

Figure S1

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20 MQLAGIRHRPESED TAVLA AHQLQVRLQTARDDVAQVEILFADSYLW---QEGTTALE-R 56
21 -----MLNAWHL PVPFVKQS-K---DQL--LITLW---LTGEDPPQ-R 34
18 ----- 0
NI ----- 0
34 ---MT-----Q-DTALDMKDVELNELDQEKVPMAG 26
4 ---MLTP-----TQ-QVGLILQYLK-TRILDIYTPEQR 28
36 ----- 0
16 ----- 0
29 ----- 0
31 ----- 0
30 ----- 0
23 ----- 0
17 ----- 0
35 ---MEEEPNSVE-----LKQKAGHE-NNGFISDHD--G--RDEDKPEKG 36

20 RIMQ-----PGLATQGNQYWQTTLTVPTN--RVVYAFLITDT 91
21 IMLRT--EHDNEEMSVPMH-----KQRSQPQPGVTAWRAAIDLSSGQPRRRYSFKL--- 83
18 ----- 0
NI ----- 0
34 G-AGDSPNGGAEKNGV-VKVKLEDEDEKSQKFTGLSKEE--LLRVAGTPTWVR----- 75
4 AGI--EKSEDWRQFSRRMDTHFPKLMNELDSVYGNNEA----- 64
36 -----M----- 1
16 -----MTSDQNM----TS-DQHSETPPIRALLGEDEER--TA----- 30
29 ----- 0
31 ----- 0
30 ----- 0
23 ----- 0
17 ----- 0
35 KSRRSKEGDAHIYSVRIN-EVPEDSPPLKPYAGMPKDV--LLQFSNRPCYRI----- 86

20 IGATVGYGEGGFFDDVATNWQTVGNYFHMPY-----MHVSD-----AELPPAWVK 136
21 -----LWHDRQRWFTPOGF SRMPPARL-----EQFAVDV-----PDIGPQWAA 121
18 ----- 0
NI -----MARDTQT-QLR 10
34 ---VRWALLILFWLG-----WAGMLAGAVV I-----VQAPRCRPLPAMEWWN 115
4 -----LLPMLEMLLAQAWQSYSQRNSSLKDIDIARENNPDWIL 102
36 -----TRNKRLRRL-----STAMLTVPMLTM-----FASGAMAEQELNGHKPPVSTG 43
16 -----D-----ARAKLEMALSLT-----QPTGAVDP-----HDTSWFE 58
29 -----MKT-----EQTPWWK 10
31 -----MEKQWWK 7
30 -----MQQVPD-----SVHLTAPT-----AHTHWWR 21
23 -----M-----SQT PWWR 8
17 -----MKSLVVVVLLL-----AVGLGAGQ-----NNKGWWK 26
35 -----AREIIFWLI-----IVATLAI-IAAT-----IAIIAIS P-----KCLDWWQ 121

20 ET--VWYQIFPERFANGVRQNDPAN-----VQPWGA---GRVHRDSFYGGDL 178
21 DQ--IFYQIFPDRFARSLPREAEQDHVYYHHAAGQE IILRDWDEPVTAQAGGSTFYGGDL 179
18 ---MKNKVQLITYADRL-----GDGTI 19
NI NE--MIYSVFVRNYS-----EAGNF 28
34 KG--PLYQVGDPA--TFQED-----GAGNI 136
4 SNKQVGGVCYVDL-----FAGDL 120
36 SG--VFYEIYINSFYDSNGD-----GHGDL 66
16 TA--VFYEV MVRSFADSSGD-----GIGDL 81
29 KA--VVYQIYPKSFNDTTGN-----GVGDL 33

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31 ES--VYQIYPRSFMDNSGD-----GIGDL 30
30 HA--VIYQIYVRSFADSNGD-----GEGDL 44
23 GA--VIYQIYPRSFLDNSGD-----GVGDL 31
17 NA--IFYQVYPRSFMDNSD-----GIGDL 49
35 RS--PMYQVYPKSFKDSNND-----GSGDL 144

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CSR VI  
β2

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20 PGITAHLLDDLA-----ALGVNGLYLCPIFTSPS-----NKKDTIDHFEIDPHFG 223
21 DGISEKLPYLK-----KLGVTALYLNPFVKAPS-----VKKDTEDYRHVDPQFG 224
18 KSMTDILRTRF-----DGVYDGVHILPFFTPFD-----GADAGFDPIDHTKVDERLG 66
NI AGVTADLQRIK-----DLGTDILWLLPINPIGEVNRKGTLSGSAIKDYRGINPEYG 80
34 QSIEKRIESLS-----SLKVKGLIIGPIHVTKK-----DQIGETQLTDIDPNYG 180
4 KGLKDKIPYFQ-----ELGLTYLHLMPLFKCPE-----GKSDGGYAVSSYRDVNPALG 168
36 KGITQKLDYLDNGKSHSGKDLQVSGLWLMPLNPSPS-----Y-KKDVTDYYQVDPQYG 119
16 AGLTEHLDYLQ-----WLGVDCLWLPFFASPM-----TDGGYDVADYRAISPDLG 127
29 NGIIEKLDYDK-----TLQVDVLWLTPIYDSPQ-----HDNGYDIRDYYSIYPEYG 79
31 RGIISKLDYDK-----ELGIDVIWLSPVYESPN-----DDNGYDISDYCKIMNEFG 76
30 NGIRERLPALV-----SLGVDAIWLTPEFYVSPL-----ADGGYDVADYRDVDPFRFG 90
23 PGIIAKLDYIS-----GLGVDAIWISPEFKSPM-----ADFGYDISDYRAVDPLFG 77
17 KGIKDKLSHFY-----ESGITAIWLSPINRSPM-----VDFGYDISDFKVDVPIFG 95
35 KGVQEKIDHFL-----YLNKIKVWVAPFYKSSL-----KDFNYAVDDFMEVDPTFG 190

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CSR I  
β3

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20 TKADFQALVDGAHARGMRVMLDAVFNFHFGES-----PQWQDVIKNG-----EQSRF 270
21 GDGALLRLRHNTQQLGMRLVLDGVFNHSGDSH-----A-WFDRHNRGTGGACHNPESPW 277
18 SWDDVAELSK-----THNIMVDAIVNHMSWES-----KQFQDVLAK-----GEESEY 108
NI TLADFKALTDRAHELGMKVMLDIVNHTSPDSVLATEHPEWIFYHDADG----- 128
34 TKEQFASLLEAARKKSIQIILDLPNYHS-EK-----SWFEKTERE----- 220
4 TIGDLREVIAALHEAGISAVVDFIFNHTSNEH-----EWAQRCAAG-----DPLFD 214
36 SLNDFRTLMEKAHRKGVKVMIDLIINHSSSDH-----PWFKEASAN-----PQSKY 165
16 TLSEFGDFIDKAHDRGIRIIDFVMNHTSDHH-----PWFEESSRH-----PDGPY 173
29 TMEDFERLVSEAHKRDLKVVMDLVVNHTSTEH-----KWFREAISS-----IDSPY 125
31 TMEDWDELLHEMHERNMKLMMDLVVNHTSDEH-----NWFIESRKS-----KDNKY 122
30 TLADFDALLATAHDLGLRVIIDIVPNHTSSAH-----RWFRRDALAA-----GPGSPE 137
23 SLADFDRLLEKAHGLGLKVMIDQVLSHTSIAH-----AWFQESRQD-----RSNPK 123
17 TIKDLEDLTAEAKQNLKVILDVLPNHTSDQH-----KWFQMSINNT-----NNNNTNKY 145
35 TMADEFESMISAMHDKGLKLIIDLIPNHTSNKH-----KWFQLSRN-----RTGKY 235

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20 ADWFH-----IHGWVPGRDP-----KTKRLNYETIAT 297
21 RDWYS-----FSDDGT-----ALDWL---G 294
18 YPMFLTMSSVFPNGATEEDL---A-----GIYRPRPGLPFTHYKFAGKTRLVWVSF 156
NI -----QLTNKV-----GD 136
34 -----SI-----VD----- 224
4 NFYYI-----FPDRRMPDQYDRTLREIFPD-----QHPG-GFS-----QLEDGRWVWTTF 258
36 HDYYV-----WADENTDLEE-----KGSWGQQIWHKNP-----NGEGYFYGTFF 203
16 GDFYV-----WRDNP---DG-----YPDARIIFIDTETSNTWTFDP---VRGQYFWHRF 215
29 RDFYI-----WKKPQ---ENG-----SVPT-NWESKFGGSAWELDE---ASGQYYLHLF 167
31 RDYYI-----WR-PG---KEG-----KEPN-NWGAASFSGSAWQYDE---MTDEYYLHLF 163
30 RDRYV-----FRPGRGENGE-----LPPN-NWQSFGGPAWTRVTEPDGTPGEWYLHLF 185
23 ADWYV-----WADPR---EDG-----TPPN-NWLSLFGGVAWQWEP---RREQYYLHNF 165
17 KDYYI-----WVDPVKDDKG-NPIKDKYPN-NWLSVFNGTGWTFHE---GRKQFYFHQF 194
35 ADYYI-----WHDCMQTGG-----LVVPPN-NWVSFYGNSAWEYDD---TRKQCYLHQF 280

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CSR V

CSR II

β4

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20 GAAMPKVNITQNPVQAYL-----IDVTKYWIEQFGIDAWTFDVADEVTHG----- 342
21 YASLPKLLIYQSESLVNEIYRGEDSIVRHWLKPWNMDGWELDVVHMLGEAGGARNN---- 350
18 TPCQVDILTDSDKGWEYL-----MSIFDQMA-ASHVSYIRLDAVGYGAKEAGTSCFMTPK 210

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NI	WSDVVKDL	YGHHELWQYQ	-----	IDTLLYWS-Q	FVDGY	CDVAPL	VPLD	-----	179
34				FEDNV	-----	TEAVNVWLERG	VGGIYFGDSE	-----	250
4	NSFQWDLN	YSNPWVFRAM	-----	AGEMFLA	NLGV	DLMDAVAF	LWKQMG	TSCENLP	311
36	WSGMPDLN	FDNPEVRKEM	-----	IKVGYWL	-QQGADG	FELDAAMH	LFRGQT	KDGADKN	256
16	YSHQPDNL	YENPKVLAEM	-----	LDALRFWL	-GFGVDG	FELDAVPY	LVEEEGT	NCE	265
29	DVTQADLN	WENEEVRKHV	-----	YDMMHFWF	-EKGIDG	FELDVINL	LISKDQR	FPNAEEG	220
31	SKKQPDNL	WDNEKVRQDV	-----	YEMMKFWL	-EKGIDG	FELDVINF	LISKEEGL	PTVETEE	217
30	DVEQPDNL	WENPEVRAEF	-----	ADILRFWL	-DRGVDG	FELDVAHG	MIKDPAL	PDIAEQ	239
23	LVDQPDNL	FHNAEVQOAT	-----	LDNVRFWL	-DRGVDG	FELDAINF	CFHDAQ	LRDNP	219
17	YKQQPDNL	YRNSDVREEM	-----	KNIMKFWL	-DKGIDG	FELDAVPH	LFE	SANISLDEPP	247
35	KKEQPDLD	FNNPDVNEEI	-----	LNI IKFWL	-EKGVDG	FELTNSAK	FLEAEHL	RDEPQVN	332

CSR III

$\beta$ 5

20						FWRALCGALRAIKPDV	YLLGES	HSSQ	364
21						MQHVAGITEAAKETQPEAY	IVGEH		374
18						TFKLI	SRLREEGVKR	GLE	228
NI						FWLEARKQVNAKYPETL	WLAE	SAGS	206
34						NFPNASSFLSEWGNMT	-AN	YSKEGKPR	VLLL 285
4						QAHALIRAFNAVMRIAAPAV	FFKSE		338
36						IAWWNEFRSEMEKVNPNV	YLAGE		281
16						NLPGTHDILKQVRKMVDEEF	PGRILLCE		296
29						DGRSFYTDGP		RVHEFLHEMNEKVF	SHYDS-MTVGEMSS 258
31						EGYVSGHKHFMNGP		NIHKYLHEMNEEVLS	HYD-IMTVGEM 259
30						KADML		DG-HTRL	PFYFDQD-GVHEIYREWRAIVDSYPGERALVAE 284
23						ADKRVGRGFSADNPYAYQYHYFNNTQ	PENLPFLERLRGLLDSYPGAVSL	GEISS	274
17						LGKLN		LSLHASLNHTLTKDQ	PETYELVKERDFVDNYAEENKR-DEIVLLTEAY 301
35						LQNPDTISNYSELFHDYTTTQVGMHDI	IRNFRQTINKYSREPGRYRFMGTE	SNDQ	390

20						SLVGN		GQFNAVMN	PL-TQPILALF	N-G	QLNPEDYVGKT	406
21						FGDARQWLQA		DVEDAAMN	RGFTFPLWGFL	ANTDI	SYDPQQIDAQT	420
18						ILIEVHSYKK		QVEIASKVDRVYDFA		LPPLL	LHALSTGHVE	269
NI						IEELRSQGYTGLSDSELYQAFDMTYD		D		VFGDFKDYWQGRS		248
34						STSTVHNNLAGPS		NETVQGTLEFR		FLDAE	NKK	NFSS 316
4						VHPDQVVQYIGQ		DECQIGYNPL		QMAIL	WNTLATREV	375
36						DKPETIAPYYGP		LHSLFNFD		LGGTI	LNSVKNGRDQGIATFAEKT	325
16						WPHDVVEYFG		D-NDECQMAFHFP		VMPRL	YMGVA	RHTR 332
29						TVDHCIRYTNPD		NKELDMTFSFH		HLKVD	YPNGE	KWALAPDFDLK 302
31						TTEEAKLYTGEE		RKELQMVQFE		HMDLD	SGEGG	KWDVKPCSLLT 303
30						ENAERVARYLRP		DELHQAFNFE		YLTAD	WDA	T 316
23						DSLATTAEYTAQ		GRLHMGYSFE		LLVQD	YSAA	Y 306
17						SSENLTKYYEVG		SNVPFNFK		FITDA	NSSS	TPEQ 335
35						AAVDKTMLYYGNS		FIQEADFPLNA		LFDLN	KANI	DGAS 428

CSR IV

$\beta$ 7

20						NLELM		MYRQ	P-NQQAMFNALDTHDTPR		LLT	435
21						CMAWMDNYRAGLSH		Q-QQLRMFNQLD	SHDTAR		FKT	454
18						PVAHWTDIRPNN			AVTVLDTHDGIG		VIDIGSDQLDRSLKGLV	310
NI						VERYVDLLQRQDATFP		GNYVKMRFL	ENHDNAR		MMS	283
34						LGATIKQYVAET			GILGNSWMV	GAPQMRH	LAS	347
4						LLHQALTYRHNLPEHTAWVNYVR		SHDDIG	WTF	FADEDAAYLGISGYDHRQFLNRFFV	431	
36						LQ-LYKSYN			KAALDAPFLSNHDQTR		VMS	352
16						EAITTILASTPPVPOGCQWAT		FLRNHDEL	T		LEMVTEDDRQYMWREYA	379
29						LKEILSDWQT			GMHAGGGWNALFWCNHDQPR		VVS	335
31						LKENLTKWQK			ALE-HTGWN	SLYWNHDQPR	VVS	335
30						LRAVVDRSLA			ANNAVGA	PTTWVLSNHDVTR	HVT	349
23						IRDTVSRLEA			TMLEGWPCWAI	SNHDVVR	AVT	337
17						FKVIIDNWIKGT			P-QNNV	PNVWVGNDRVR	VGT	367
35						IFSMVDLWMMKAM			P-SGKW	PNWVGGPSSSR	IAS	460

20	-----TLH-----G	439
21	-----LLG-----R	458
18	PDEDVDNLVNTIHANTHGESQAATGAAASNLD-lyQVNSTYYSALG-----C	356
NI	-----L-----MH	286
34	-----MV	349
4	NRF-----D-----GSFARGVPFQYNPSTGDCRVSGTAAALVGLAQDDPH	471
36	-----ELG-----G	356
16	P-----DPRMRLNLGIRRR---LAPLMGN	400
29	-----RYG-----DDGAY	343
31	-----RFG-----NDGMV	343
30	-----RFG-----GGAQ	356
23	-----RWG-----GAQA	344
17	-----RYP-----	370
35	-----RVG-----	463

CSR VII

$\beta 8$

20	QLTKFKSALTLLMLLPgSPCIYYGTEVAMAGGA-----	473
21	DIARLPLAVVWLFTWPGVPCIIYYGDEVGLDGKN-----	492
18	NDQHYIAARAVQFFLPGVPQVYYVGALAGKNDMELLRKTNN-----	397
NI	SKAEAVNNLTWIFMQRGIPLIYNGQEF LAEHQPSLFDRDTM-----	327
34	NENLLRVYQLLLFTLPGTPI SLYGDEI GLKDL SGLAAQ-----	387
4	AVDRIKLLYSIALSTGGLPLIYLGDVGTLNDDVWSQDSNK-----	512
36	DVRKAKLAASILLTLPGQPFLYYGEEIGMKGEKPD-----	391
16	DPDKIRLMNAMLLSLPGSPVLYYGDEI GMGDDIW-----	434
29	RVKSAKMLATAIHMMQGTPIYQGEELGMTNPKFTDISSYRDVESLNMYHAFK-EKGMAD	402
31	RIESAKMLATVLHMMKGTPIYQGEELGMTNVRFESIDEYRDIETLNMYKEKVMERGED	403
30	GLARARAALLMLALPGSVYLYQGEELGLPEVTLPPEALQD-----P	399
23	TPAFARMVVALLCSLRGSICLYQGEELGLSEAEV-AFEDLQD-----P	386
17	-GR-ADHMIMLEMILPGVAVTYYGEEIGMVDNNTTIY--KYD-----	407
35	-RQYVNVMMNMLLLTLPGTPTTYYGEEELGMEDGSPQV--STEN-----	502

\*

20	-----PDMRCMNWQPDEQ-----	487
21	-----PFCRKPFPWQVEKQ-----	506
18	-----GRDINRHYYST-----T-----	408
NI	-----VADRHGDVTPLIQKLVTIKQLPLLRAADYQLAVVEEGIVKITYRAAGEALTA	379
34	-----LSGPIMQWGEVSV-----SN---NSP-----	405
4	-----SDDSRWAHRPR-----	523
36	-----EYLREPMPRWYKGDG-----PGQTT-----	410
16	-----LHDRDGVTPMQWTADPS-----AGFST---ATP---DKF	463
29	QDITAILQAKSRDNSRTPVQWDATEN-----GGFTT---GTP-----	436
31	EKVMQSIYIKGRDNARTPMQWDDQNH-----AGFTT---GEP-----	437
30	TWKRSGYTERGRDGCSTPMPWTDAP-----PFGFGCSA---ERS-----	436
23	YGITFWPTFKGRDGCSTPMPWTDAP-----SA--GFTS---GKP-----	420
17	-----VRDGCSTPMPWTDAP-----AGFSK---IAENLLEKN	437
35	-----PQEYNPTEYPEKTPMQWDSSSN-----AGFSE---AN---RT	533

20	-----EQQVRQFVTRLIKFRQQADFLATSQLTWTIDGHC	522
21	-----DTALFALYQRMIALRKKSQALR-----HGGC	532
18	-----AEIDENLKRVPVKALNALAKFRNELDAFD-----GTF	440
NI	WIPLK-----GQ---VTAVATKLAAGSY---QNLITDGP---TEVV-----DGKL	415
34	---QI--A---TDVNAVNTFKGQDADKGSFLNVYRKLSDLRGKERSLL-----HGDF	449
4	-----YNEALYAQRNDPSTAAGQIYQGLRHMIAVRQSNPRFD-----GGRL	564
36	WEKP---KYNTGE---VSVEAQLRDDDSLLESYRTLIRLREEHDALR-----SDSL	455
16	FLPLLADPYSPQQ---VNVTDQMAPGSLLVWMSMLTTRRQFPVFG-----RGEF	511
29	WIPV---AGNYRE---INAEAAALRDQNSVFYHYQKLIQIRKMYDIVT-----EGTY	481
31	WITV---NPNYKE---INVKQAIQNKDSIFYYYKKLIELRKNNEIVV-----YGSY	482

30	WLPV---PAEWR---LTREVQERDPDSTLSLYKKALRLRRELLLP-----EDAL	481
23	WLPL---AASHRA---AAVSVQQDDAHSVLRVRAFLAWRKEMPALR-----EGSI	465
17	WLPV---HTSYKSG---LNLEQEKKDSISHYHLYTNLTALRKRDLK-----GNF	482
35	WLSV---NPDYEA---VNVEAQKNEQYSTLNLYRELNHLRNNELPLH-----RGWL	578
.		
20	LILTR-TDVE-----QTIQGRFNLG--AQAVSTVSGVSPILT-AGITA---	561
21	QVLYA-EDNVVVFVRVLNQ-----QRVLVAINRG--EA-CEVVLPASPFLN-AVQWQ---	579
18	SYTTDD-DTSISFTWRGETS-----QA---TLTFE--PKRGLGVDNTTP--VAMLEWED---	486
NI	TVD--GQPVLIKVVTNTAVT-----KVADQSN-----	440
34	ALLYNS-DQAISFLRSWDQNE-----RYVTALNFNYEGEAEFLKQDGDKEL---PEQGTV	501
4	VTFNTNKKHIIIGYIRN-----NALLAFGNFS--EYPQVTAHTLQAMP----FKAHD	610
36	QPIQAGSASVTAFKRTSDK-----ESLYVYHNLS--GEPVTLQMKDFD----KGKWKVVF	504
16	IDMGGQNDAVLSFLRVLDDDKHGSQRLLCLNLS--PEEQDVLV--YLPDDAGTKPVS---	565
29	EIIAKDDPNIFAYLR-----HGSNEKLLVINNFY--GTEAAF---TLPDSLAPDEWKAEV	531
31	DLILENNPSIFAYVR-----TYGVEKLLVIANFT--AEECIF---ELPEDISYSEVE--L	530
30	HWADAP-QNVLAFR-----EPGFT---CAVNFG--ADPVTL---PFEDEV-----	518
23	AFYDTA-EPVLMFRR-----EHAGQVLLAFNLS--ADPAEL---ALPAGE----WEQID	510
17	TIEIL-NKTVLAVVRQSEEE-----AVSLLINF--KNNTIVDISKLVNKRNNAK-----I	530
35	CYTWS-DNVFAYVRELDGLNK---VFMMVLNFG--QAWTINLRQAVPDLPGAEK-----I	628
.		
20	-----NE-----MAPGGFELTVA-----	574
21	-----CKEGHGQLTDGILALPAISATVWMN-----	604
18	-----SAGDHRSDDLIANPPV-VA-----	504
NI	-----	440
34	VLSS-NPQRKDGDTVSLKSL-K-----LGAGEALLLKYPYSG-----	536
4	-----LIGGKTVSLNQDLTLQP-YQVMWLEIA-----	636
36	STSK---DV---KVKKGTITIPA-YSSLITKEDRKS-----	533
16	LLTS---QAMAPIAANGEFHDTLPA-WGFAWLDLSKGSDEHESE-----	605
29	LLT---NDEARE-GLQNMTLR-PY-ESIVYR-LTKPC-----	561
31	LIHN---YDVENG-PIENITLR-PY-EAMVFK-LK-----	558
30	VLSS---GPVE---QDGTHLVLPD-DTAVWL-RQ-----	544
23	VPGV---ELGA---MDGGHLRLAG-HAVVAA-VGRG-----	538
17	YTSSVNSNLTVNQTVNPAI-NIPG-DTSIIVDSSTSGATIVN--YS--IMIFLSAVFIS	584
35	RLSTEGSRV--GKAVSTDSIQTPG-EGL-ILEYKTNKPVHVRDTEFKDKCFISEKACYTS	684
.		
20	-----	574
21	-----	604
18	-----	504
NI	-----	440
34	-----	536
4	-----	636
36	-----	533
16	-----	605
29	-----	561
31	-----	558
30	-----	544
23	-----	538
17	FFQR-----	588
35	AFDLLYNSC	693

**Fig. S1.** Sequence alignment of the  $\alpha$ -amylase representatives of thirteen different GH13 subfamilies with focus on the intermediary group with MPDLN as CSR V (Majzlová et al., 2013). The sequences from GH13\_4 (*Neisseria polysaccharea*, accession Q9ZEU2), GH13\_16 (*Propionibacterium freudenreichii* subsp. *Shermanii*, A1XGB1), GH13\_17 (*Apis mellifera*, Q25BT8), GH13\_18 (*Bifidobacterium adolescentis*, Q84HQ2), GH13\_20 (*Lactobacillus plantarum* WCFS1, F9URM8),

GH13\_21 (*Escherichia coli*, P21517), GH13\_23 (*Xhantomonas campestris*, Q76LB0), GH\_29 (*Bacillus subtilis*, P39795), GH13\_30 (*Thermonospora curvata*, Q60027), GH13\_31 (*Bacillus cereus*, P21332), GH13\_34 (*Xenopus leavis*, Q7ZYR3), GH13\_35 (*Xenopus leavis*, Q32NL8), GH13\_36 (*Paenibacillus polymyxa* E681, E0RLH8) subfamilies and Lp\_0179 (NI, not included in a subfamily, F9USZ) are represented. Alignment was done using the program ClustalOmega. Residues that are identical (\*), conserved (:), or semiconserved (.) in all sequences are indicated. Dashes indicated gaps introduced to maximize similarities. The GH13 three domains are highlighted in blue (domain A), green (domain B), and yellow (domain C). The catalytic triad is highlighted in pink. The seven GH13 CSRs are boxed. Conserved residues in amylolytic enzymes are highlighted in red (Lee et al., 2002)