



1	MSNKKKKDLD	TSYMPYLDPA	NYADYITNEE	IPQDELNRNDP	QISNGYTKIP
VLXT	DDDDDDDDDD		DD	DDDDDDDDDD	DDDDDDDDDD
51	NNQNINNLYP	NNVNHYPKSS	NSPNNLPNTN	NTSGNMNYNT	SATNNMPNNM
VLXT	DDDDDDDDDD	DDDDDDDDDD	DDDDDDDDDD	DDDDDDDDDD	DDDDDDDDDD
101	NNNTGMPNNM	SNNMNSNMGM	PNNMSNNMNS	NMGMPNNMPN	NMNSNMGMPN
VLXT	DDDDDDDDDD	DDDDDDDDDD	DDDDDDDDDD	DDDDDDDDDD	DDDDDDDDDD
151	NVPNNMNSNM	GMPNNMSNNM	NSNMGMPNNM	SGNMNNNMYG	NTGMPNNMNS
VLXT	DDDDDDDDDD	DDDDDDDDDD	DDDDDDDDDD	DDDDDDDDDD	DDDDDDDDDD
201	NMGYNMNNM	GIPNFSCNQ	MPPNVLMIP	GVICHNTMQG	MPVVPSTMP
VLXT	DDDDDD	D	DDDDDD	DDDDDDDDDD	DDDDDDDDDD
251	PNIYPTPYGS	SNMSIQGIPQ	ATNIEEFDEE	EM	
VLXT	DDDDDDDDDD	DDDDDDDDDD	DDDDDDDDDD	DD	

FIG S8. PONDR plot analysis of GerG. The heavy horizontal black bars indicate regions of predicted disorder as determined by PONDR using the VL-XT algorithm. The exact residues predicted to be disordered are indicated by a blue “D.”