**Supplementary Table 2**

N-glycosylation acceptor site

XBP1u arrest peptide (21 residues)

Flanking GGPG….GPGG tetrapeptides

H segment

Linker

Amino acid sequences of constructs representing the red curve in Figure 6B (mutation S255A in the XBP1u arrest peptide)

L69:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGTWIVPPGQYFMMGDNRDNSADSRYWGFVPEANLVGRATAGDPVPYQPPFLCQWGRHQPAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L63:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGGQYFMMGDNRDNSADSRYWGFVPEANLVGRATAGDPVP YQPPFLCQWGRHQPAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L61:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGYFMMGDNRDNSADSRYWGFVPEANLVGRATAGDPVPYQPPFLCQWGRHQPAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L59:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGMMGDNRDNSADSRYWGFVPEANLVGRATAGDPVP YQPPFLCQWGRHQPAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L56:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGDNRDNSADSRYWGFVPEANLVGRATAGDPVP YQPPFLCQWGRHQPAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L53:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGDNSADSRYWGFVPEANLVGRATAGDPVP YQPPFLCQWGRHQPAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L51:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGSADSRYWGFVPEANLVGRATAGDPVPYQPPFLCQWGRHQPAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L48:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGSRYWGFVPEANLVGRATAGDPVPYQPPFLCQWGRHQPAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L46:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGYWGFVPEANLVGRATAGDPVPYQPPFLCQWGRHQPAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L45:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGWGFVPEANLVGRATAGDPVPYQPPFLCQWGRHQPAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L43:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGFVPEANLVGRATAGDPVPYQPPFLCQWGRHQPAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L42:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGVPEANLVGRATAGDPVPYQPPFLCQWGRHQPAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L41:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGPEANLVGRATAGDPVPYQPPFLCQWGRHQPAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L39:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGANLVGRATAGDPVPYQPPFLCQWGRHQPAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L38:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGNLVGRATAGDPVPYQPPFLCQWGRHQPAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L36:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGVGRATAGDPVPYQPPFLCQWGRHQPAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L34:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGRATAGDPVPYQPPFLCQWGRHQPAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L33:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGATAGDPVPYQPPFLCQWGRHQPAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L31:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGAGDPVPYQPPFLCQWGRHQPAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L30:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGGDPVPYQPPFLCQWGRHQPAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L29:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGDPVPYQPPFLCQWGRHQPAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L25:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAADPVPYQPPFLCQWGRHQPAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

Amino acid sequence list of constructs representing the blue curve in Figure. 6B (mutations P254C and S255A in the XBP1u arrest peptide)

L69:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGTWIVPPGQYFMMGDNRDNSADSRYWG FVPEANLVGRATAGDPVPYQPPFLCQWGRHQCAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L63:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGGQYFMMGDNRDNSADSRYWGFVPEANLVGRATAGDPVP YQPPFLCQWGRHQCAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L61:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGYFMMGDNRDNSADSRYWGFVPEANLVGRATAGDPVPYQPPFLCQWGRHQCAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L59:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGMMGDNRDNSADSRYWGFVPEANLVGRATAGDPVP YQPPFLCQWGRHQCAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L56:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGDNRDNSADSRYWGFVPEANLVGRATAGDPVP YQPPFLCQWGRHQCAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L53:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGDNSADSRYWGFVPEANLVGRATAGDPVP YQPPFLCQWGRHQCAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L51:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGSADSRYWGFVPEANLVGRATAGDPVPYQPPFLCQWGRHQCAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L48:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGSRYWGFVPEANLVGRATAGDPVPYQPPFLCQWGRHQCAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L46:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGYWGFVPEANLVGRATAGDPVPYQPPFLCQWGRHQCAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L45:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGWGFVPEANLVGRATAGDPVPYQPPFLCQWGRHQCAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L43:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGFVPEANLVGRATAGDPVPYQPPFLCQWGRHQCAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L42:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGVPEANLVGRATAGDPVPYQPPFLCQWGRHQCAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L41:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGPEANLVGRATAGDPVPYQPPFLCQWGRHQCAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L39:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGANLVGRATAGDPVPYQPPFLCQWGRHQCAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L38:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGNLVGRATAGDPVPYQPPFLCQWGRHQCAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L36:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGVGRATAGDPVPYQPPFLCQWGRHQCAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L34:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGRATAGDPVPYQPPFLCQWGRHQCAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L33:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGATAGDPVPYQPPFLCQWGRHQCAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L31:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGAGDPVPYQPPFLCQWGRHQCAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L30:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGGDPVPYQPPFLCQWGRHQCAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L29:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAAGPGGDPVPYQPPFLCQWGRHQCAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*

L25:

MANMFALILVIATLVTGILWCVDKFFFAPKRRERQAAAQAAAGDSLDKATLKKVAPKPGWLETGASVFPVLAIVLIVRSFIYEPFQIPSGSMMPTLNSTDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDPKLDYIKRAVGLPGDKVTYDPVSKELTIQPGCSSGQACENALPVTYSNVEPSDFVQTFSRRNGGEATSGFFEVPKQETKENGIRLSETSGGPGAAAALALALALALALAAAADPVPYQPPFLCQWGRHQCAWKPLMNGSSDKQEGEWPTGLRLSRIGGIH\*