

	protein OS= <i>Apis mellifera</i>	Q27_API ME						
Triple	Alpha-glucosidase OS= <i>Apis mellifera</i>	A0A0B4J2P5_API ME	66,596.7	100	7	7	13.1	105
Triple	Uncharacterized protein OS= <i>Apis mellifera</i>	A0A087ZTY7_API ME	75,404.6	100	3	3	6.11	42
Triple	Alpha-glucosidase; Uncharacterized protein OS= <i>Apis mellifera</i>	Q25BT8_API ME	67,359.4	100	4	4	7.99	80
Triple	Aconitate hydratase, mitochondrial OS= <i>Apis mellifera</i>	A0A087ZXX3_API ME	85,998.7	100	20	22	28.8	234
Triple	Transferrin OS= <i>Apis mellifera</i>	A0A088AFH7_API ME	78,630.7	100	30	43	49.9	760
Triple	Uncharacterized protein OS= <i>Apis mellifera</i>	A0A088AJI5_API ME	76,681.3	100	19	29	34.1	612
Triple	Uncharacterized protein OS= <i>Apis mellifera</i>	A0A088AQB0_API ME	75,709.1	100	9	10	21.8	230

Fig. 1:

A:

MLLLTLLFAGTVAADFQHNWQVGNEYTYLVRSRTLTSLGDLSDVHTGILIKALLTVQAKDSNVLAALKVWNGQYARVQQSMPDGWE
TEISDQMLELRDLPIGKPFQIRMKHGLIRDLIVDRDVPTWEVNILKSIVGQLQVDTQGENAVKVNSVQVPTDDEPYASFKAMEDSVGGK
CEVLYDIAPLSDFVIHRSPELVPMPTLKGDRHMEVIKKNFDNCDQRINYHFGMTDNSRLEPGTNKNGKFFSRSSSTRIVISESLKHFTIQ
SSVTTSKMMVSPRLYDRQNGVLVSRMNLTLAKMEKTSKPLPMVDNPESTGNLVYTYNNPFSDEERRVSKTAMNSNQIVSDNSLSSSEE
KLKQDILNLRTDISSSSSSISSEENDFWQPKPTLEDAPQNSLLPNFVGYYKQKHGKSGKYDVTNAAKELIFQIANELEDASNIPVHATLEK
FMILCNLMRTMNRKQISELESNMQISPNEKPNKDSQVIKQNTWTVFRDAITQTGTGPAFLTIKEWIERGTTKSMEANIMSKLPKTVRT
PTDSYIRSFPELLQNPQVSNQFLNTAATLSFCEMIHNQVKNRSIHNNYPVHTFGRLTSKHDNSLYDEYIPFLERELRKAHQEKDSPRIQ
TYIMALGMIGEPKILSVFEPYLEGKQQMTVFQRTLMVQSLGKLTETNPKLARSVLYKIYLNMTESHEVRCITAVFLLMKTNPPLSMLQRM
AEFTKLDNLRQVNSAVKSTIQSLMKLKSPEWKDLAKKARSVNHLLTHHEYDVELSRGYIDEKILENQNIITHMILNYVGSSEDSVIPRILYL
TWYSSNGDIKVPSTKVLAMISSVKSFMELSLRSVKDRETIISAAEKIAEELKIVPEELVPLEGNLMNNKYALKFFPFDKHILDKLPTLISN
YIEAVKEGKFMNVNMLDYESVHSFPTETGLPFVYTFNVIKLTKTSGTVQAQINPDFAFIVNSNLRLTFSKNVQGRVGFVTPFEHRHFISG
IDSNLHVYAPLKISLDVNTPKGNMQWKIWPMMKGEESRLFHYSVVPFVSNDHILNLRPLSMEKGTRPMIPDDNTSLALPKNEGPFRLNV
ETAKTNEEMWELIDTEKLTDRLPYPWTMDNERYVKVDMYMNLEGEQKDPVIFSTSFDSKVMTRPDTSENWTPKMMAVEPTDKQAN
SKTRRQEMMREAGRGIESAKSYVVDVRVHVPGESESETVTLAWSESNVESKGRLLGFWRVEMPRSNADYEVCIQSQIMVSPETLLSY
DEKMDQKPKMDFNVDIRYGKNGKGERIDMNGKLRQSPRLKELVGATSHKDCVEDMKRGNKILRTCQKAVVLSMLLDEVDSMEVPS
DALIALYSQGLFSLSEIDNLDVSLDVSNPKNAOKKKIDVRAKLNEYLDKADVINTPIMDAHFKDVKLSDFGFGSTEDILDTADEDLLINN
VFYEDETSCMLDKTRAQTFDGKDYPLRLGPCWHAVMTTYPRINPDNHNKHLHIPKDKSVSVLSRENEAGQKEVKVLLGSDKIKFVPGT
TSQPEFVNGEKIVVSRNKAYQKVEENEIIFEIYKMGDRFIOLTSDFVSLALDGERVMLKASEDYRYSVRGLCGNFDHDSNDNFVGP
KNCLFRKPEHFVASYALISNQCEGDSLNVAKSLQDHDCIRQERTQQRNVISDSSESGRLDTEMSTWGYHHNVNKHCTIHTQVKETDDKI
CFTMRPVVSCASGCTAVETKSKPYKFHCLKNTAAAMKLNKRIEKGANPILSQKPVSTTEELTVPFVCKA

B:

