
MS3	UPTR:Q9VZD8_DROME	QPEEGAGGDAGEDDPKPAAGGT*SDDDDLEAAAAK	0.9689	0.007
MS2	UPTR:Q24593_DROME	QPSAAASGLLTVP*SFTLQLSLR	0.9922	0.291
MS3	UPTR:Q24593_DROME	QPSAAASGLLTVP*SFTLQLSLR	0.9893	0.265
MS2	UPTR:Q86NT4_DROME	QS*GLGSSSNSSNLVEFR	1	0.323
MS3	UPTR:Q86NT4_DROME	QS*GLGSSSNSSNLVEFR	0.9998	0.252
MS2	UPTR:Q7KV69_DROME	QS*QENLVVMR	0.9995	0.345
MS3	UPTR:Q7KV69_DROME	QS*QENLVVMR	0.9923	0.204
MS3	UPTR:Q8T0I8_DROME	QVSLEAAVTDNINQT*IS*GS*VR	0.9214	0.199
MS3	UPTR:O76903_DROME	QYNKTSVADGVAAVLNGNLDS*FIY*	0.9646	0.229
MS2	UPTR:Q9VUZ8_DROME	RAAIDS*DDEDGYGC	0.9767	0.146
MS3	UPTR:Q9VUZ8_DROME	RAAIDS*DDEDGYGC	0.9984	0.405
MS2	UPTR:Q9WVF0_DROME	RAS*AVAGPTK	0.9633	0.168
MS3	UPTR:Q9WVF0_DROME	RAS*AVAGPTK	0.9178	0.272
MS2	HSP27_DROME	RAS*GGPNALLPAVGK	0.9971	0.292
MS3	HSP27_DROME	RAS*GGPNALLPAVGK	0.9983	0.298
MS2	UPTR:Q8IGS1_DROME	RAS*LGLPLQSSVPTPSTAEEQQQQR	0.985	0.136
MS3	UPTR:Q8IGS1_DROME	RAS*LGLPLQSSVPTPSTAEEQQQQR	0.9849	0.136
MS2	UPTR:Q7KNC5_DROME	RAS*QDVSSLR	0.9553	0.211
MS2	MCM2_DROME	RDLGFGQGS*DDEDDVGPR	0.9962	0.259
MS3	MCM2_DROME	RDLGFGQGS*DDEDDVGPR	0.9528	0.185
MS2	UPTR:Q86NR4_DROME	RDS*ESFQMPQLDEIEQAK	0.9813	0.107
MS3	UPTR:Q86NR4_DROME	RDS*ESFQMPQLDEIEQAK	0.98	0.107
MS2	UPTR:Q86LC4_DROME	RDS*FCEFLDAQGPR	0.988	0.131
MS3	UPTR:Q86LC4_DROME	RDS*FCEFLDAQGPR	0.989	0.236
MS2	UPTR:Q59E35_DROME	RDS*SVLPVAEQPPAK	0.9832	0.065
MS3	UPTR:Q59E35_DROME	RDS*SVLPVAEQPPAK	0.937	0.075
MS2	UPTR:Q9W002_DROME	RENS*DFFPLAK	0.9981	0.342
MS3	UPTR:Q9W002_DROME	RENS*DFFPLAK	0.9967	0.347
MS2	UPTR:Q95RK8_DROME	RES*VLGTIDEAMFAK	0.9604	0.176
MS3	UPTR:Q95RK8_DROME	RES*VLGTIDEAMFAK	0.9924	0.313
MS2	UPTR:Q86G33_DROSI	RES*WLHPNNLEK	0.958	0.13
MS2	UPTR:Q9NHN6_DROME	RFS*DDIADQR	0.9703	0.21
MS2	UPTR:Q9VY91_DROME	RFVS*EGDGGHVVKPTTF	0.9916	0.292
MS3	UPTR:Q9VY91_DROME	RFVS*EGDGGHVVKPTTF	0.9929	0.349
MS2	LASP1_DROME	RIGS*VSDIDPANGIY GSL TAAEQAHQQQK	0.9632	0.123
MS3	UPTR:Q9NFR7_DROME	RKPLVQQNS*LFVDP TL N P GLK	0.9625	0.273
MS2	UPTR:Q7YU91_DROME	RLS*ADELN VLLPTLN A PK	1	0.362
MS3	UPTR:Q7YU91_DROME	RLS*ADELN VLLPTLN A PK	1	0.407
MS2	UPTR:Q95RW5_DROME	RLS*NLLADNDVQPVFK	0.9998	0.262
MS3	UPTR:Q95RW5_DROME	RLS*NLLADNDVQPVFK	0.9992	0.214
MS3	UPTR:Q9V6Q6_DROME	RNS*FYLSNEESPLEVR	0.9219	0.301

MS Level	Protein	Sequence	Peptide probability	dCn
MS2	UPTR:Q9I7D3_DROME	RNS*GNYQR	0.9975	0.279
MS3	UPTR:Q9I7D3_DROME	RNS*GNYQR	0.9944	0.353
MS2	UPTR:Q9VLK2_DROME	RPLILAPPES*PAAPAPAAK	0.9759	0.185
MS3	UPTR:Q8T9F1_DROME	RPLILAPPES*PAAPAPAAK	0.9963	0.173
MS2	UPTR:Q7KR73_DROME	RQDS*VELLNQTPVSVVISK	0.9988	0.298
MS3	UPTR:Q7KR73_DROME	RQDS*VELLNQTPVSVVISK	0.9994	0.368
MS2	UPTR:Q7KR73_DROME	RQDS*VELLNQTPVSVVISKPR	0.9597	0.369
MS3	UPTR:Q7KR73_DROME	RQDS*VELLNQTPVSVVISKPR	0.9419	0.358
MS2	GP:AE003493_34	RQS*LELTPEQLER	0.9965	0.212
MS3	GP:AE003493_34	RQS*LELTPEQLER	0.9993	0.355
MS2	UPTR:Q8T3Q6_DROME	RQS*LHVPSPLEAAK	0.9569	0.149
MS3	UPTR:Q8T3Q6_DROME	RQS*LHVPSPLEAAK	0.9321	0.207
MS2	HIRA_DROME	RQS*LPFDPGQSNELLR	0.9834	0.194
MS3	HIRA_DROME	RQS*LPFDPGQSNELLR	0.9866	0.194
MS2	UPTR:Q9NFR7_DROME	RQS*MEQLDLIK	0.95	0.04
MS3	UPTR:Q9NFR7_DROME	RQS*MEQLDLIK	0.9366	0.047
MS3	UPTR:Q961X5_DROME	RQVIVIMPS*LT*NAEYMLDMAAT*LR	0.9463	0.25
MS2	UPTR:Q7KR73_DROME	RS*SQDGFLQSELSPVQQQLSEINNR	0.9591	0.016
MS3	UPTR:O96936_DROME	RS*SQDGFLQSELSPVQQQLSEINNR	0.9269	0.016
MS2	UPTR:Q9VX75_DROME	RSS*DPNLLASLK	0.998	0.201
MS3	UPTR:O96782_DROME	RSS*DPNLLASLK	0.9947	0.204
MS2	UPTR:O96958_DROME	RSS*LPVGQPVLTR	0.9985	0.262
MS2	UPTR:Q8WRQ7_DROME	RSS*NISALLEAAANEK	0.9777	0.092
MS3	UPTR:Q8WRQ7_DROME	RSS*NISALLEAAANEK	0.9896	0.074
MS2	UPTR:Q7KR73_DROME	RSS*QDGFLQSELSPVQQQLSEINNR	0.9377	0.131
MS3	UPTR:Q7KR73_DROME	RSS*QDGFLQSELSPVQQQLSEINNR	0.9537	0.138
MS2	HP1_DROME	RT*TDAEQDTIPVSGSTGFDR	0.9971	0.001
MS2	UPTR:Q8IMS6_DROME	RTS*TTVLDLSQAFK	0.9922	0.046
MS3	UPTR:Q8IMS6_DROME	RTS*TTVLDLSQAFK	0.9718	0.087
MS2	UPTR:Q9W3W1_DROME	RTS*TVFGK	0.966	0.135
MS3	UPTR:Q9W3W1_DROME	RTS*TVFGK	0.9588	0.141
MS3	HP1_DROME	RTT*DAEQDTIPVSGSTGFDR	0.9573	0.002
MS2	GP:M14131_1	RTTDAEQDT*IPVSGSTGFDR	0.9455	0.147
MS3	GP:M14131_1	RTTDAEQDT*IPVSGSTGFDR	0.9565	0.147
MS2	UPTR:Q9GTU6_DROME	RVS*ELAGIPGGSAR	0.9992	0.265
MS3	UPTR:Q9GTU6_DROME	RVS*ELAGIPGGSAR	0.9421	0.373
MS3	UPTR:Q7K2Q3_DROME	RVS*PVPAK	0.9953	0.2
MS2	UPTR:Q9W2U7_DROME	S*ASPAVVGSFR	0.937	0.09
MS2	CDC37_DROME	S*DDEDDTHPNIDTPSLFR	0.9045	0.235
MS2	UPTR:Q9Y162_DROME	S*DSDDEDGDDPEK	0.93	0.013
MS3	UPTR:Q9Y162_DROME	S*DSDDEDGDDPEK	0.9871	0.02
MS2	UPTR:Q9V426_DROME	S*EEELEYDPALYPQR	0.9968	0.289
MS3	UPTR:Q9V426_DROME	S*EEELEYDPALYPQR	0.9996	0.289
MS2	UPTR:Q9VAW4_DROME	S*FKSWSEEAAAEEAGESPIVGSVSLAQTGEK	0.9748	0.028
MS3	UPTR:Q9VAW4_DROME	S*FKSWSEEAAAEEAGESPIVGSVSLAQTGEK	0.9754	0.028
MS2	UPTR:Q5LK13_DROME	S*GEETDFVADPAETSLLIK	0.9954	0.023
MS3	DBP80_DROME	S*GEETDFVADPAETSLLIK	0.995	0.024
MS2	UPTR:Q8IGG3_DROME	S*GSVSSFPDALDENNTSSGLNSPTDSLPK	0.9607	0.008
MS3	UPTR:Q8IGG3_DROME	S*GSVSSFPDALDENNTSSGLNSPTDSLPK	0.9458	0.013
MS3	UPTR:Q8MT43_DROME	S*IGCACGTFLAGYLFR	0.9651	0.199
MS2	UPTR:Q8SY41_DROME	S*ILDSAIGFINDVTLANQPVQDPK	0.9522	0.076
MS2	UPTR:Q95TN8_DROME	S*LSDDEMPINHLLGPEANVANVFSTPVSSQK	0.9725	0.34
MS3	UPTR:Q95TN8_DROME	S*LSDDEMPINHLLGPEANVANVFSTPVSSQK	0.9635	0.317
MS3	PNUT_DROME	S*NAVNGGSGGAISALPSTLAQLALR	0.9977	0.072
MS2	UPTR:Q7K765_DROME	S*NSQEQLDQPQVK	0.9351	0.017
MS3	UPTR:Q7K765_DROME	S*NSQEQLDQPQVK	0.9709	0.286
MS3	FUTSC_DROME	S*PLDS*KDTS*RPGSMVESVTAEDEK	0.9272	0.223
MS2	UPTR:Q9NL57_DROME	S*RQSSVEQELLFSSELDIQHNHQK	0.9423	0.021
MS3	UPTR:Q9NL57_DROME	S*RQSSVEQELLFSSELDIQHNHQK	0.9697	0.032
MS2	UPTR:Q7KR74_DROME	S*SSNVNSQVGEGAGSSVDADAPGR	0.9051	0.022
MS3	UPTR:Q7KR74_DROME	S*SSNVNSQVGEGAGSSVDADAPGR	0.9983	0

MS Level	Protein	Sequence	Peptide probability	dCn
MS2	CH18_DROSU	S*SY	0.9966	0.077
MS2	UPTR:Q86S06_DROME	S*TSQQQQGVSSAVNATIDQLTK	0.9085	0.007
MS3	UPTR:Q86S06_DROME	S*TSQQQQGVSSAVNATIDQLTK	0.9364	0.038
MS2	UPTR:Q9Y095_DROME	S*VSPTPLDAKPLDR	0.9792	0.134
MS2	UPTR:Q9VXF9_DROME	SANRPVGGNPAISTLDFSニアVPGTSSGGS*PPSR	0.9761	0.071
MS3	UPTR:Q9VXF9_DROME	SANRPVGGNPAISTLDFSニアVPGTSSGGS*PPSR	0.9962	0.088
MS2	UPTR:Q8MR13_DROME	SAVSSPEQLPS*PTSPIAAEIGDKPYGR	0.9894	0.19
MS3	UPTR:Q8MR13_DROME	SAVSSPEQLPS*PTSPIAAEIGDKPYGR	0.9478	0.085
MS2	UPTR:Q86B44_DROME	SDLMLESGCPELS*PR	0.9999	0.437
MS3	UPTR:Q86B44_DROME	SDLMLESGCPELS*PR	0.9996	0.382
MS2	UPTR:Q9VQI0_DROME	SDLNLTGS*VELPVSPYFR	0.9943	0.31
MS3	UPTR:Q9VQI0_DROME	SDLNLTGS*VELPVSPYFR	0.9809	0.31
MS2	CAF1_DROME	SDNAAES*FDDAVEER	0.967	0.168
MS3	CAF1_DROME	SDNAAES*FDDAVEER	0.9113	0.157
MS2	UPTR:O46093_DROME	SDPLLQDSVGVS*PIR	0.9976	0.291
MS3	UPTR:O46093_DROME	SDPLLQDSVGVS*PIR	0.9889	0.243
MS2	UPTR:Q9Y162_DROME	SDS*DDEDGDDPEK	0.9939	0.254
MS3	UPTR:Q9Y162_DROME	SDS*DDEDGDDPEK	0.9718	0.274
MS2	H1_DROME	SDSAVATSAS*PVAAPPATVEK	0.9516	0.06
MS3	H1_DROME	SDSAVATSAS*PVAAPPATVEK	0.9578	0.06
MS2	MODU_DROME	SEGADEVDES*DDDEEAPVEKPVSK	0.98	0.223
MS3	MODU_DROME	SEGADEVDES*DDDEEAPVEKPVSK	0.9965	0.327
MS3	UPTR:Q7KRS5_DROME	SESAKEMLLS*QMPSLGPLPPS*PPNS*NPD	0.9676	0.284
MS2	DNK_DROME	SESSIFDAISSNQQQPSPVLVS*PSKR	0.9832	0.112
MS3	DNK_DROME	SESSIFDAISSNQQQPSPVLVS*PSKR	0.988	0.113
MS2	UPTR:Q9VAW4_DROME	SFKS*WSEEAAAEEAGESPIVGSVSLAQTGEK	0.9295	0.022
MS3	UPTR:Q9VAW4_DROME	SFKS*WSEEAAAEEAGESPIVGSVSLAQTGEK	0.9175	0.022
MS2	UPTR:Q9VFE9_DROME	SFLPFDAADIPENDVS*LVSGR	0.9986	0.242
MS3	UPTR:Q9VFE9_DROME	SFLPFDAADIPENDVS*LVSGR	0.9986	0.242
MS2	DBP80_DROME	SGEET*DFDVADPAETSLLIK	0.9968	0.102
MS3	UPTR:Q5LK13_DROME	SGEET*DFDVADPAETSLLIK	0.9963	0.104
MS2	UPTR:Q5LK13_DROME	SGEETDFDVADPAET*SLLIK	0.9281	0.031
MS3	UPTR:Q5LK13_DROME	SGEETDFDVADPAET*SLLIK	0.9221	0.031
MS2	UPTR:Q5LK13_DROME	SGEETDFDVADPAETS*LLIK	0.9145	0.073
MS3	UPTR:Q5LK13_DROME	SGEETDFDVADPAETS*LLIK	0.9954	0.064
MS2	UPTR:Q8IGG3_DROME	SGS*VSSFPDALDENNTSSGLNSPTDSLPK	0.991	0.05
MS3	UPTR:Q8IGG3_DROME	SGS*VSSFPDALDENNTSSGLNSPTDSLPK	0.9678	0.025
MS2	UPTR:Q8IGG3_DROME	SGSVS*SFPDALDENNTSSGLNSPTDSLPK	0.9954	0.003
MS3	UPTR:Q8IGG3_DROME	SGSVS*SFPDALDENNTSSGLNSPTDSLPK	0.985	0.001
MS2	UPTR:Q8IGG3_DROME	SGSVSS*FPDALDENNTSSGLNSPTDSLPK	0.9575	0.015
MS2	UPTR:Q8IGZ9_DROME	SGSVSSASSSVSSS*TENLK	0.9965	0.073
MS3	UPTR:Q4VIW7_DROBU	SGSVSSASSSVSSS*TENLK	0.9988	0.047
MS2	UPTR:Q8IGG3_DROME	SGSVSSFPDALDENNTSSGLNS*PTDSLPK	0.9216	0.028
MS2	UPTR:Q9VVA0_DROME	SHSPNASLQLPS*PIITR	0.9822	0.203
MS2	UPTR:Q9NL57_DROME	SIS*AVDTAAAQR	0.9986	0.312
MS3	UPTR:Q9NL57_DROME	SIS*AVDTAAAQR	0.9995	0.263
MS2	UPTR:Q9VZL5_DROME	SIS*ECQVGGFVR	0.916	0.067
MS2	UPTR:Q7KQM6_DROME	SIS*TVATLSTDR	0.9714	0.099
MS3	UPTR:Q7KQM6_DROME	SIS*TVATLSTDR	0.9817	0.093
MS2	UPTR:Q8IGE9_DROME	SISLKEEDT*DVEQHQNNR	0.9992	0.239
MS3	UPTR:Q8IGE9_DROME	SISLKEEDT*DVEQHQNNR	0.9961	0.222
MS2	UPTR:Q9VP57_DROME	SLEES*PSADLLRPR	0.9091	0.084
MS2	UPTR:Q8MRY4_DROME	SLES*DEDDILEK	0.9871	0.161
MS3	UPTR:Q8MRY4_DROME	SLES*DEDDILEK	0.9772	0.118
MS2	UPTR:Q9XZ07_DROME	SLQEGERGDLI*IAEDR	1	0.444
MS3	UPTR:Q9XZ07_DROME	SLQEGERGDLI*IAEDR	0.9915	0.391
MS2	UPTR:Q95TN8_DROME	SLS*DDEMPLNHLLGPEANVANVFSTPVSSQK	0.9856	0.041
MS3	UPTR:Q95TN8_DROME	SLS*DDEMPLNHLLGPEANVANVFSTPVSSQK	0.9922	0.042
MS2	UPTR:Q8T3Q6_DROME	SLS*GAPEDLEEMEIK	0.9439	0.085
MS3	UPTR:Q8T3Q6_DROME	SLS*GAPEDLEEMEIK	0.952	0.085
MS2	UPTR:Q8MSB4_DROME	SLS*PVSLILEMEK	0.9708	0.052

MS Level	Protein	Sequence	Peptide probability	dCn
MS3	UPTR:Q8MSB4_DROME	SLS*PVSLILEMEK	0.9717	0.053
MS3	UPTR:Q9VMA0_DROME	SLVELSFYLSNNHADNIKNCT*L	0.9857	0.258
MS2	PNUT_DROME	SNAVNGGS*GGAISALPSTLAQLALR	0.9841	0.085
MS3	PNUT_DROME	SNAVNGGS*GGAISALPSTLAQLALR	0.9845	0.085
MS3	UPTR:Q9VWS2_DROME	SNISFATSPGGSS*PHELNR	0.9051	0.016
MS2	UPTR:Q7K764_DROME	SNS*LEELR	0.9856	0.167
MS3	UPTR:Q7K764_DROME	SNS*LEELR	0.9492	0.136
MS2	UPTR:Q8MQI1_DROME	SPLS*ADMSLGLAK	0.9916	0.407
MS3	UPTR:Q8MQI1_DROME	SPLS*ADMSLGLAK	0.9651	0.333
MS2	UPTR:O16048_DROME	SQS*SENILNEK	0.9951	0.11
MS3	UPTR:O16048_DROME	SQS*SENILNEK	0.9953	0.109
MS2	UPTR:Q9NL57_DROME	SRQS*SVEQUELLFSSELDIQHNHQK	0.9317	0.015
MS3	UPTR:Q9NL57_DROME	SRQS*SVEQUELLFSSELDIQHNHQK	0.915	0.016
MS2	UPTR:Q8T3W9_DROME	SS*GLTIDTNPDATPAGGFR	0.956	0.117
MS2	UPTR:Q8IGZ9_DROME	SS*IPFGQNTTEAVAAQK	0.9804	0.002
MS2	UPTR:Q94885_DROME	SS*LQFQEQQPQEKS	0.9627	0.002
MS3	UPTR:Q94885_DROME	SS*LQFQEQQPQEKS	0.955	0.002
MS2	UPTR:Q7KR74_DROME	SS*SNVNSQVGEGAGSSVDADAPGR	0.9404	0.004
MS3	UPTR:Q7KR74_DROME	SS*SNVNSQVGEGAGSSVDADAPGR	0.9401	0.004
MS2	GP:AE003526_24	SS*TTLVYSSEPR	0.971	0.01
MS3	LASP1_DROME	SS*TTLVYSSEPR	0.9855	0.008
MS2	UPTR:Q6AWQ1_DROME	SS*VEYAGPAVNTIDLRC	0.9942	0.005
MS3	UPTR:Q6AWQ1_DROME	SS*VEYAGPAVNTIDLRC	0.9791	0.005
MS2	UPTR:Q8INM3_DROME	SSIS*ETELER	0.98	0.149
MS2	UPTR:Q7KR73_DROME	SSS*IPALTGFGFKPIR	0.9716	0.151
MS3	UPTR:Q7KR73_DROME	SSS*IPALTGFGFKPIR	0.9795	0.142
MS2	UPTR:Q7KR74_DROME	SSS*NVNSQVGEGAGSSVDADAPGR	0.9961	0
MS3	UPTR:Q7KR74_DROME	SSS*NVNSQVGEGAGSSVDADAPGR	0.9959	0
MS2	UPTR:Q8MME2_DROME	SSS*SENVNEPTLK	0.9591	0.035
MS3	UPTR:Q8IQN4_DROME	SSSAATTTPAALES*PVR	0.9572	0.29
MS3	UPTR:Q4TZM6_DROME	SSSAGPS*VT*GLTVAGSGGDGNANATGGDAS*DK	0.9824	0.161
MS2	CPD1_DROME	SSTAAVAIAIS*PGIK	0.9992	0.281
MS3	GP:U56393_1	SSTAAVAIAIS*PGIK	0.9989	0.365
MS2	UPTR:Q9VA36_DROME	SSTS*SATTSSATTVATGLTSSSVSK	0.9989	0.004
MS3	UPTR:Q9VA36_DROME	SSTS*SATTSSATTVATGLTSSSVSK	0.9983	0.005
MS2	UPTR:Q86S06_DROME	ST*SQQQQGVSSAVNATIDQLTK	0.9441	0.001
MS3	UPTR:Q86S06_DROME	ST*SQQQQGVSSAVNATIDQLTK	0.976	0.025
MS2	UPTR:Q8T3Q6_DROME	STS*FMDQMSGAK	0.9418	0.074
MS3	UPTR:Q8T3Q6_DROME	STS*FMDQMSGAK	0.9744	0.107
MS2	UPTR:Q86S06_DROME	STS*QQQQGVSSAVNATIDQLTK	0.978	0.036
MS3	UPTR:Q86S06_DROME	STS*QQQQGVSSAVNATIDQLTK	0.9605	0.014
MS2	UPTR:P91675_DROME	SVAMLMASPSS*EEQSVATSTTEPAIISDAR	0.914	0.016
MS3	UPTR:P91675_DROME	SVAMLMASPSS*EEQSVATSTTEPAIISDAR	0.9113	0.014
MS2	UPTR:P91675_DROME	SVAMLMASPSEEQS*VATSTTEPAIISDAR	0.9338	0.023
MS2	UPTR:Q9I7T7_DROME	SVATSTS*TENLSAAATASK	0.9984	0.043
MS3	UPTR:Q9I7T7_DROME	SVATSTS*TENLSAAATASK	0.9988	0.044
MS2	UPTR:Q9VGE4_DROME	SVS*QQEDEEAEMAAR	0.9736	0.033
MS3	UPTR:Q9VGE4_DROME	SVS*QQEDEEAEMAAR	0.9093	0.037
MS2	UPTR:O16040_DROME	T*ADSPAKEPQEICEVK	0.9371	0.042
MS2	UPTR:Q24452_DROME	T*ASAAAAMMSLTAAAAPK	0.962	0.014
MS3	UPTR:Q9VZZ9_DROME	T*ASAAAAMMSLTAAAAPK	0.9195	0.014
MS2	UPTR:Q8MZB3_DROME	T*KSETEDPIELLK	0.9811	0.045
MS3	UPTR:Q8MZB3_DROME	T*KSETEDPIELLK	0.9264	0.05
MS2	UPTR:Q5KTT4_DROME	T*LLNTSPNLLPITTATDTFNNLK	0.9139	0.021
MS3	UPTR:Q5KTT4_DROME	T*LLNTSPNLLPITTATDTFNNLK	0.9033	0.021
MS3	UPTR:Q9N618_DROSI	T*S*NVFAMFDQAQIAEFK	0.9445	0.274
MS2	UPTR:Q9W4L2_DROME	T*SPIQVNGAALACPLVR	0.9845	0.015
MS3	UPTR:Q9W4L2_DROME	T*SPIQVNGAALACPLVR	0.9933	0.024
MS3	HP1_DROME	T*TDAEQDTIPVSGSTGFDR	0.9562	0.004
MS2	GP:AY071367_1	T*VGT*FIT*RQPQLLVLDPALAHEILVD	0.9612	0.308
MS3	CP391_DROME	T*VGT*FIT*RQPQLLVLDPALAHEILVD	1	0.33

MS Level	Protein	Sequence	Peptide probability	dCn
MS2	UPTR:O16040_DROME	TADS*PAKEPQEICEVK	0.9426	0.07
MS3	UPTR:O16040_DROME	TADS*PAKEPQEICEVK	0.9234	0.091
MS2	UPTR:Q8IRB9_DROME	TANLMSTS*LIVTSSSSR	0.9948	0.106
MS3	UPTR:Q8IRB9_DROME	TANLMSTS*LIVTSSSSR	0.9956	0.095
MS2	UPTR:Q8IGG3_DROME	TASVFGS*ITSGISSK	0.9985	0.149
MS3	UPTR:Q8IGG3_DROME	TASVFGS*ITSGISSK	0.9984	0.143
MS2	UPTR:P91675_DROME	TATVGADS*DEEDIEPPQPDAGDLTR	0.9742	0.001
MS3	UPTR:P91675_DROME	TATVGADS*DEEDIEPPQPDAGDLTR	0.9387	0.001
MS2	UPTR:Q8MLI7_DROME	TDNQKS*PLFTTSATTGPHVESTR	0.9196	0.144
MS3	41_DROME	TDNQKS*PLFTTSATTGPHVESTR	0.9068	0.136
MS2	PPAN_DROME	TDS*DPEDDAEYYKEEVGEEPDEELFK	0.9522	0.071
MS3	PPAN_DROME	TDS*DPEDDAEYYKEEVGEEPDEELFK	0.9387	0.076
MS2	GP:U01842_1	TEQVLTTQAQEILAAAADLATDDTHQLHGT*IER	0.9488	0.053
MS3	GP:U01842_1	TEQVLTTQAQEILAAAADLATDDTHQLHGT*IER	0.9073	0.053
MS2	UPTR:O96046_DROME	TGGIGNAISAFNQMQS*PVSETPPAR	0.9916	0.098
MS3	UPTR:O96046_DROME	TGGIGNAISAFNQMQS*PVSETPPAR	0.9889	0.086
MS2	BICD_DROME	TGIEQEDALLNES*AAR	0.9998	0.291
MS3	BICD_DROME	TGIEQEDALLNES*AAR	0.9994	0.382
MS3	UPTR:Q9VQK3_DROME	TGVCEGDFIFSIGGGPGGNFS*L	0.9995	0.308
MS2	UPTR:Q8ML45_DROME	TIS*GTQTVATAVGNLATISQQQPVQQSPLGK	0.9806	0.024
MS3	UPTR:O17142_DROME	TIS*GTQTVATAVGNLATISQQQPVQQSPLGK	0.9857	0.009
MS2	UPTR:O17142_DROME	TISGT*QTVATAVGNLATISQQQPVQQSPLGK	0.9536	0.051
MS3	UPTR:Q8ML45_DROME	TISGT*QTVATAVGNLATISQQQPVQQSPLGK	0.9623	0.061
MS2	UPTR:Q9VNA2_DROME	TIVPTHFSES*PPR	0.9966	0.297
MS3	UPTR:Q9VNA2_DROME	TIVPTHFSES*PPR	0.924	0.151
MS2	UPTR:Q8MZH3_DROME	TKS*ETEDPIELLK	0.9526	0.026
MS2	GNL3_DROME	TLES*MVEDADMR	0.9986	0.178
MS3	GNL3_DROME	TLES*MVEDADMR	0.9988	0.178
MS2	UPTR:Q5KTT4_DROME	TLLNT*SPNLLPITTATDTFNNLK	0.9319	0.039
MS3	UPTR:Q5KTT4_DROME	TLLNT*SPNLLPITTATDTFNNLK	0.9734	0.012
MS2	UPTR:Q5KTT4_DROME	TLLNTS*PNLLPITTATDTFNNLK	0.9917	0.002
MS3	UPTR:Q5KTT4_DROME	TLLNTS*PNLLPITTATDTFNNLK	0.999	0.328
MS2	UPTR:Q6UBD8_DROME	TLS*DIGSITEFPEPDVER	0.9575	0.015
MS3	UPTR:Q6UBD8_DROME	TLS*DIGSITEFPEPDVER	0.9668	0.015
MS2	GP:U01842_1	TLVATS*PHQEIVR	0.9841	0.013
MS3	GP:U01842_1	TLVATS*PHQEIVR	0.9829	0.012
MS2	UPTR:Q24496_DROME	TPFASTPNDS*PDVILK	1	0.226
MS3	UPTR:Q24496_DROME	TPFASTPNDS*PDVILK	0.999	0.229
MS2	UPTR:Q95R63_DROME	TQDS*DEFNLEPGPSK	0.9995	0.129
MS3	UPTR:Q95R63_DROME	TQDS*DEFNLEPGPSK	0.9988	0.177
MS2	UPTR:Q8I1D4_DROVI	TQFFGLDNLPS*PTADR	0.9767	0.414
MS3	UPTR:Q8I1D4_DROVI	TQFFGLDNLPS*PTADR	0.9793	0.001
MS2	UPTR:Q8I1J2_DROER	TQFFGLDNLPS*PTADRK	0.9917	0.02
MS2	UPTR:Q8I1D4_DROVI	TQFFGLDNLPSPT*ADR	0.9984	0.055
MS3	UPTR:Q8I1D4_DROVI	TQFFGLDNLPSPT*ADR	0.9929	0.055
MS2	EAS_DROME	TQGLS*PVQSEDPVIIKEKDDDEFTDDR	0.9386	0.15
MS3	EAS_DROME	TQGLS*PVQSEDPVIIKEKDDDEFTDDR	0.9618	0.147
MS2	EF1D_DROME	TQVS*LLNELLTATVK	0.9941	0.098
MS3	EF1D_DROME	TQVS*LLNELLTATVK	0.9933	0.098
MS2	UPTR:Q6NP13_DROME	TRQS*EDLLVER	0.9573	0.188
MS3	UPTR:Q6NP13_DROME	TRQS*EDLLVER	0.9894	0.12
MS2	UPTR:Q23980_DROME	TS*GAQVLDGTATPQMAFLQR	0.9941	0.001
MS3	UPTR:Q23980_DROME	TS*GAQVLDGTATPQMAFLQR	0.9782	0.001
MS2	UPTR:Q9W4L2_DROME	TS*PIQVNNGAACPLVR	0.9515	0.004
MS3	UPTR:Q9W4L2_DROME	TS*PIQVNNGAACPLVR	0.9567	0.004
MS2	UPTR:Q9VHU6_DROME	TS*SGDDDAPLLTAK	0.9172	0.005
MS2	UPTR:Q9VDI1_DROME	TSAAVAGAATATAASAAS*NRNSSVTNGNGK	0.9919	0.09
MS3	UPTR:Q9VDI1_DROME	TSAAVAGAATATAASAAS*NRNSSVTNGNGK	0.9911	0.09
MS2	UPTR:Q9VWY7_DROME	TSAIPVRLS*PPVPGGGLPAPATCEVEQALNR	0.9799	0.084
MS3	UPTR:Q9VWY7_DROME	TSAIPVRLS*PPVPGGGLPAPATCEVEQALNR	0.9808	0.084
MS2	UPTR:Q9XYZ7_DROME	TSLFSCADSKDS*PK	0.9938	0.164

MS Level	Protein	Sequence	Peptide probability	dCn
MS3	UPTR:Q9XYZ7_DROME	TSLFSCADSKDS*PK	0.9898	0.159
MS2	UPTR:Q9VYB2_DROME	TSRPLS*PMPDFTDSLQR	0.9165	0.062
MS2	UPTR:Q9VHU6_DROME	TSS*GDDDAPLLTAK	0.9425	0.068
MS3	UPTR:Q9VHU6_DROME	TSS*GDDDAPLLTAK	0.9363	0.081
MS2	UPTR:Q7KV88_DROME	TSS*VLPDLLSQASPATPPR	0.9503	0.01
MS3	UPTR:Q7KV88_DROME	TSS*VLPDLLSQASPATPPR	0.9666	0.016
MS2	UPTR:Q8IMS6_DROME	TSTISNPNSARPS*FNVIEDDVQALSK	0.9458	0.294
MS3	UPTR:Q8IMS6_DROME	TSTISNPNSARPS*FNVIEDDVQALSK	0.9966	0.136
MS3	UPTR:Q9UB07_DROME	TSTS*PSPVLNALR	0.9415	0.08
MS3	HP1_DROME	TT*DAEQDTIPVSGSTGFDR	0.9768	0.002
MS2	UPTR:Q8MQK4_DROME	TT*SIGNQTTTANPSECIRR	0.9329	0.005
MS2	UPTR:Q7KRU0_DROME	TT*SVSVGVPPEHIVK	0.9445	0.012
MS3	UPTR:Q7KRU0_DROME	TT*SVSVGVPPEHIVK	0.9366	0.058
MS3	UPTR:Q6NLK4_DROME	TTGETS*PQAEEKEDS*ANEQSADPAVAEEEDESK	0.9036	0.023
MS2	UPTR:Q6NLK4_DROME	TTGETS*PQAEKEDSANEQSADPAVAEEEDESK	0.9539	0.04
MS3	UPTR:Q6NLK4_DROME	TTGETS*PQAEKEDSANEQSADPAVAEEEDESK	0.9108	0.042
MS2	UPTR:Q6NLK4_DROME	TTGETSPQAEKEDS*ANEQSADPAVAEEEDESK	0.9184	0.111
MS3	UPTR:Q6NLK4_DROME	TTGETSPQAEKEDS*ANEQSADPAVAEEEDESK	0.9433	0.09
MS2	UPTR:Q8IGE9_DROME	TTKS*EGDQSGVEAGAK	0.9653	0.194
MS3	UPTR:Q8IGE9_DROME	TTKS*EGDQSGVEAGAK	0.9957	0.2
MS2	UPTR:Q8MQK4_DROME	TTS*IGNQTTTANPSECIRR	0.9321	0.034
MS2	UPTR:Q8IGE9_DROME	TTS*QTDNEQPQGETAQK	0.9873	0.007
MS3	UPTR:Q8IGE9_DROME	TTS*QTDNEQPQGETAQK	0.9894	0.069
MS2	UPTR:Q7KRU0_DROME	TTS*VSvgvppehivk	0.927	0.04
MS3	UPTR:Q7KRU0_DROME	TTS*VSvgvppehivk	0.9271	0.077
MS2	UPTR:Q8T0P5_DROME	TTVSNAGIVGGLGFMS*PR	0.976	0.232
MS3	UPTR:Q8IGQ1_DROME	TTVSNAGIVGGLGFMS*PR	0.9989	0.254
MS2	UPTR:Q8MPP2_DROME	TVQDTTS*EVGVVTK	0.9502	0.21
MS3	UPTR:Q8MPP2_DROME	TVQDTTS*EVGVVTK	0.9538	0.187
MS2	UPTR:Q6XHQ8_DROYA	VAADDVS*AVKDDLK	0.9943	0.281
MS3	UPTR:Q6XHQ8_DROYA	VAADDVS*AVKDDLK	0.9903	0.289
MS3	UPTR:Q8IRH5_DROME	VAEIEPSTQES*DKK	0.9577	0.173
MS2	GP:AE003417_4	VAIVSTGSELCS*PR	0.9861	0.315
MS3	GP:AE003417_4	VAIVSTGSELCS*PR	0.9879	0.315
MS3	UPTR:Q8MR14_DROME	VALQIGNTT*ITPLTK	0.9049	0.045
MS2	UPTR:Q9VNE0_DROME	VEIFDNLFGSSS*PISNIR	0.9152	0.008
MS3	UPTR:Q9VNE0_DROME	VEIFDNLFGSSS*PISNIR	0.9524	0.066
MS2	UPTR:Q86BS3_DROME	VENSEAPAPVS*PAPVPQK	0.9992	0.4
MS3	UPTR:Q86BS3_DROME	VENSEAPAPVS*PAPVPQK	0.9992	0.4
MS2	UPTR:Q9W0N9_DROME	VEPEAELES*ELDQDPADLDEDANNGR	0.999	0.389
MS3	UPTR:Q9W0N9_DROME	VEPEAELES*ELDQDPADLDEDANNGR	0.9989	0.33
MS2	UPTR:O46307_DROME	VEPEDDS*DEELVR	0.9985	0.21
MS3	UPTR:Q8MR29_DROME	VEPEDDS*DEELVR	0.9986	0.274
MS2	UPTR:Q960P4_DROME	VEPMHSVSEEKTS*PVK	0.9472	0.238
MS3	UPTR:Q960P4_DROME	VEPMHSVSEEKTS*PVK	0.9492	0.061
MS2	GP:AE003707_12	VES*GADLKDYFDR	0.9882	0.19
MS3	GP:AE003707_12	VES*GADLKDYFDR	0.9539	0.214
MS2	UPTR:Q8T3Q6_DROME	VEVGNDFCPSQS*FVDMVAEK	0.9982	0.231
MS3	UPTR:Q8T3Q6_DROME	VEVGNDFCPSQS*FVDMVAEK	0.9979	0.23
MS2	UPTR:Q8IRM8_DROME	VFGS*SIKVDSSLAK	0.9216	0.086
MS2	UPTR:Q9V6S4_DROME	VFGSLKPSNQGDS*DGE	0.973	0.143
MS3	UPTR:Q9V6S4_DROME	VFGSLKPSNQGDS*DGE	0.9327	0.146
MS2	UPTR:Q9VM93_DROME	VGS*LEHVNLAR	0.9861	0.169
MS3	UPTR:Q9VM93_DROME	VGS*LEHVNLAR	0.9953	0.29
MS2	UPTR:Q9VA36_DROME	VGVFPSNFVQHIEPS*PVЛАSK	0.9758	0.036
MS3	UPTR:Q7YU85_DROME	VGVFPSNFVQHIEPS*PVЛАSK	0.9033	0.068
MS2	UPTR:Q7YU85_DROME	VGVFPSNFVQHIEPSPVLAS*K	0.9109	0.256
MS3	UPTR:Q9VA36_DROME	VGVFPSNFVQHIEPSPVLAS*K	0.9394	0.015
MS2	UPTR:Q8IGK0_DROME	VIQGLEDNEDS*QGEAPNLK	1	0.496
MS3	UPTR:Q8IGK0_DROME	VIQGLEDNEDS*QGEAPNLK	1	0.481
MS2	UPTR:O76755_DROME	VIS*AGVSAVLSEPEKPGGDNFLR	0.9732	0.398

MS Level	Protein	Sequence	Peptide probability	dCn
MS3	UPTR:O76755_DROME	VIS*AGVSAVLSEPEKPGGDNFLR	0.9186	0.337
MS2	UPTR:Q9VWS3_DROME	VIS*EDEDEFVFDNLSHKS*S*GSSLNIQR	0.9489	0.32
MS2	UPTR:Q86B47_DROME	VLDEEDEQEKGDS*DDDGDIPLLQGLR	0.9826	0.16
MS3	UPTR:Q86B47_DROME	VLDEEDEQEKGDS*DDDGDIPLLQGLR	0.9831	0.16
MS2	UPTR:Q9VYV4_DROME	VLDGDDT*NDGVGVLDLDES*QGAGGR	0.9982	0.189
MS3	UPTR:Q9VYV4_DROME	VLDGDDT*NDGVGVLDLDES*QGAGGR	0.9971	0.189
MS2	UPTR:Q8IGC9_DROME	VLRPPGGGS*SDIFGSEMPQTPR	0.9239	0.36
MS2	UPTR:Q8IGC9_DROME	VLRPPGGSSDIFGSEMPQT*PR	0.9912	0.149
MS2	UPTR:Q8IRB5_DROME	VLS*DDESEENQNEK	1	0.354
MS3	UPTR:Q8IRB5_DROME	VLS*DDESEENQNEK	1	0.408
MS2	UPTR:Q9VTU0_DROME	VMNKEDDS*EDEFGGIFK	0.964	0.243
MS3	UPTR:Q9VTU0_DROME	VMNKEDDS*EDEFGGIFK	0.9739	0.362
MS2	UPTR:Q9XZ31_DROME	VNFS*PILATELGPR	0.9664	0.195
MS3	UPTR:Q9XZ31_DROME	VNFS*PILATELGPR	0.995	0.174
MS3	UPTR:Q7KVC1_DROME	VNS*RDLVVT*AAR	0.9406	0.157
MS2	MODU_DROME	VQEEETVVPQPS*PSK	0.9571	0.203
MS3	MODU_DROME	VQEEETVVPQPS*PSK	0.9125	0.203
MS2	MODU_DROME	VQEEETVVPQSPS*K	0.9294	0.246
MS3	MODU_DROME	VQEEETVVPQSPS*K	0.9398	0.246
MS2	UPTR:Q7KQ11_DROME	VQS*MVGIIGNR	0.9597	0.135
MS3	UPTR:Q7KQ11_DROME	VQS*MVGIIGNR	0.9656	0.093
MS2	UPTR:Q8MQX4_DROME	VRDFS*PVIGQNVGR	0.9349	0.126
MS2	HP1_DROME	VS*DAEEEEEEYAVEK	0.9762	0.154
MS3	HP1_DROME	VS*DAEEEEEEYAVEK	0.9763	0.179
MS2	UPTR:Q76NQ9_DROME	VS*ISGEDTSGVPLEDLER	0.9937	0.187
MS3	UPTR:Q76NQ9_DROME	VS*ISGEDTSGVPLEDLER	0.9879	0.164
MS3	UPTR:Q9V9I8_DROME	VS*TYYVMPGHQSSISPMNDNLRLER	0.9721	0.264
MS2	UPTR:Q9V544_DROME	VSVLDEDLDELPS*DEEK	0.9954	0.283
MS3	UPTR:Q9V544_DROME	VSVLDEDLDELPS*DEEK	0.9966	0.283
MS2	UPTR:Q9V544_DROME	VSVLDEDLDELPS*DEEKADETNRPK	0.9436	0.145
MS3	UPTR:Q9V544_DROME	VSVLDEDLDELPS*DEEKADETNRPK	0.9886	0.242
MS2	UPTR:Q24050_DROME	VTPLDGGLPAGAS*PK	1	0.364
MS3	UPTR:Q24050_DROME	VTPLDGGLPAGAS*PK	0.9998	0.364
MS2	UPTR:Q9VUB8_DROME	VTTGEAIP*PETVPAR	0.9553	0.24
MS3	UPTR:Q9VUB8_DROME	VTTGEAIP*PETVPAR	0.9616	0.24
MS2	GP:L14644_1	VVLMETDDS*LPSTSK	0.9989	0.35
MS3	HYD_DROME	VVLMETDDS*LPSTSK	0.999	0.373
MS3	UPTR:Q9V5J7_DROME	VYTHVSRLQFDSGENLHNQQT*FEGLNYWDQLSVK	0.9624	0.195
MS2	UPTR:Q9VVA0_DROME	WEEPFYGGSS*PAK	0.9846	0.264
MS3	UPTR:Q9VVA0_DROME	WEEPFYGGSS*PAK	0.9763	0.033
MS2	YC17_DROME	WRDES*DDEEGDQK	0.964	0.216
MS3	YC17_DROME	WRDES*DDEEGDQK	0.9895	0.257
MS2	UPTR:Q9VB23_DROME	YRNS*QDVELQQLPPLK	0.9964	0.162
MS3	UPTR:Q9VB23_DROME	YRNS*QDVELQQLPPLK	0.9794	0.186
MS2	UPTR:Q95TU6_DROME	YS*ISNAEFDIEDVVQR	0.9827	0.05
MS3	UPTR:Q95TU6_DROME	YS*ISNAEFDIEDVVQR	0.9449	0.052