

Supplementary data

6ETZ	1	MSVETPSALADSSPHTAPGSAGRSLELGAADIQDLESFEAGRGALPARAYLQSDAPRLSL	60
5EUV	1	-----	0
6ETZ	61	NGEWQFRLSPGSRVAP--DDGQWLGEALNGFESLPVPSWPMHGHGAPAYTNVQFFFAVE	118
5EUV	1	-----MRVTQKLNHGWIIFAE-----GAADPA-----TPLAGE	27
6ETZ	119	PPHVPEANPIGDHLVVE--AGPEFFPH-----ALLRFDGIESAGTVWLNQ	163
5EUV	28	TVTLPH-NAVDLPLSYFDETSYQRAFTYQRVIAWDDAWQGRVQLRFDGAMADNVVWVNG	86
6ETZ	164	VELGTTGRSRLAHE-----FDVSGILEQGENTLAVRV-----AQFSAASYV	202
5EUV	87	VQV-----VAHPDGYTPFVADLTDHLRPGDNLVTVRIDGSENPAIPFPGAQIDVLYTA	140
6ETZ	203	EDQDMWWLPGIFRDVTLQARPAAGIDDDVVFHAGYDHTGEGILKVEASRGGQAIDAVRV	263
5EUV	141	-----GIYRDVWLMVLPER-----HLTNARILTPDALSDAKTV--VIR-	175
6ETZ	264	PELAL-----ELAAG-----TEVVRVPAVEPWSAEVPKLY--EAAVSAAGES	302
5EUV	176	PEVTAPGPVRRARLLDGDREIAATEGEGELTLAGLTGLSLWS TDNPQLYTVELTLPSGDV	235
6ETZ	303	VALQIGFRSIAIEDAQFKVNGRRILLRQVNRHEHHPRLGRVPRDVVEAELRLMKQHNI-	342
5EUV	236	TTHRFGRFTAEWTPQGFLLNGQPMKLRGLNRHQSWAHQGYAAGRHAQERDAEIVR-HDLC	295
6ETZ	343	-NAIRTSHPYPHPQFLALADQLGFYVLECDLETHGFESAGWAQNPSDDPQWEDALVDRM	397
5EUV	296	CNMVRTSHYPQSTWFLDRCDIEGL-LVFE-----EIPGWQH--IGDQAWQDRSDVNV	343
6ETZ	398	RRTVERDKNHASVVMWSLG-NEAGTGRNL-AAMSRWTKDRDPSRPIHYEGD---WSSEH	448
5EUV	344	RAMITRDWNHPSIVIWGVRLNESPDNHDIFYVRTNALARELDPTRAI---GGVRCITDSEM	399
6ETZ	449	V-DVYSR--MYASQAETALIGQ---GIEPALNDAALDARRRAMPFVLCQEVHAMGNPGGG	528
5EUV	400	LEDVYTMNDFILDESELPLINRPTALRPTEEVGTI---KKPVPYLVTEY-----NGH	450
6ETZ	529	MSEYQALFEKYPRLMGGFVWEWLEHGI---TVSTADG-----VDHYGGDFG	573
5EUV	451	MFPTKA---QDPEL-----RQMEHVIRHLEVLNAAHGDPAISGCIWGMCFDYNTHKDFG	501
6ETZ	574	EEVHDGNFVT-DGLVDADRRPR-----PGLLDFKKVIEPLRIDVARDWTGFT	619
5EUV	502	A---GDRI CHHGVM DIWREPKFAAHAYGSQKPPSEGI-----VMEPVTF-----W----	543
6ETZ	620	LRNGQDFADTSAFSFRYEAVEADGGALDGGTVDVAPVAPQSETVVELPGSVAALAAGLSDG	679
5EUV	544	-----ARGERNIGGVLPLIVLTCDEVEFECAG-----	571
6ETZ	680	RPAVLTVRAVLGADSAWADAGHEVAVGQSVREPGAPVPPAPVEPVQVQDSELTLPVVF-	739
5EUV	572	-----VTRRVGPDRE-----RFPHLRPPVIIDHRHISAEELGQWGMWSH	610
6ETZ	740	-SRATGMPTSIGGVV-----EKLGLTLWVAPTDNDLGREWGADERPLATQWKDAGL	790
5EUV	611	PGRITGW---LNQEVALREYVADPLPTTLQIAP-DRD TLPADGDIDLRVMLRALDQVG-	666
6ETZ	791	NRL-----HTRLLGISANPGQDGGETLTVR-----TRVSAADKQYGLVD	830
5EUV	667	NRLPFLDAGIAVTVDGPARLIGPDLRMLQGGTGMMLRLTGDAGTIRITARHPQFPEAVA	726
6ETZ	831	YTWSTDGETVGLRTQVRRDGTWVNRGFEVEWARIGLEFVLGEETELVSWFGQPHQSYPD	890
5EUV	727	TV-----TVG-----	731
6ETZ	891	TGQGARAGWFSFLAKMDVEYVRPQECGARSRSAAALQLGGRTLEICGDPFALTVPYYS	950
5EUV	732	-----	731
6ETZ	951	QDVLDAAAHRPDLKADGRTYLYVDHALRGVGTAAACGPGVLEQYRLKPRDADFILTLKQRS	1010
5EUV	732	-----	731

Figure S1. The sequence alignment of *Arth* β DG and *Par* β DG performed using EMBOSS Needle Pairwise Sequence Alignment. The sequence similarity is 35%, and identity only 17.6% with 47.3% gaps. Catalytic amino acids marked with red boxes.

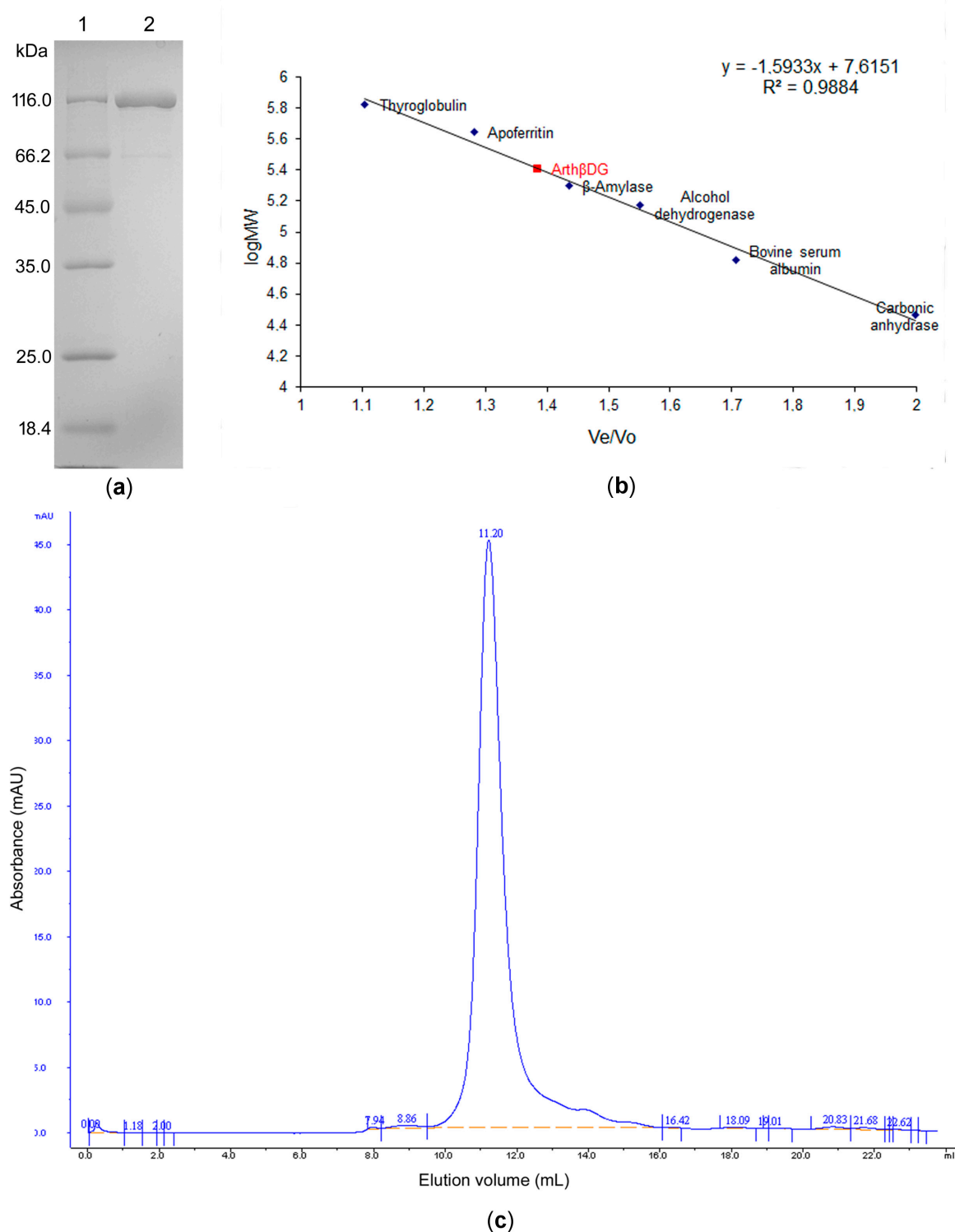


Figure S2. Biochemical oligomerization assays of *Arth*βDG. (a) SDS-PAGE analysis stained with Coomassie Brilliant Blue G; lane 1 protein molecular-weight markers (Thermo Fisher Scientific), lane 2 *Arth*βDG; (b) V_e/V_0 versus log MW calibration curve for separation of proteins on a Superdex 200 10/200 GL column with *Arth*βDG marked red (V_e , elution volume; V_0 , void volume); (c) chromatographic separation of the fraction containing active *Arth*βDG by gel filtration on a Superdex 200 10/300 GL column.