

Figure S1. Negative stain electron microscopy of purified T33-23. *Left:* Computational design model and the PDB entry from which each of the two trimeric components (A, purple; B, blue) were derived. *Right:* Negatively stained electron micrograph of the co-expressed tetrahedral nanoparticle. Scale bar: 50 nm.

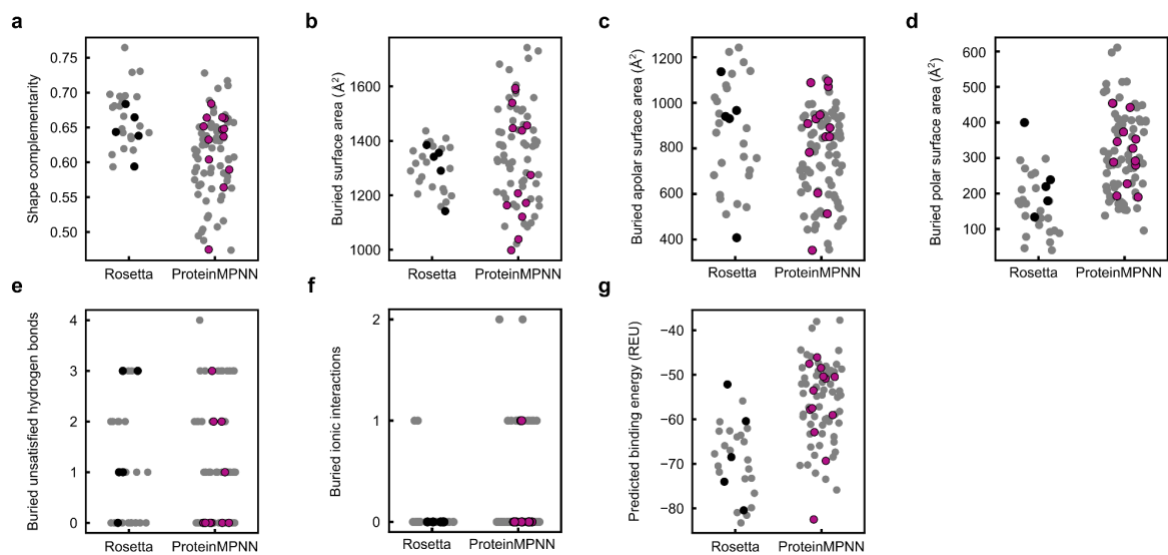


Figure S2. Detailed scoring metrics of tetrahedral nanoparticle interface design with Rosetta and ProteinMPNN. Interface scoring metrics plotted: **(a)** shape complementarity, **(b)** buried surface area in \AA^2 , **(c)** buried apolar surface area, **(d)** buried polar surface area, **(e)** buried unsatisfied hydrogen bonds, **(f)** ionic interactions where at least one of the side chains is buried, and **(g)** predicted binding energy (ddG). Designs that failed to assemble into the target assemblies are shown in gray, while successful designs are shown in black (5 Rosetta designs) or purple (13 ProteinMPNN designs).

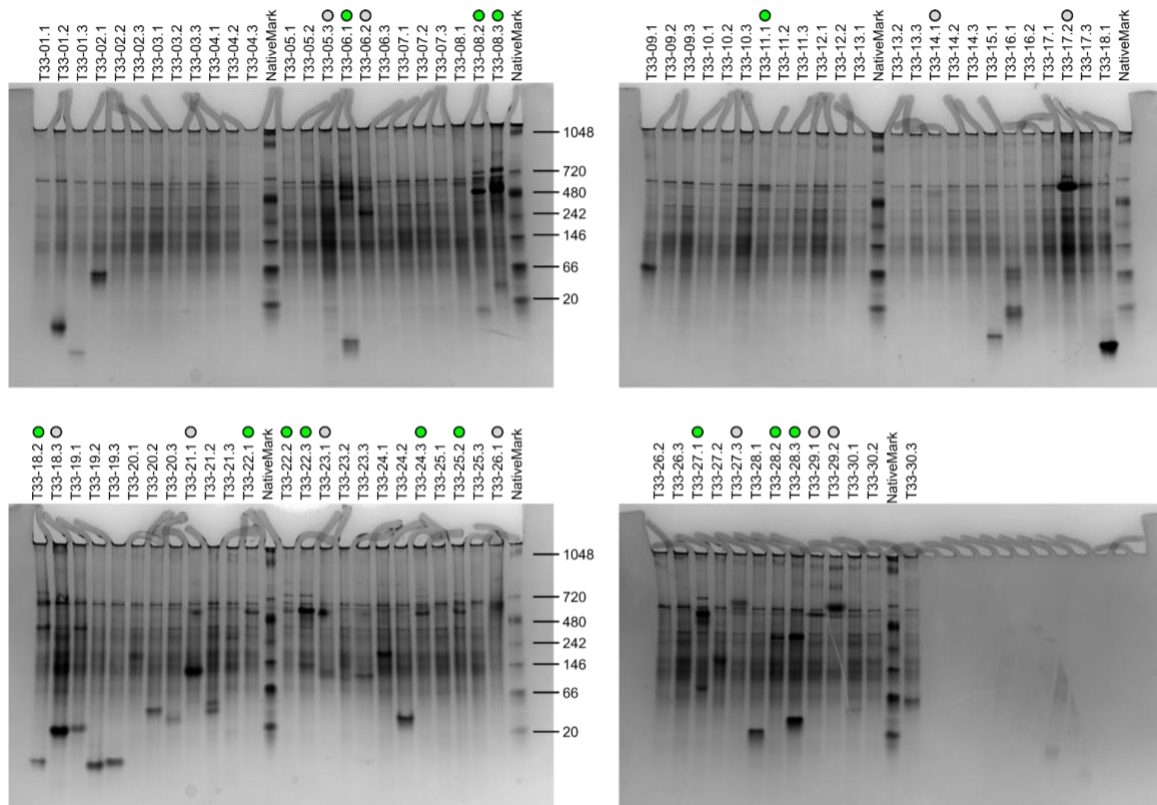


Figure S3. Lysate screening of bicistronically expressed ProteinMPNN-designed tetrahedral nanoparticles. Assembly into tetrahedral nanoparticles results in slower migration in native PAGE. 24 Designs yielding bands that migrated in ~ 0.5 -1 MDa range were selected for further characterization. Circles indicate selected designs, green circles indicate designs that were eventually confirmed to assemble into tetrahedral nanoparticles. NativeMark (ThermoFisher Scientific) is loaded as reference with molecular weight in kDa as indicated. Note: apart from the 76 designs representing the 27 experimentally characterized docks described in King et al. (ref. ²⁰), an additional 9 ProteinMPNN designs were tested based on T33-19, T33-20, and T33-30, which were designed but not experimentally tested in King et al. None of the 9 ProteinMPNN designs exhibited indications of nanoparticle assembly. To ensure fair comparison of docks for which experimental data was available for both the Rosetta and ProteinMPNN design sets, these 9 designs were not further considered.

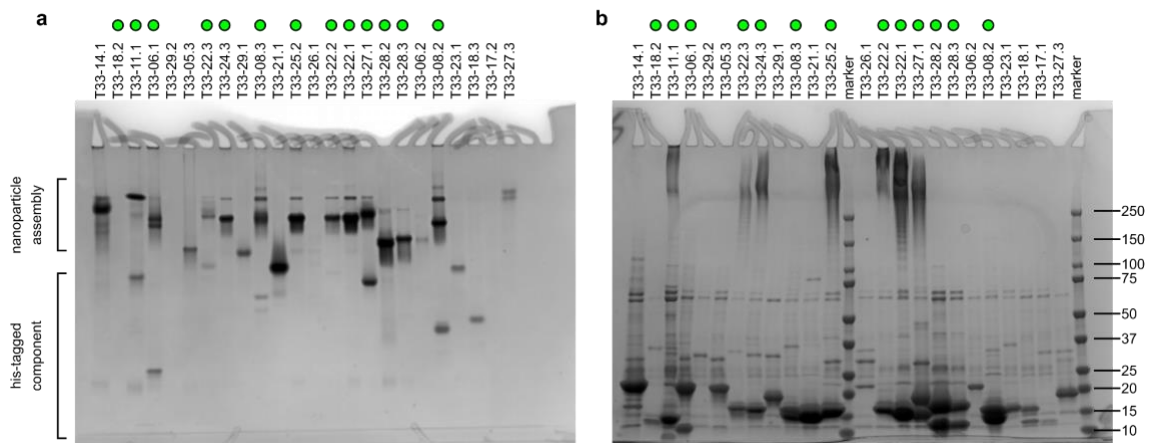


Figure S4. Co-purification of 24 potential ProteinMPNN-designed tetrahedral nanoparticles. (a) (Non)-denaturing PAGE of Ni-NTA purified tetrahedral assembly candidates. Assembled nanoparticles migrated slower in the gel compared to individual components. **(b)** Denaturing PAGE of Ni-NTA purified tetrahedral nanoparticle candidates. A and B components with different molecular weights (between ~10 and ~20 kDa) can be observed, indicating co-purification since only one of the two components contained a hexahistidine tag. Protein marker with molecular weights indicated in kDa is shown. Green colored circles indicate designs that were eventually confirmed to assemble into tetrahedral nanoparticles.

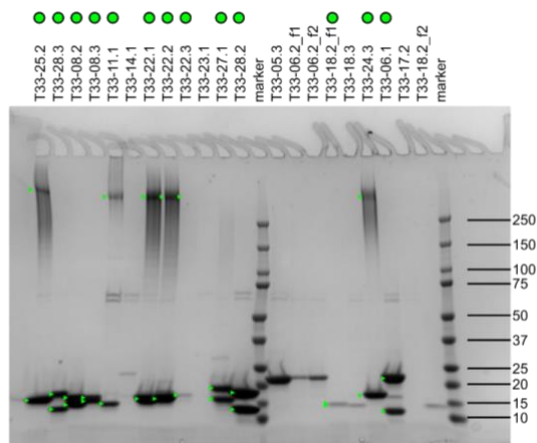


Figure S5. Denaturing PAGE of isolated size exclusion chromatography nanoparticle peaks. Nanoparticle peak (~13 mL) of a superdex S200 10/300 Increase column (Cytiva) is isolated. “f1” indicates peak isolated at ~13 mL and “f2” indicates peak isolated at ~14 mL. Marker with molecular weight indicated in kDa in figure. Green triangles indicate the two components. Green colored circles indicate designs that were eventually confirmed to assemble into tetrahedral nanoparticles. Note that for T33-25.2, T33-28.3, T33-11.1 T33-22.1, T33-22.2, T33-22.3 and T33-24.3 one of the two components does not fully migrate into the gel.

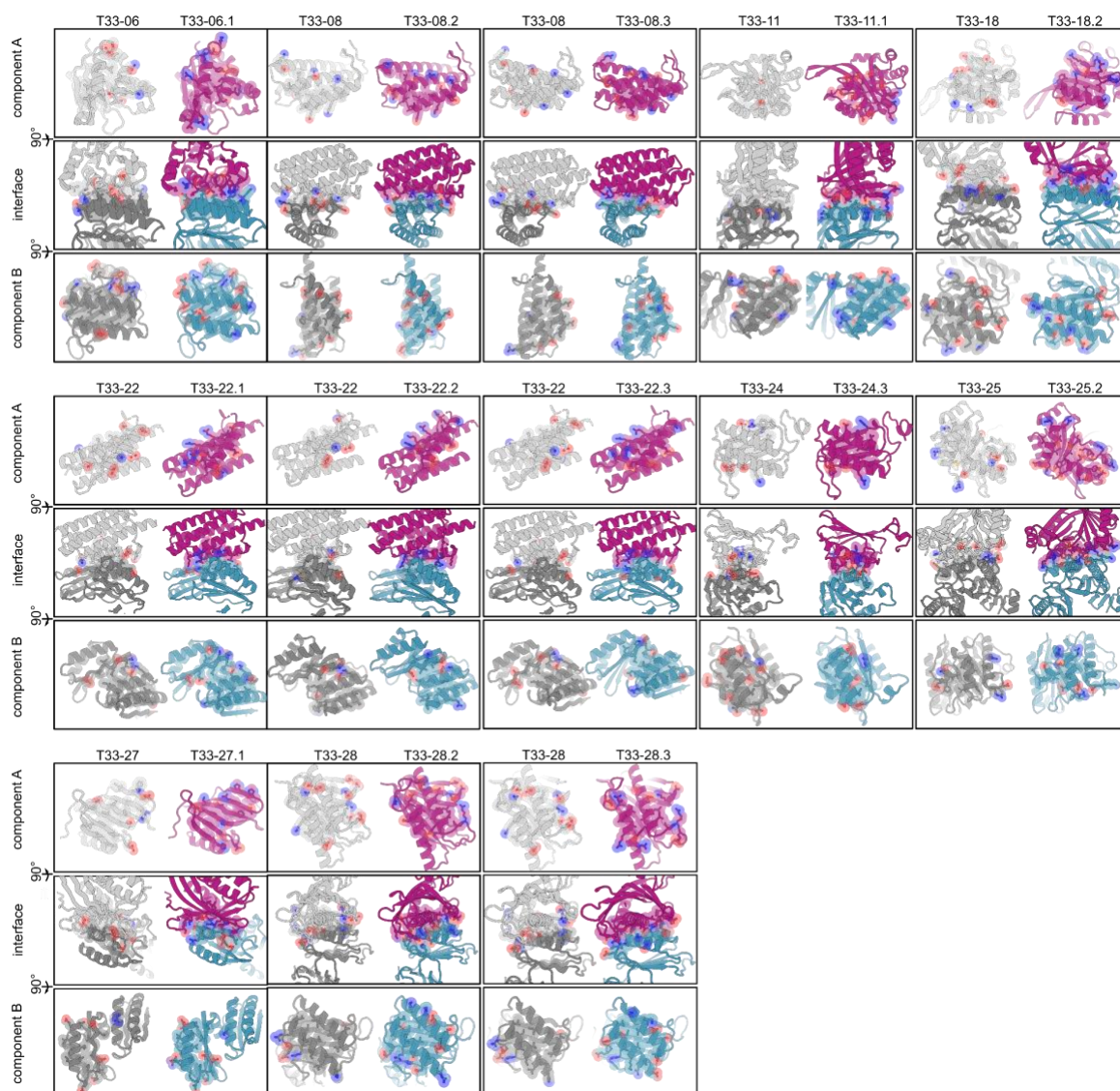


Figure S6. Comparison of Rosetta-designed interfaces and ProteinMPNN-designed interfaces. for all 13 confirmed ProteinMPNN-designed tetrahedral nanoparticles. All interface residue side chains within 5.5 Å distance across the interface are displayed as sticks, with oxygen and nitrogen atoms colored red and blue respectively, to highlight polar residues.

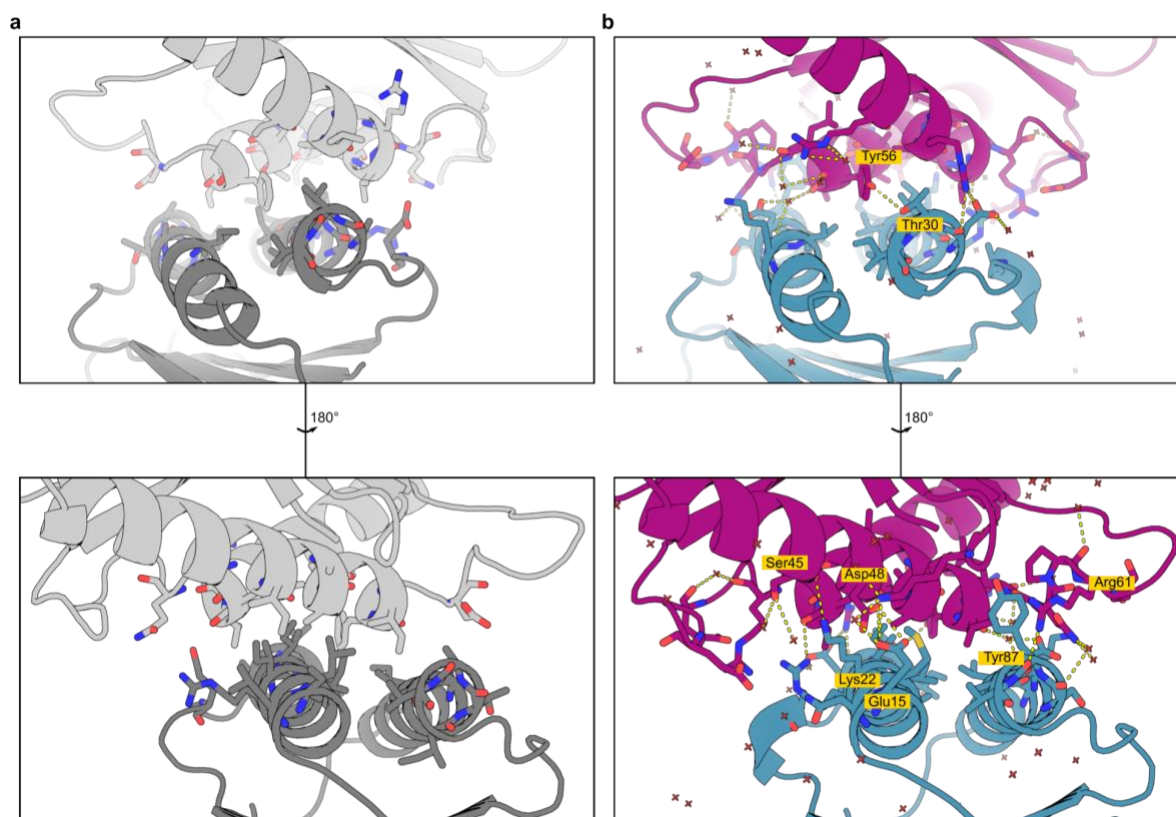


Figure S7. Interface comparison of crystal structure of T33-28 and T33-28.3. Two orientations at 180° of the interface of crystal structures T33-28 (PDB ID: 4NWR²⁰) **(a)** and T33-28.3 (PDB ID: 8T6E) **(b)** are shown. All residues with heavy atoms at less than 5.5 \AA across the interface are visualized as sticks. All possible hydrogen bonding and ionic interactions across the interface and with water molecules at less than 3.5 \AA distance were visualized (yellow dotted lines). For the T33-28 crystal structure zero polar interactions were observed, but for T33-28.3 more than 10 interactions across the interface were present. Key polar mutations are highlighted in yellow in T33-28.3. Water molecules are visualized as red plusses.

Table S1. Data collection and refinement statistics (molecular replacement).

	T33-18.2 (8T6C)	T33-27.1 (8T6N)	T33-28.3 (8T6E)
Data collection			
Space group	R3	P 2 ₁ 3	P 1
Cell dimensions			
<i>a, b, c</i> (Å)	138.81, 138.81, 129.11	176.51, 176.51, 176.5	113.74, 114.05, 114.20
<i>a, b, g</i> (°)	90, 90, 120	90.00, 90.00, 90.00	62.09, 77.86, 89.41
Resolution (Å)	56.87 - 1.92 (1.96 - 1.92)*	100 - 3.63 (3.69 - 3.63)*	48.47 - 2.48 (2.52 - 2.48)*
R _{sym} or R _{merge}	0.085 (0.162)	0.229 (0.063)	0.062 (0.630)
I / σI	9.8 (0.1)	22.69 (1.5)	6.3 (0.7)
Completeness (%)	100 (100)	100 (100)	98.1)97.5)
Redundancy	6.7 (6.7)	21.5 (21.4)	2.4 (2.2)
Refinement			
Resolution (Å)	56.87 - 1.92 (1.95 - 1.92)	48.96 - 3.63 (3.72 - 3.63)	48.47 - 2.48 (2.54 - 2.48)
No. reflections	70444	20763	171172
<i>R</i> _{work} / <i>R</i> _{free}	0.1977 (0.4685)/ 0.2423 (0.5712)	0.2142 (0.2654)/ 0.2585 (0.3624)	0.2053 (0.3513)/ 0.2389 (0.4115)
No. atoms			
Protein	7211	1175	25202
Ligand/ion	n/a	n/a	n/a
Water	424	n/a	593
B-factors			
Protein	38.44	91.68	55.66
Ligand/ion	n/a	n/a	n/a
Water	40.79	n/a	50.57
R.m.s. deviations			
Bond lengths (Å)	0.004	0.002	0.002
Bond angles (°)	0.600	0.432	0.460

*A single crystal was used for each structure in the data collection. Values in parentheses are for the highest-resolution shell.

Table S2. Amino acid sequences of novel proteins designed in this study.

Design	Component A	Component B	MW Comp A (kDa)	MW Comp B (kDa)
T33-01.1	MPIFTLNTNIKATDVPSD FLARTSRLVALILNKPGS YVAVHINTDQQLSFGGS TNPAAFGTLMSIGGIEP GLNHAINCALTAELEHEL GIAPERMYIHFVNLNGD DVGWGYGTG	MTEKEKMLAEKWYDANF DQELIERRAKAAAICWAL NNTRPSDTGRIKALIDALF GKVTDNVSISIPFDTDY ENVKLGKNVYVNTNCYF MDGGQITIGDNVFIGPNC GFYTATHPLNFHHRNEG FEKAGPIHIGSNTWFGGH VAVLPGVTIGEGSVIGAG SVVTKDIPPHSLAVGNPC KVVRKIDNDEGSHHHHH H	12.1	21.5
T33-01.2	MPIFTLNTNIKATDVPSD FLARTSEAVSRILNKPG SYVAVHINTDQQLSFGG STNPAAFGTLMSIGGIEP ENNEKLNVLTTLLEHE LGIPADRMYYIHFVNLNG DDVGWGYGTG	MTEKEKMLAEKWYDANF DQELIARRTRAILCYILN NTRPSDKELRKLIDALF RTKTDNVSISIPFDTDY ENVKLGKNVYVNTNCYF MDGGQITIGDNVFIGPNC GFYTATHPLNFHHRNEG FEKAGPIHIGSNTWFGGH VAVLPGVTIGEGSVIGAG SVVTKDIPPHSLAVGNPC KVVRKIDNDEGSHHHHH H	12.3	21.8
T33-01.3	MPIFTLNTNIKATDVPSD FLDVT SRLVADLLEKPG SYVAVHINTDQQLSFGG STNPAAFGTLMSIGGIEP GLNAAINAALTAVLEDLL GIRGDRMYIHFVNLNGD DVGWGYGTG	MTEKEKMLAEKWYDANF DQELIAERARAEICWAL NNTRPSNKGRIRGLIEGL FGKVTDNVSISIPFDTDY GKNVKGKNVYVNTNCY FMDGGQITIGDNVFIGPN CGFYTATHPLNFHHRNE GFEKAGPIHIGSNTWFG GHVAVLPGVTIGEGSVIG AGSVVTKDIPPHSLAVGN PCKVVRKIDNDEGSHHH HHH	12.0	21.5
T33-02.1	MHQIRVGVLTVDSCFR NLAPDRSGEALKLYVQD KDELGGTISAYKIVPDEI EEIKETLIDWCDEKELNL ILTTGGTGAFAPRDVTP ATKEVIEREAPGMALAM LMAASLSPEGMLSRPV CGIRGKTLIINLPGSLIGS LHCFDAILPALPHAIDLL RDAIVKVKVHVLGSHHH HHH	MPVIQTFVSTPLDHHKRE ELAEVYRRVTREVLGKP EDLVMMTFHDSTPMHFF GSTDPVACVRVEALGGY KENQPSVVTRTVSAAISL ECGIVLERIFVLYFSPLHC GWNGTNP	19.4	12.7
T33-02.2	MHQIRVGVLTVDSCFR NLAKDRSGNALKWLQ	MPVIQTFVSTPLDHHKRE NLAEVYRAVTREILGKPE	19.5	12.8

	DPDLLGGTISAYKIVPDE IEEIKETLIDWCDEKELN LILTTGGTGAFPRDVTP EATKEVIEREAPGMALA MLMASLEVSPGMLSR PVCGIRGKTLIINLPGST VGSRLRCFLAILPALPHAI DLLRDAIVKVKEVHHGS HHHHH	DLVMMTFHDSTPMHFFG STDPVACVRVEALGGYR EGEPELVTLIVTYAIEDEC GIVKDRIFVLYFSPLHCG WNGTNE		
T33-02.3	MHQIRVGVLTVSDSCFR NLAPDWSGNALKRLVQ DPELLGGTISAYKIVPDE IEEIKETLIDWCDEKELN LILTTGGTGAFPRDVTP EATKEVIEREAPGMALA MLMHLSVSPRGMLSR PVCGIRGKTLIINLPGSQI GSLRCFLAILPALPHAID LLRDAIVKVKEVHHGSH HHHHH	MPVIQTFVSTPLDHHKRE ALAERYRAVTKEILGKPE DLVMMTFHDSTPMHFFG STDPVACVRVEALGGYK EDEPELVTLIVTLSIEEEC GIVKERIFVLYFSPLHCG WNGTNP	19.5	12.8
T33-03.1	MHQIRVGVLTVSDSCFR NLERPLSGRALELYVQD PKLLGGTISAYKIVPDEIE EIKETLIDWCDEKELNLIL TTGGTGAFPRDVTPEAT KEVIEREAPGMALAMLM GSLNITPLGMLSRPVCGI RGKTLIINLPGSLLGSRV CFKFILPALPHAIDLLRD AIVKVKEVHHGSHHHHH H	MPVIQTFVSTPLDELRR SLVLVYRLVTEEVLGKPA DLVMMTFHDSTPMHFFG STDPVACVRVEALGGYG PSEPEKVTEIVTRAITEVC GIVADRIFVLYFSPLHCG WNGTNL	19.6	12.5
T33-03.2	MHQIRVGVLTVSDSCFR NLIPPLSGEALKIFVQDP KLLGGTISAYKIVPDEIEE IKETLIDWCDEKELNLILT TGGTGAFPRDVTPEATK EVIEREAPGMALAMLMG SLNVTPLGMLSRPVCGI RGKTLIINLPGSLLGSLQ CFQFILPALPHAIDLLRD AIVKVKEVHHGSHHHHH H	MPVIQTFVSTPLDELRRQ SLVLTYRIVTEKILGKPAD LVMMTFHDSTPMHFFGS TDPVACVRVEALGGYGP SEPEKVTEIVTRAITEVCG IVADRIFVLYFSPLHCGW NGTNL	19.5	12.5
T33-03.3	MHQIRVGVLTVSDSCFR NLRPLSGRALEIFVQD PELLGGTISAYKIVPDEIE EIKETLIDWCDEKELNLIL TTGGTGAFPRDVTPEAT KEVIEREAPGMALAMLM GSLNLTPLGMLSRPVCG IRGKTLIINLPGSLLGSLS CFRFILPALPHAIDLLRD AIVKVKEVHEGSHHHHH H	MPVIQTFVSTPLDELRR SLCLVYRIVTEEILGKPAD LVMMTFHDSTPMHFFGS TDPVACVRVEALGGYGP SEPERVTRVVTEAITEVC GIVADRIFVLYFSPLHCG WNGTNL	19.6	12.6
T33-04.1	MHQIRVGVLTVSDSCFR	MPVIQTFVSTPLDEDRE	19.6	12.5

	NLRPDLSGKALEILVQD PAFLGGTISAYKIVPDEI EEIKETLIDWCDEKELNL ILTTGGTGFAPRDVTPE ATKEVIEREAPGMALAM LMGSLKITPLGMLSRPV CGIRGKTLIINLPGSLLG SLRCFRFILPALPHAIDL RDAIVKVKEVHHGSHHH HHH	ALCLVYRIVTEEILGKPAD LVMMTFHDSTPMHFFGS TAPVACVRVEALGGYGP SEPERVTEIVTKAITEVCG IVADRIFVLYFSPLHCGW NGTNL		
T33-04.2	MHQIRVGVLTVSDSCFR NLRPDLSGRALARYVQ DPRELGGTISAYKIVPDE IEEIKETLIDWCDEKELN LILTTGGTGFAPRDVTP EATKEVIEREAPGMALA MLMGSLKITPLGMLSRP VCGIRGKTLIINLPGSLL GSLECFR FILPALPHAID LLRDAIVKVKEVHHGSH HHHHH	MPVIQTFVSTPLNEARRE ALVLVYRLVTKEILGKPE DLVMMTFHDSTPMHFFG STAPVACVRVEALGGYG PSEPEKVTAVVTEAITEV CGIVADRIFVLYFSPLHC GWNGTNL	19.6	12.4
T33-04.3	MHQIRVGVLTVSDSCFR NLRPDLSGRALRRYVQ DPAELGGTISAYKIVPDE IEEIKETLIDWCDEKELN LILTTGGTGFAPRDVTP EATKEVIEREAPGMALA MLMGSLKITPLGMLSRP VCGIRGKTLIINLPGSLL GSLRCFR FILPALPHAID LLRDAIVKVKEVHHGSH HHHHH	MPVIQTFVSTPLDEDRE ALFLVYQLVTEEILGKPA DLVMMTFHDSTPMHFFG STAPVACVRVEALGGYG PSEPEKVTAVVTKAITEV CGIVADRIFVLYFSPLHC GWNGTNL	19.7	12.5
T33-05.1	MHQIRVGVLTVSDSCFR NLATDWSGEALKLYVSN PKRLGGTISAYKIVPDEI EEIKETLIDWCDEKELNL ILTTGGTGFAPRDVTPE ATKEVIEREAPGMALAM LMGSLAVTPLGMLSRPV CGIRGKTLIINLPGSLG SLRCFEFILPALPHAIDL RDAIVKVKEVHEGSHHH HHH	MPVIQTFVSTPLDHHKRE NLAQAYRDVTRRILGKPE DLVMMTFHDSTPMHFFG STDPVACVRVEALGGYG RGEPELVTLVVSLAIEKE CGIVLERIFVLYFSPLHCG WNGINF	19.5	12.7
T33-05.2	MHQIRVGVLTVSDSCFR NLARDRSGRALRLYVAN PKELGGTISAYKIVPDEI EEIKETLIDWCDEKELNL ILTTGGTGFAPRDVTPE ATKEVIEREAPGMALAM LMGSLAVTPLGMLSRPV CGIRGKTLIINLPGSLRG SLRCFEFILPALPHAIDL RDAIVKVKEVHHGSHHH HHH	MPVIQTFVSTPLDHHKRE NLAQVYRDVTREILGKPE DLVMMTFHDSTPMHFFG STDPVACVRVEALGGYG KDEPELVNLVVSLAIQEE CGIVLDRIFVLYFSPLHCG WNGINV	19.6	12.7

T33-05.3	MHQIRVGVLTVSDSCFR NLAEDWSGRALEYVVT NPNELGGTISAYKIVPDE IEEIKETLIDWCDEKELN LILTTGGTGFAPRDVTP EATKEVIEREAPGMALA MLMGSLKVTPLGMLSR PVCGIRGKTLIINLPGSL EGSLRCFRFILPALPHAI DLLRDAIVKVKEVHAGS HHHHHH	MPVIQTFVSTPLDHHKRE NLAQVYRDVTRRILGKPE DLVMMTFHDSTPMHFFG STDPVACVRVEALGGYG REQPELVTLVVSLAIDKE CGIVLDRIFVLYFSPLHCG WNGINF	19.6	12.8
T33-06.1	MHQIRVGVLTVSDSCFR NLRPDLSGRALERYVQ DPKLLGGTISAYKIVPDE IEEIKETLIDWCDEKELN LILTTGGTGFAPRDVTP EATKEVIEREAPGMALA MLMGSLNITPLGMLSRP VCGIRGKTLIINLPGSLL GSLRCFDFILPALPHAID LLRDAIVKVKEVHHGSH HHHHH	MPVIQTFVSTPLDEDDR ALSLVYRYATEKILGKPA DLVMMTFHDSTPMHFFG STDPVACVRVEALGGYG PSEPEEVTKLVTAATEV CGIVADRIFVLYFSPLHC GWNGTNV	19.6	12.4
T33-06.2	MHQIRVGVLTVSDSCFR NLRPDLSGEALKIFVQD PELLGGTISAYKIVPDEIE EIKETLIDWCDEKELNLIL TTGGTGFAPRDVTPEAT KEVIEREAPGMALAMLM GSLNRTPLGMLSRPVC GIRGKTLIINLPGSLLGSL RCFRFILPALPHAIDLLR DAIVKVKEVHHGSHHHH HH	MPVIQTFVSTPLDEDDRT ALCLVYRIVTERILGKPAD LVMMTFHDSTPMHFFGS TDPVACVRVEALGGYGP SEPEEVTRVVTAATEVC GIVADRIFVLYFSPLHCG WNGTNV	19.6	12.4
T33-06.3	MHQIRVGVLTVSDSCFR NLRPDLSGEALRRIVQD PALLGGTISAYKIVPDEIE EIKETLIDWCDEKELNLIL TTGGTGFAPRDVTPEAT KEVIEREAPGMALAMLM GSLNITPLGMLSRPVCGI RGKTLIINLPGSLLGSLA CFR FILPALPHAIDLLRD AIVKVKEVHEGSHHHHH H	MPVIQTFVSTPLDELDRA SLDLVYRIATERILGKPAD LVMMTFHDSTPMHFFGS TDPVACVRVEALGGYGP SEPEEVTRLVTEATEVC GIVADRIFVLYFSPLHCG WNGTNV	19.5	12.4
T33-07.1	MALYFMGHMILVYSTFP SEKIAEITGKALLAQRLIA CFNAFEIRSGYWWKGE VVQDKEWAAIFKTTEEK EKELYEALRELHPEETP AIFTLKVENILTEYMNWL RESVLGE	MQAIGILELTSIAKGMELG DAMLKSANVDLLVSKTIS PGKFLMLGGDVPAIAKA VIVGIGNAGEMLVDSRVIL DIHPSVLP AISGLNSVDK RQAVGIVETWSVAACIKA ADAAVKGSNVTLVRVHM AFGIGGKCYMVVAGDVS DVNNAVTVASESAGEKG LLVYRSVIPRPHEAMWR QMVEGGSHHHHHH	13.0	20.0

T33-07.2	MALYFMGHMILVYSTFP NELLAIEITGKALLAKRLIA CFNAFEIRSGYWWKGEI VQDKEWAAIFKTTEEKE KELYEALREHVHFETPAI FTLKVENILTEYMNWLR ESVLGG	MSQAIGILELTSIAKGMEL GDAMLKSANVDLLVSKTI SPGKFLMLGGDVLAIK AVAVGLGAAGEMLVDSR LITNIHPSVLP AISGLNSV DKRQAVGIVETWSVAACI KAADKAVKGSNVTLVRV HMAFGIGGKCYMVVAGD VSDVNNAVTVASESAGE KLLLVYRSVIPRPHEAM WRQMVEGGSHHHHHH	13.0	20
T33-07.3	MALYFMGHMILVYSTFP NEAQAQIVGKALLAQRLI ACFNAFEIRSGYWWKGEI EIVQDKEWAAIFKTTEEK EKELYEALRELHVEETP AIFTLKVENILTEYMNWL RESVLGA	MSQAIGILELTSIAKGMEL GDAMLKSANVDLLVSKTI SPGKFLMLGGDVLAIK AVSVGLGNAGEMLVDSA LLTNIHPSVLP AISGLNSV DKRQAVGIVETWSVAACI KAADKAVKGSNVTLVRV HMAFGIGGKCYMVVAGD VSDVNNAVTVASESAGE KLLLVYRSVIPRPHEAM WRQMVEGGSHHHHHH	13.0	20
T33-08.1	MSPVVEVQGTIDELNSFI GYALVLSRWDDIRNDLF RIQNDFVLGEDVSTGG KGRTVTLEMILDVKKTE KMLKEIGKIELFVPPGG VESASLHMARAVSRRL RRIRAAAELTPINALVEL YAEALSKILFMHALISNK RLNIPEKIL	MREPIIEANGTDELTSFI GEAKHYVDEEMKGILEEI QNDIYKIMGEIGSKGKIEG IPLSSLNRLVDLIEREEM VNKSFVLPGGTLES AKLD VCRTIARRALLKVETVLR EFGIGLVAVLYLEVELSELL FLLARVIEIEKNKKGSHH HHHH	16.8	17.2
T33-08.2	MSPVVEVQGTIDELNSFI GYALVLSRWDDIRNDLF RIQNDFVLGEDVSTGG KGRTVTLEMIAELVKKK YKMKKEIGKIELFVPPG GSVESASLHMARAVSR RLERRIEAAAKLTEINEL VLLYAQALSRLFMHALI SNKRLNIPEKIY	MNQPIIEANGTDELTSFI GEAKHYVDEEMKGILEEI QNDIYKIMGEIGSKGKIEG ISDESLVKLLDLIEREEM VNKSFVLPGGTLES AKLD VCRTIARRATLKVKTVLE EFGIGFNAVLYLEVELSELL FLLARVIEIEKNKEGSHH HHHH	16.9	17.2
T33-08.3	MSPVVEVQGTIDELNSFI GYALVLSRWDDIRNDLF RIQNDFVLGEDVSTGG KGRTVTEEMVIELIKRYV KMKKEIGKIELFVPPG SVESASLHMARAVSRRL ERRIEAAARLTPINELVL AYAQALSRLFMHALISN KRLNIPEKIL	MNQPIIEANGTDELTSFI GEAKHYVDEEMKGILEEI QNDIYKIMGEIGSKGKIEG ISDES VKLWDLIEREEM MVNKS FVLPGGTLES AK LDVCRTIARRAYLKVLT VREFGIGLTAVLYLKLSE LLFLLARVIEIEKNKEGSH HHHHH	16.9	17.3
T33-09.1	MEEVVLITVPSAEEAVRI AYTLVEERLAACVNIIPG VVKIYRWQGRV RVASTL LLL VKTTTHAFPKL KERV KALHPYTVPEIVALPIAE	MVRGIRGAITVAADTDEA ILAATIELLREMLRANGIQ SYEELAAVIFTVTEDLTAA FPARAAELIGMHRVPLLS AREVPVPGSLKNVIRVLA	11.7	14.3

	GNREYLDWLRENTK	LWNTDTPQDRVRHVYLD EAVRLRPDLESPGSHHH HHH		
T33-09.2	MEEVVLITVPSAEEAVRI AYALVEERLAACVNIIPG LVRIYRWQGRVVRVDHV LLLLVKTTHAFPKLKER VKALHPYTVPEIVALPIA EGNREYLDWLRENTK	MVRGIRGAITVAADTPEAI YAATIELLRMLEANGIQ SYEELAAVIFTVTEDLTAA FPAAEARLIGMHRVPLLS AREVPVPGSLKNVIRVLA LWNTDTPQDRVRHVYLG EAVRLRPDLESPGSHHH HHH	11.8	14.3
T33-09.3	MEEVVLITVPSAEDAVRI ARALVEERLAACVNIIPG VVEIYRWQGRVKVKHVL LLLLVKTTHAFPKLKERV KALHPYTVPEIVALPIAE GNREYLDWLRENTK	MVRGIRGAITVKADTPEAI YAATVELLERMLAANGIQ SYEELAAVIFTVTEDLTAA FPADAARTIGMHRVPLLS AREVPVPGSLKNVIRVLA LWNTDTPQDRVRHVYLG EAVRLRPDLESPGSHHH HHH	11.7	14.2
T33-10.1	MEEVVLITVPSEEVAIEIA VALVEERLAACVNLPVPG LIRIYRWNNRVVIEKELL LLVKTTHAFPKLKERV KALHPYTVPEIVALPIAE GNREYLDWLRENTKGS HHHHH	MGAMGPVDEQWIEILRIQ ALCARYCLTINTQDGEG WAGCFTDDGSFSFDGW TITGRPALREYADAHARV VRGRHLTTDLLYTVIGNIA TGRSASVVTATAAGYKI LGSGEYHDLKKKDGQW RIHRDLRNDRLVSDPSV AVNVADADVAAVVGHLL AAARRLGTQDKN	12.8	18.4
T33-10.2	MEEVVLITVPSEGVASEI ACALVHERLAACVNIVP GLTRVYRWNNRVKVEN ELLLLKTTTHAFPKLKE RVKALHPYTVPEIVALPI AEGNREYLDWLRENTK GSHHHHH	GHMGPVDEQWIEILRIQA LCARYCLTINTQDGEGW AGCFTEDGSFSFDGWTI TGRPALREYADAHARVV RGRHLTTDLLYTVSGNV ASGRSASVVTATAAGY KILGSGEYHDLVKKKDGQ WRIHRDLRNDRLVSDP SVA NVADADVAAVVGH LLAAARRLGTQDKE	12.7	18.3
T33-10.3	MEEVVLITVPSEEVAIEIA LALVEERLAACVNIVPGL IRIYRWDNRVVIDKELL LVKTTHAFPKLKERVK ALHPYTVPEIVALPIAEG NREYLDWLRENTKGS HHHHH	MGAMGPVDEQWIEILRIQ ALCARYCLTINTQDGEG WAGCFTEDGSFSFDGW TITGRPALREYADAHARV VRGRHLTTDLLYTVIGNL ATGRSASVVTATAAGY KILGSGEYHDVLLKKKDGQ WRIASRDLRNDRLVSDP SVA NVADADVAAVVGH LLAAARRLGTQDES	12.8	18.4
T33-11.1	MEEVVLITVPSDEEAVTI AATLVSERLAACVNIVP GLTSLYRWNNKVKSEK EYLLLKTTTHAFPKLKE	MSQAIGILELTSIAKGMEL GDAMLKSANVDLLVSKTI SPGKFLMLGGDIGAIQQ AIETGVGQAGEMLVDSL	12.6	19.2

	RVKALHSYTVPEIVALPI AEGNREYLDWLRENTK GSHHHHHH	VLENIHPSVLP AISGLNSV DKRQAVGIVETWSVAACI KAANVALESSDVT LVRVH MAFGIGGKCYM VVAGDV AQVELAVTAASLVAGSR GLLVYRSVIPRPHEAMW RQMVEG		
T33-11.2	MEEVVLITVPSLEEALVI AGTLVNERLAACVNIVP GLTSLYRWNNEVKS EYLLLVKTTTHAFPKLKE RVKALHRYTVPEIVALPI AEGNREYLDWLRENTK GSHHHHHH	MSQAIGILELTSIAKGMEL GDAMLKSANVDLLVSKTI SPGKFLMLGGDIGAIQQ AIETGREQAGEMLVDSL LEDVHPSVLP AISGLNSV DKRQAVGIVETWSVAACI RAANVALASSDVT LVRV HMAFGIGGKCYM VVAGD VGSVRRAVEAAAIEAGS RGLLVYRSVIPRPHEAM WRQMVEG	12.7	19.3
T33-11.3	MEEVVLITVPSLHEAYVI AATLVRERLAACVNIVP GLTSLYRWDGVVVKVER EYLLLVKTTTHAFPKLKE RVKALHSYTVPEIVALPI AEGNREYLDWLRENTK GSHHHHHH	MSQAIGILELTSIAKGMEL GDAMLKSANVDLLVSKTI SPGKFLMLGGDIGAIQQ AIETGREQAGEMLVDSL LENIHPSVLP AISGLNSVD KRQAVGIVETWSVAACIR AANVALAGSNVT LVRVH MAFGIGGKCYM VVAGDV AEVEEAVALASEVAGRR GLLVYRSVIPRPHEAMW RQMVEG	12.7	19.3
T33-12.1	MILVYSTFPNLIEAVRIGI KLEKRLIACFNAPITA AYWWKGEIRIDRETAI FKTTEEKEKELYEELRK LHPYETPAIFTLKVENVL TEYMNWLRESVKGSHH HHHH	MVYMYVVSQDSLTPPEAK QAVADAIVDAHRSLTGTQ HFLAQVNFQEQPAGNVF LGGVQQGGYTIFVHGLH REGRSADLKGQLAEDIIL LVSAAANIDPKHIWVYFG EMPAQQMVEYGRS	13.0	12.9
T33-12.2	MILVYSTFPDLITAATIGI KLEKRLIACFNTPITA VYWWKGEIRVDRETAI FKTTEEKEKELYEELRK LHPYETPAIFTLKVENVL TEYMNWLRESVKGSHH HHHH	MVYMYVVSQDFLTPEAK AAVARAITDAHRALTGTQ HFLAQVNFQEQPAGNVF LGGVQQGGYTIFVHGLH REGRSADLKGQLARDIIL LVSVAANIDEKHIWVYFG EMPAQQMVEYGRE	12.9	13.1
T33-13.1	MHNFIYITASSAEEAVEI AVRILLEKKLAACVNLYPI VELFWWEGRIRAEQEV AMIVKTRSEKFAEVRDE VKAMHSYTTPCICAIPIE RGLKEFLDWIDETVE	MVRGIRGAI TVKRNTPLAI YASTVALLREMLEANGIQ SYEELAAVIFTVTEDLTAA SPADAARAIGMHRVPLLS AREVPVPGSLKNVIRVLA LWNTDTPQDRVRHVYLG EAVRLRPDLESPGSHH HHH	11.8	14.2
T33-13.2	MHNFIYITAKSGVEAVGI AYRILLEKKLAACVNLYPI	MVRGIRGAI TVGRDTPLA ISAATIALLEKMLEANGIQ	11.7	14.1

	VELFWWEGRVHAETEVE AMIVKTRSEKFAEVRDE VKAMHSYTTPCICAIPIE RGLKEFLDWIDETVN	SYEELAAVIFTVTEDLTAA DPADAARAIGMHRVPLLS AREVPVPGSLKNVIRVLA LWNTDTPQDRVRHVYLS EAVRLRPDLESPGSHHH HHH		
T33-13.3	MHNFYITADSGIEAVAIA MRLLEKKLAACVNIYPIV ELFWWEGEIRVRQETA MIVKTRSEKFAEVRDEV KAMHSYTTPCICAIPIER GLKEFLDWIDETVY	MVRGIRGAITVARDTEIEI AAATMVLLKRMLKANGIQ SYEELAAVIFTVTEDLTAA NPADAARAIGMHRVPLLS AREVPVPGSLKNVIRVLA LWNTDTPQDRVRHVYLD EAVRLRPDLESPGSHHH HHH	11.9	14.2
T33-14.1	MKIRIGHGFDVHKFGEP RPLILCGVEVPYETGLV AHSDDGVVLHAISDAILG AMALGDIGKHFPDTPDAA YKGADSIDLLRECVELA RAKGFELGNLDVTIIAQA PKMAPYIKLMQLNLSIVL DADIADINVKATTTEKLG FTGRKEGIAVEAVVLLS RK	MSEKKAVIGVVTISDRAS KGIYKDYSGEAIIYLKTVI ITPFEVEYRVIPDERDLIE KTLIELADEKGCSLILTTG GTGPAPRDVTPEATEAV CEKMLPGFGELMRQVSL KQVPTAILSRQTAGIRGS CLIVNLPDGPESILLCLKA VMPAIPYCIDLIGGAYIDT DPRIVKAFRPKPGSHHH HHH	17.0	20.3
T33-14.2	MKIRIGHGFDVHKFGEP RPLILCGVEVPYETGLV AHSDDGVVLHAISDAILG AMALGDIGKHFPDTPDAA YKGADSLDLLRHCIDLA RAKGFELGNLDVTIIAQA PKMAPYIKLMQLNLSVL LDADIADINVKATTTEKL GFTGRKEGIAVEAVVLL SRK	MSEKKAVIGVVTISDRAS KGIYKDYSGLTIINLLKTVII TPFEVEYRVIPDERDLIEK TLIELADEKGCSLILTTGG TGPAPRDVTPEATEAVC EKMLPGFGELMRQVSLK QVPTAILSRQTAGIRGSC LIVNLPDGPESIVICLKAV MPAIPYCIDLIGGAYIDTD PRIVKAFRPKPGSHHHH HH*	17.0	20.2
T33-14.3	MKIRIGHGFDVHKFGEP RPLILCGVEVPYETGLV AHSDDGVVLHAISDAILG AMALGDIGKHFPDTPDAA YKGADSLDLLRECIDLA RAKGFELGNLDVTIIAQA PKMAPYIKLMQLNLSVL LDADAADINVKATTTEKL GFTGRKEGIAVEAVVLL SRK	MSEKKAVIGVVTISDRAS KGIYKDYSGEAIIILLKTTII TPFEVEYRVIPDERDLIEK TLIELADEKGCSLILTTGG TGPAPRDVTPEATEAVC EKMLPGFGELMRQVSLK QVPTAILSRQTAGIRGSC LIVNLPGDIDSIVLCLKAV MPAIPYCIDLIGGAYIDTD PRIVKAFRPKPGSHHHH HH	17.0	20.2
T33-15.1	MVRGIRGAVSVLEDTRL VISHATRLLLRLMLKAN GIQSYEELAAVIFTVTED LTSAFPAAARRIGMHR VPLLSAREVPVPGSLPR VIRVLALWNTDTPQDRV RHVYLD DAVRLRPDLES	MSKAKIGIVTVSDRASAGI EEDVSGQAIIDWLKAYLT SEWEPIYQVIPDEQDVIE TTLIKMADEQDCCLIVTT GGTGPAPRDVTPEATEA VCDRMMPGFGELMRATL LRFNPTAILSRQTAGLRG	14.5	19

	PGSHHHHHH	DSLIVNLPGAPDSIILCLE AVFPAIPYCIDLMEGPYL ECDESVLKPFRRP		
T33-16.1	MSLILVYSTFPNRTEAVT IGVKLLKKRLIACFNAPFI VSAYEEDGVIELKEEWA AIFKTTEEKEKELYEELR KLHPYETPAIFTLKVENV LTEYMNWLRESV	MPVIQTFVSTPLDKEKRE ALALEYRVITETVLGKDP ALVMMTFHDSTPMFFNG NTDPVACVRVEALGGYG PSEPEKVTRLVTKAITDIC GIVADRIFVLYFSPLHCG WNGTNLGSHHHHHH	12.0	13.4
T33-16.2	MSLILVYSTFPNLHEAVV IGVELLRKRLIACFNAPFI VSVYEEEDGVIVVREEWA AIFKTTEEKEKELYEELR KLHPYETPAIFTLKVENV LTEYMNWLRESI	MPVIQTFVSTPLDEEKRE ALALQYRVVITYTILKKEP DLVMMTFHDSTPMRFRG STAPVACVRVEALGGYG PSEPERVTRVVTAITAV CGIVADRIFVLYFSPLHC GWNGTNLGSHHHHHH	12.0	13.5
T33-17.1	MSLILVYSTFPDLVSAIAI GIKLLKRLIACFNAPFIT SVYWWKGEIRVEKETA AIFKTTEEKEKELYEELR KLHPYETPAIFTLKVENV LTEYMNWLRESVGS HHH	MVYMYVVSQGRLTPEQK AAVARAIVDAHRALTGTQ HFLAQVNFQECPKGNVF LGGKRQDGNTIFVHGLH REGRSADLKGQLARDIIL LVSAAADIPEKHIWVYFG EMPAQQMVEYGRE	13.0	13.2
T33-17.2	MSLILVYSTFPSTLAEVA IGIELIEKRLIACFNAPFIT SVYWWKGEIRVERETA AIFKTTEEKEKELYEELR KLHPYETPAIFTLKVENV LTEYMNWLRESVGS HHH	MVYMYVVSQGGLSPEQ KAAVADAIVQAHRRLTGT QHFLAQVNFQECPKGNV FLGGVRQDGNTIFVHGL HREGRSADLKGQLAHDII LLVSAAANIPEKHIWVYF GEMPAQQMVEYGRA	13.0	13.1
T33-17.3	MSLILVYSTFPNRVTAIAI GLKLIKRLIACFNAPFIT TVYWWKGEIRVERETA AIFKTTEEKEKELYEELR KLHPYETPAIFTLKVENV LTEYMNWLRESVGS HHH	MVYMYVVSQGYLTPQQK ADVAAAIVTAHRDLTGTQ HFLAQVNFQECPKGNVF LGGVRQDGNTIFVHGLH REGRSADLKGQLARDIIL LVSAAANIPEKHIWVYFG EMPAQQMVEYGRS	13.1	13.1
T33-18.1	MSLILVYSTFPNRLEALLI GLELLEKRLIACFNAFEI TSAYWEKGRIRIEREWA AIFKTTEEKEKELYEELR KLHPYETPAIFTLKVENV LTEYMNWLRESVGS HHH	MVYMYVVSQDRLTPSAK HAVAQAITDAHLAHTGEE HTLAQVNFQECPAGNVF LGGVQQGGDTIFVHGLH REGRSDELKRDLITDIQV LVSHAANIDPKHIWVYFG EMPASQMVEYGGL	13.2	13
T33-18.2	MSLILVYSTFPNLLAEKLI GLKLLKKRLIACFNAFEI TSAYWEKGRIRTRREW AAIFKTTEEKEKELYEEL RKLHPYETPAIFTLKVEN VLTEYMNWLRESVGS HHHH	MVYMYVVSQDRLTPSAK HAVAQAITDAHLTHTGEE HSLAQVNFQECPAGNVF LGGVQQGGDTIFVHGLH REGRSDELKQRLITDIIAK VSIAADIDPKHIWVYFGE MPASQMVEYGGL	13.2	13

T33-18.3	MSLILVYSTFPNLEALYI GLLLLDKRLIACFNAFEI VSAAYWEKGRIRIRREWA AIFKTTEEKEKELYEELR KLHPYETPAIFTLKVENV LTEYMNWLRRESVGS HHHH	MVYMYVVSQDRLTPSAK HDVARAITDAHLAFTGEE HRLAQVNFQEQPAGNVF LGGVQQGGDTIFVHGLH REGRSDELKRDLITAIH VSLAANIDPKHIWVYFGE MPRVQMMMEYGGL	13.2	13.2
T33-19.1	MDSPIIEANGTDELTSF IGEAKHYVDEEMKGILE EIQNDIYKIMGEIGSRGKI EGISPERLRWLLDLIDRY SEMVKKENVLPGGTLES AKLDVCRTIAERAARKV KTVVEEKGIGETALHYL EVLSELLARVIEIEKN KEGSHHHHHH	MKKIIETQRAPGAIGPYV QGVDLGSMVFTSGQIPV PKTGKIPSTIAEQARLSLE NVKAIVVAAGLSVGDIIKM TVFITDLSLPLIELVYER FFDEHQATYPTRSCVQV ARLPKDVKLEIEAIAVRD	17.2	13.8
T33-19.2	MDSPIIEANGTDELTSF IGEAKHYVDEEMKGILE EIQNDIYKIMGEIGSRGKI EGISEERLLFLLDLIDRY SEMVPLSGVLPGGTLES AKLDVCRTIAERAARKV KTVVEETGIGIVALRYL EVLSELLARVIEIEKN KEGSHHHHHH	MKKIIETQRAPGAIGPYV QGVDLGSMVFTSGQIPV PETGEIPEHVYEQARLSL ENVKAIVVAAGLSVGDIIKM MTVFITDSSDLPIELVYK RFFDEHQATYPTRSCVQ VARLPKDVKLEIEAIAVRP	17.0	14.0
T33-19.3	MDSPIIEANGTDELTSF IGEAKHYVDEEMKGILE EIQNDIYKIMGEIGSRGKI EGISEERLDELDDLYNR YSEMVPRDNVLPGGTL ESAKLDVCRTIAERAAR KVKTVEETGIGRVALQ YLEVLSLLELLARVIEIE KNKEGSHHHHHH	MKKIIETQRAPGAIGPYV QGVDLGSMVFTSGQIPV PETGRIPAHVAEQARLSL ENVKAIVVAAGLSVGDIIKM MTVFITDLEDLPLIEAVYK RFFDSHQATYPTRSCVQ VARLPKDVKLEIEAIAVRE	17.2	13.8
T33-20.1	MSPIEEANGTDELTSFI GEAKHYVDEEMKGILEE IQNDIYKIMGEIGSKGKIP GIPQRSRLDWLLDLIERK EMVNRKFVLPGGTLESA KLDVCRTIARRATRQVL KVVEEFGIGRVAVQYLL VLVELLFLARVIEIEKNK EGSHHHHHH	MLYFQGMPHLVIEATANL RLETSPGELLEQANAALF DSGQFGEADIKSRFVTLE AYRQGTAAVERAYLHAC LSILDGRSVLERTRLALRL RAVLAVAGGGGEEGVQ VSVEVREMERISYAKAVV AR	17.2	13.8
T33-20.2	MKPIEEANGTDELTSFI GEAKHYVDEEMKGILEE IQNDIYKIMGEIGSKGKIP GIPESRLEWLLSLIARYS EMVNREFVLPGGTLESA KLDVCRTIARRAARKVQ EVLEEFGIGDVALKYLLV LVELLFLARVIEIEKNKE GSHHHHHH	MLYFQGMPHLVIEATANL RLETSPGELLEQANAALF ASGQFGEADIKSRFVTLE AYRQGTAAVERAYLHAC LSILDGRSAETRLRLSIRL CAVLASAVAGGGGEEGVQ VSVEVREMERISYAKAVV AP	17.1	13.7
T33-20.3	MEPIEEANGTDELTSFI	MLYFQGMPHLVIEATANL	17.2	13.7

	GEAKHYVDEEMKGILEE IQNDIYKIMGEIGSKGKIP GISEDRLDWLLDLIDRYK EMVNRKFLVLPGGTLESA KLDVCRTIARRAARKVL KVLEEFVIGDVALKYL LEELLFLLARVIEIEKNKE GSHHHHHH	RLETSPGELLEQANAALF DSGQFGEADIKSRFVTLE AYRQGTAAVERAYLHAC LSILDGRSTETRLRLSLRL LAVLAGAVAGGGEVQ VSVEVREMERISYAKAVV AA		
T33-21.1	MDSPIIEANGTDELTSF IGEAKHYVDEEMKGILE EIQNDIYKIMGEIGSKGKI PGIPQSSRLRWDLIKR YSEMVNKSFVLPGGTLE SAKLDVCRTIARRAARK VATVVEEFGIGVALAY LDVLSSELLFLLARVIEIEK NKEGSHHHHHH	MLDFQGMPLVIEATANL RLETSPGELLEQANAALF ASGQFGEADIKSRFVTLE AYRQGTAAVERAYLHAC LSILDGRSIGELRALGARL CAVLAAVAGGGEVQ VSVEVREMERLSYAKRV VAA	16.9	13.5
T33-21.2	MDSPIIEANGTDELTSF IGEAKHYVDEEMKGILE EIQNDIYKIMGEIGSKGKI PGISEESLVKLFDLIKRY SEMVNKSFVLPGGTLES AKLDVCRTIARRAARKV ATVVEEFGIGAVALAYLE LSELLFLLARVIEIEKNK EGSHHHHHH	MLDFQGMPLVIEATANL RLETSPGELLEQANRALF DSGQFGEADIKSRFVTLE AYRQGTAAVERAYLHAC LSILDGRDIGTRTALAARL LAVLAGAVAGGGEVQ VSVEVREMERLSYAKRV VAA	16.9	13.6
T33-21.3	MDSPIIEANGTDELTSF IGEAKHYVDEEMKGILE EIQNDIYKIMGEIGSKGKI PGISYESIARLFDLIRRY KEMVNKSFVLPGGTLES AKLDVCRTIARRAARKV ATVLEEFVIGAVALAYLE LSELLFLLARVIEIEKNK EGSHHHHHH	MLDFQGMPLVIEATANL RLETSPGELLEQANAALF DSGQFGEADIKSRFVTLE AYRQGTAAVERAYLHAC LSILDGRSTGELTALAAR LCAVLAVAGGGEVQ QVSVEVREMERLSYAKR VVAA	17.1	13.5
T33-22.1	MDSPIIEANGTDELTSF IGEAKHYVDEEMKGILE EIQNDIYKIMGEIGSKGKI EGISEDRLADLLELLRY SAMVNKSFVLPGGTLES AKLDVCRTIARRAERKV ATVLEEFVIGKVALRYL RVLERLLFLLARVIEIEKN KEGSHHHHHH	MSQAIGILELTSIAKGMEL GDAMLKSANVDLLVSKTI SPGKFLMLGGDYGAIQ QAIETGTSQAGEMLVDS ELLKNIHPSVLP AISGLNS VDKRQAVGIVETWGVTA CIVAADFAVKNSNVT LVR VHMAFGIGGKCYMVVAG DVSDVNNAV DVASAVAG ALGKLVYRSVIPRPHEAM WRQMVEG	17.2	19.2
T33-22.2	MDSPIIEANGTDELTSF IGEAKHYVDEEMKGILE EIQNDIYKIMGEIGSKGKI EGISEERLVDLLELLRY SKMVNKSFLVLPGGTLES AKLDVCRTIARRAERKV ATVLEEFVIGKVALRYL RVLERLLFLLARVIEIEKN	MSQAIGILELTSIAKGMEL GDAMLKSANVDLLVSKTI SPGKFLMLGGDYGAIQ QAIETGTSQAGEMLVDS ALLKDIHPSVLP AISGLNS VDKRQAVGIVETWGVTA CIIAADFAVKNSNVT LVR VHMAFGIGGKCYMVVAG	17.3	19.2

	KEGSHHHHHH	DVSDVNNAVEVASAVAG ALGRLVYRSVIPRPHEAM WRQMVEG		
T33-22.3	MDSPIIEANGTDELTSF IGEAKHYVDEEMKGILE EIQNDIYKIMGEIGSKGKI EGISED RVAYLLELLRY EKMVNKSFVLPGGTLES AKLDVCRTIARRAERKV ATVLRREFGIGKVALRYLK VLERLLFLLARVIEIEKN EGSHHHHHH	MSQAIGILELTSIAKGMEL GDAMLKSANVDLLVSKTI SPGKFLMLGGDTGAIQ QAIETGTSQAGEMLVDS DLIKDIHPSVLP AISGLNS VDKRQAVGIVETWGVTA CIIAADFAVKGSNVT LVR VHMAFGIGGKCYMVVAG DVSDVNNAVDVASRVAG ALGLLVYRSVIPRPHEAM WRQMVEG	17.3	19.2
T33-23.1	MDSPIIEANGTDELTSF IGEAKHYVDEEMKGILE EIQNDIYKIMGEIGSKGKI PGISSYVWLVLIRRY EEMVNKSFVLPGGTLES AKLDVCRTIARRAHRKV KTVVEEFGIGEDAAAYL ELLSRLLFLLARVIEIEKN KEGSHHHHHH	MSQAIGILELTSIAKGMEL GDAMLKSANVDLLVSKTI SPGKFLMLGGDIGAIQQ AIETGTSQAGEMLVDSL IPDIHPSVLP AISGLNSVD KRQAVGIVETWSVVACIR AANA AVASSNVT LVRVH MAFGIGGKCYMVVAGDV SDVNEAVTVASAVAGAT GLLVYRSVIPRPHEAMW RQMVEG	17.1	19
T33-23.2	MDSPIIEANGTDELTSF IGEAKHYVDEEMKGILE EIQNDIYKIMGEIGSKGKI PGIPWESLLWLRDLIKR YEEMVNKSFVLPGGTLE SAKLDVCRTIARRAYRK VKT VVEEFGIGEVAVQY LRELSRLLFLLARVIEIEK NKEGSHHHHHH	MSQAIGILELTSIAKGMEL GDAMLKSANVDLLVSKTI SPGKFLMLGGDIGAIQQ AIETGTSQAGEMLVDSL LPDIHPSVLP AISGLNSVD KRQAVGIVETWSVEACIR AADMAVRTSNVT LVRVH MAFGIGGKCYMVVAGDV SDVNEAVTAASATAGAL GKLVYRSVIPRPHEAMW RQMVEG	17.5	19.2
T33-23.3	MDSPIIEANGTDELTSF IGEAKHYVDEEMKGILE EIQNDIYKIMGEIGSKGKI PGIPLSSYIWLLELIRRY EEMVNKSFVLPGGTLES AKLDVCRTIARRAFRKV RTVVEEFGIGEVAAVYL RVLSELLFLLARVIEIEKN KEGSHHHHHH	MSQAIGILELTSIAKGMEL GDAMLKSANVDLLVSKTI SPGKFLMLGGDIGAIQQ AIETGTSQAGEMLVDSL IPDIHPSVLP AISGLNSVD KRQAVGIVETWSVTACII AANA AVAGSNVT LVRVH MAFGIGGKCYMVVAGDV SDVNEAVTVASLTAGAL GRLVYRSVIPRPHEAMW RQMVEG	17.3	19.1
T33-24.1	MPLLKFDLFYGRSDEQI KSLIDAHAAMVLAFGV APTDRYQTVSQHREGE MVLED TGLGYGRTEAV VLLTVISRPRSEEQK VLF NRLLVAALESVCGISPD DVIVALVENSADWSFG	MSKAKIGIVTVSDRAYAGI YEDISGKAIIDTLNDY LTS EWEPIYRVIPDNLEQIKVA LGYMALIEDCCLIVTTGG TGPAKRDTVPEATEAVC DRMMPGF GELMRAESLK FVPTAILS RQTAGLLGDS	15.2	19

	GGRAEFLTGDLVGGSH HHHHH	LIVNLPGKPKSIRECLDAV FPAIPYCIDLMEGPYLEC NEAVIKPFRP		
T33-24.2	MPLLKFDLFYGRSDEQI KSLIDAAWAAMVLAFGV PATDRYQTVSQHREG MVLEDTGLGYGRTRAV VLLTVISRPRSEEQKVL NRLLCAALEVVCGISPD DVIVALVENSADWSFG RGRAEFLTGDLVGGSH HHHHH	MSKAKIGIVTVSDRAFAGI YEDISGKAIIDTLNDYLTS EWEPIYRVIPDELGLIEAA LAYMALVEDCCLIVTTGG TGPAKRDTVPEATERVC DRMMPGFGELMRAESLK FVPTAILSRQTAGLLGDS LIVNLPGKPKSIRECLDAV FPAIPYCIDLMEGPYLEC NEAVIKPFRP	15.4	19.0
T33-24.3	MPLLKFDLFYGRSDEQI KSLIDAAGAMVLAFGV PASDRYQTVSQHRPGE MVLEDTGLGYGRTRAV VLLTVISRPRSEEQKVL NRLLTAALEVLCGISPDD VIVALVENSADWSFGG GRAEFLTGDLVGGSHH HHHH	MSKAKIGIVTVSDRAFAGI YEDISGKAIIDTLNDYLTS EWEPIYRVVPDDKDIIVTT LAYMALIEDCCLIVTTGGT GPAKRDTVPEATEAVCD RMMPGFGELMRAESLKF VPTAILSRQTAGLLGDSLI VNLPGKPKSIRECLDAVF PAIPYCIDLMEGPYLECN EAVIKPFRP	15.2	19.0
T33-25.1	MSRVYLIFSTCPDLPSA EISRVLVQERLAACVTQ LPGAVSTYRWQGGKIETT QEIQLLIKTNRKTVALAM LKLKDLHPYRLPETIAVQ VSTGYPRFEKWIEDEIE	MSRTMVSSGSLFEEIFGY SRAVRIGPLVVVAGTTGS GSTIGAQTLDALRRIEIAL GQAGATLADVVRTRIYVT DISLYDVVGMAYDAFRKI RPVTSMVEVTALIAPGLL VEIEADAYGGSHHHHHH	12.0	13.6
T33-25.2	MSSVYLIFSTCPDLPSA EISRVLVQERLAACVTQ LPGAVSTYRWQGGKIETT QEIQLLIKTNRRTVSLAIL KLQDLHPYRLPETIAVQ VSTAYPEFEKWIYDEIE	MSRTMVSSGSLLEEVTG YSRAVRIGPLVVVAGTTG SGKDIGAQTLDALRRIEIA LGQAGATLADVVRTRIYV TDIRFDDVALAINRAFR KIRPVTSMVEVTALIAPGL LVEIEADAYGGSHHHHH H	12.0	13.5
T33-25.3	MSNVYLIFSTCPDLPSA EISRVLVQERLAACVTQ LPGAVSTYRWQGGKIETT QEIQLLIKTNRDTIVRAIL KLKELHPYRLPETIAVQV ATAYAGFEKWIWDEIA	MSRTMVSSGSLLEERLG YSRAVRIGPLVVVAGTTG SGDTIGMQTLDALRRIEIA LGQAGATLADVVRTRIYV TDIRIDVGLAIAEAFGK IRPVTSMVEVTALIAPGLL VEIEADAYGGSHHHHHH	11.9	13.4
T33-26.1	MKSELEKMLAGHLYNP ADPELQDLVLLARRLVD HYNRTSADEYKERQTL RALFGSTGERLFIENF RCDYGENIHVGENFFM NFDGVILDVCEVRIGDH CFIGPGVHIYTATHPLDP HERNSGLEYGKPVVIGH	MPVIQTFVSTPLDERTRS LLAAVYARVTREVLGKDP TRVMMTFHDSTPMHHK GSTAPVACVRVEALGGY GPSEPEKVTIVTRAITDL CGIVADRIFVLYFSPLHC GWNGTNV	21.3	12.4

	NVWIGGRAVINPGVTIG DNAVIASGAVVTKDVPA NAVVGGNPAKVIKWLK GSHHHHHH			
T33-26.2	MKSELEKMLAGHLYNP ADPELQDLRLLARRLVD AYNETSADEYEERKLLL DTLFGSTGERLFIENF RCDYGDNIHVGENFFM NFDGVILDVCEVRIGDH CFIGPGVHIYTATHPLDP HERNSGLEYGKPVVIGH NVWIGGRAVINPGVTIG DNAVIASGAVVTKDVPA NAVVGGNPAKVIKWLK GSHHHHHH	MPVIQTFVSTPLDERDRL LLAAVYARVTEKVLGKDP SKVMMTFHDSTPMHHR GSTAPVACVRVEALGGY GPSEPEKVTIVTDAITEV CGIVADRIFVLYFSPLHC GWNGTNV	21.3	12.3
T33-26.3	MKSEKEKMLAGHLYNP ADKELQNELLTARRLVD LYNETGADEYDERRVLL RTLFGSTGERLFIENF RCDYGRNIHVGENFFM NFDGVILDVCEVRIGDH CFIGPGVHIYTATHPLDP HERNSGLEYGKPVVIGH NVWIGGRAVINPGVTIG DNAVIASGAVVTKDVPA NAVVGGNPAKVIKWLK GSHHHHHH	MPVIQTFVSTPLDERERT LLAAVYARVTREVLGKPS EKVMMTFHDSTPMHHR GSTAPVACVRVEALGGY GPSEPEKVTIVTAAITDV CGIVADRIFVLYFSPLHC GWNGTNV	21.3	12.3
T33-27.1	MTMADETIILNVLGQYT RAHRRDPDAMAALFA PDASIVVDAVGGASKPI SVLHGRDAIRVAVRQM MAPHGYRAWSQNVVN APVIHIGDTARLDAQF MVFSILAAEVPDGGWPT GTFGAQGRIVPIEAGTY TLFLRTVPDGVVIAHMY IKHRLPMAFG	MSQAIGILELSSIAKGMEL GDAMLKAANVDLLVSKTI SPGKFLMLGGDLDDIILA VAVGMERAGDSDLSEVI PDIHPSVLPASGLNSVD KRQAVGIVETWSVAACIK AADRAVKGSNVTLVRVH MAFGIGGKCYMVVAGDV SDVNNAVTVASESAGEK GLLVYRSVIPRPHEAMW RQMVEGGSHHHHHH	17.3	20.2
T33-27.2	MTMADETIILNVLGQYT RAHRRDPDAMAALFA PDATIVVDAVGGANRRII SLLDGRDAIRVAVRQM MAPHGYRAWSQNVVN APVIHINGDKALLDAQF MVFSILAAEVPDGGWPT GTFGAQGRIVPIEAGEY LLMLETVPDGVVISMII KHRLPMAFG	MSQAIGILVLSSIAKGMEL GDAMLKAANVDLLVSKTI SPGKFLMLGGDESAIKQ AVAVGVERAGDALLDSA VISDIHPSVLPASGLNSV DKRQAVGIVETWSVAACI EAADRAVKGSNVTLVRV HMAFGIGGKCYMVVAGDV VSDVNNAVTVASESAGE KLLVYRSVIPRPHEAM WRQMVEGGSHHHHHH	17.3	20.0
T33_27.3	MTMADETIILNVLGQYT RAHRRDPDAMAALFA PDATIVVDAVGGAFRVI SILKGRDAIRVAVRQMM	MSQAIGILVLSSIAKGMEL GDAMLKAANVDLLVSKTI SPGKFLMLGGDEGAIK QAVAVGVRNAGDDLDS	17.4	20.1

	APHGYRAWSQNVVNP VIHIKGDKALLDAQFMVF SILAAEVPDGGWPTGTF GAQGRIVPIEAGTYLLML ETVEDGWVISRMIIEHRL PMAFG	KVIDNIHPSVLP AISGLNS VDKRQAVGIVETWSVAA CIRAADRAVKGSNVT LVR VHMAFGIGGKCYMVVAG DVSDVNNAVTVASESAG EKGLLVYRSVIPRPHEAM WRQMVEGGSHHHHHH		
T33-28.1	MSVNTSFLSPSLVTIRDF DHGQFAVLRIGRTGFPA DKGDIDLCLSKMQGVLS AQLFLGNPREPGFKGP HIRIRCVDIDDKHTYNAM VYVDLIVGTGASEVERE TAEKARAALAVLRVD EADHSCVTQFEMKLR EELLSSDSFHPDKDEYY KDFL	MPVIQTFVSTPLDHEKRT LLFRQYRIVTAVILGKPAE LVMMTFHDSTPMHFFGS TDPVACVRVEALGGYGP SEPEKVTEVVTKAISYVC GIVADRIFVLYFSPLHCG WNGTNGSHHHHHH	17.6	13.5
T33-28.2	MSVNTSFLSPSLVTIRDF DNGQFAVLRIGRTGFPA DKGDIDLCLRKMEGVLA AQIYLGNPREGPKGPH IRIRCVDIDDKHTYNAMV YVDLIVGTGASEVERET AEELAKAALDIALEVDKA NEHSCVTQFEMKLREEL LSSDSFHPDKDEYYKDF L	MPVIQTFVSTPLDHRKRE MLSTVYRIVTATILGKPE LVMMTFHDSTPMHFFGS TDPVACVRVEALGGYGP SEPEKVTKVVTEAISYLC GIVADRIFVLYFSPLHCG WNGTNIGSHHHHHH	17.6	13.5
T33-28.3	MSVNTSFLSPSLVTIRDF DKGQFAVLRIGRTGFPA DKGDIDLCLSKMDGVLA AQLYLGNPREGPKGPH HIRIRCVDIDDKHTYNAM VYVDLIVGTGASEVERE TAEERARRALAVLRVD EADHSCVTQFEMKLR EELLSSDSFHPDKDEYY KDFL	MPVIQTFVSTPLDHEKRN MLTKVYRIVTDTILGKPAE LVMMTFHDSTPMHFFGS TDPVACVRVEALGGYGP SEPEKVTKVVTD AISYVC GIVADRIFVLYFSPLHCG WNGTNLGSHHHHHH	17.7	13.5
T33-29.1	MSRTMVSSGSRYERIM GYSRAVRIGPLVVVAGT TGSGRGIGDQTEDALR RIEIALGQAGATLADVVR TRIVYTDISEFAAVAIQH YVAFRKIRPVTSMVEVT ALIAPGLLVEIEADAYGG SHHHHHH	MKKIEAIIRPFLDEVKIAL VNAGIVGMTVSEVRGFG RQKRGSEYTFEFLQKLG LEIVLDEDVAEVILKIRE AARTGENGDGKIFVSPVL RVVRIRDGAMDEAAISA WA	13.7	12.2
T33-29.2	MSRTMVSSGSKEEIEFG YSRAVRIGPLVVVAGTT GSGRTIAAQTEDALRRI EIALGQAGATLADVVRT RIYVTDISRWDEVGLVH KNAFAKIRPVTSMVEVT ALIAPGLLVEIEADAYGG SHHHHHH	MKKIEAIIRPFLDEVKIAL VNAGIVGMTVSEVRGFG RQKRGSEYTFEFLQKLG LEIVLDEDVPLVINKIRE AARTGENGDGKIFVSPV ERVVRIRDGAMDELAISA WS	13.7	12.3

T33-30.1	MSKAKIGIVTVSDRASA GTLTDTNGLAIRSCLDM YLTSEWEPIYQVIPDEQ DVIETTLIKMADEQDCCL IVTTGGTGPAKRDVTPE ATEAVCDRMMPGFGEL MRAESLKFVPTAILSQR TAGLRGDSLIVNLPGSP ESIFECLKAVFPAIPYCID LMEGPYLECNERVIKPF RPGSHHHHHH	MPFLELDTNLPANRVPA GLEKKLCEQAAAAILGKPA DRVNVTVRPGLAMALSG STEPCAQLSISSIGVVGE AERNLISRGFTDFLTKE LALGQDRILIRFFPLESW QIGKIGLVMTFE	20.0	12.8
T33-30.2	MSKAKIGIVTVSDRASA GTLTDTNGLAIRTALRRY LTSEWEPIYQVIPDEQD VIETTLIKMADEQDCCLI VTTGGTGPAKRDVTPE ATEAVCDRMMPGFGEL MRAESLKFVPTAILSQR TAGLRGDSLIVNLPGSP ESIIECLKAVFPAIPYCID LMEGPYLECNEKVIKPF RPGSHHHHHH	MPFLELDTNLPANRVPA GLEKRLCEVAAEILGKPA DRVNVTVRPGLAMALSG STEPCAQLSISSIGVVGT AERNAVISAGFTDFLTKE LALGQDRILIRFFPLESW QIGKIGLVMTFD	20.0	12.7
T33-30.3	MSKAKIGIVTVSDRASA GVRLNRNGLAIETWLDL YLTSEWEPIYQVIPDEQ DVIETTLIKMADEQDCCL IVTTGGTGPAKRDVTPE ATEAVCDRMMPGFGEL MRAESLKFVPTAILSQR TAGLRGDSLIVNLPGDP DSIIECLKAVFPAIPYCID LMEGPYLECNEKVIKPF RPGSHHHHHH	MPFLELDTNLPANRVPA GLEKKLCRAAAEILGKPE DRVNVTVRPGLAMALSG STEPCAQLSISSIGVVGT AERNALISRRFTDFLTKE LALGQDRILIRFFPLESW QIGKIGLVMTFD	20.1	12.9

Table S3. Amino acid sequence of individual T33 components for *in vitro* assembly.

Design	Sequences	MW
T33-06.1A	MHQIRVGVLTVSDSCFRNL RPDLSGRALERYVQDPKLL GGTISAYKIVPDEIEEIKETL IDWCDEKELNLILTTGGTG FAPRDVTPEATKEVIEREA PGMALAMLMGSLNITPLG MLSRPVCGIRGKTLIINLPG SLLGSLRCFDFILPALPHAI DLLRDAIVKVKEVHHGSHH HHHH	19.6
T33-06.1B	MPVIQTFVSTPLDEDDRRA LSLVYRYATEKILGKPADLV MMTFHDSTPMHFFGSTDP VACVRVEALGGYGPSEPE EVTKLVTAAITEVCGIVADR IFVLYFSPLHCGWNGTNVG SHHHHHH	13.4
T33-08.2A	MSPVVEVQGTIDELNSFIG YALVLSRWDDIRNDFRIQ NDLFVLGEDVSTGGKGRT VTLEMIAELVKKSYKMKKEI GKIELFVVPGGSVESASLH MARAVSRRLERRIEAAKL TEINELVLLYAQALSRILFM HALISNKRLNIPEKIYGSHH HHHH	17.9
T33-08.2B	MNQPIIEANGTDELTSFIG EAKHYVDEEMKGILEEQN DIYKIMGEIGSKGKIEGSD ESLVKLLDLIERYEEMVNK SFVLPGGTLES AKLDVCRT IARRATLKVKTVLEEFGIGF NAVLYLEVELSELLFLLARVI EIEKNKEGSHHHHHH	17.2
T33-11.1A	MEEVVLITVPSDEEAVTIAA TLVSERLAACVNIVPGLTSL YRWNNKVKSEKEYLLL VKT TTHAFPCLKERVKALHSYT VPEIVALPIAEGNREYLDW LRENTKGSHHHHHH	12.6
T33-11.1B	MSQAIGILELTSIAKGMELG DAMLKSANVDLLVSKTISP GKFLMLGGDIGAIQQAIET GVGQAGEMLVDSLVL ENIH PSVLP AISGLNSVDKRQAV	20.1

	GIVETWSVAACIKAANVAL ESSDVTLVVRVHMAFGIGGK CYMVVAGDVAQVELAVTA ASLVAGSRGLLVYRSVIPR PHEAMWRQMVEGGSHHH HHH	
T33-18.2A	MSLILVYSTFPNLEAKLIG LKLLKKRLIACFNAFEITSA YWEKGRIRTRREWAAIFKT TEEKEKELYEELRKLHPYE TPAIFTLKVENVLTEYMNW LRESVGSHHHHHH	13.2
T33-18.2B	MVYMVVYSQDRLTPSAKH AVAQAITDAHLTHTGEEHS LAQVNFQEQPAGNVFLGG VQQGGDTIFVHGLHREGR SDELKQRLITDIIAKVSIAAD IDPKHIWVYFGEMPASQM VEYGGLGSHHHHHH	14
T33-22.3A	MDSPIIEANGTDELTSFIG EAKHYVDEEMKGILEEIQN DIYKIMGEIGSKGKIEGISE DRVAYLLELLLRYEKMNK SFVLPGGTLES AKLDVCRT IARRAERKVATVREFGIG KVALRYLKVLERLLFLLARV IEIEKNKEGSHHHHHH	17.3
T33-22.3B	MSQAIGILELTSIAKGMELG DAMLKSANVDLLVSKTISP GKFLMLGGDTGAIQQAIE TGTSQAGEMLVSDLIKDI HPSVLP AISGLNSVDKRQA VGIVETWGV TACIIAADF AV KGSNVTLVVRVHMAFGIGG KCYMVVAGDVSDVNNAVD VASRVAGALGLLVYRSVIP RPHEAMWRQMVEGGSHH HHHH	20.2
T33-24.3A	MPLLKFDLFYGRSDEQIKS LIDAAHGAMVLAFGVPASD RYQTVSQHRPGEMVLEDT GLGYGR TDAVVLLTVISRP RSEEQKVLFNRLLTAALEV LCGISPDDVIVALVENS DA DWSFGGGRAEFLTGD LVG GSHHHHHH	15.2
T33-24.3B	MSKAKIGIVTVSDRAFAGIY EDISGKAIIDTLNDYLTSEW	19.9

	EPIYRVVPDDKDIIVTTLAY MALIEDCCLIVTTGGTGPA KRDVTPEATEAVCDRMMP GFGELMRAESLKFVPTAIL SRQTAGLLGDSLIVNLPK PKSIRECLDAVFPAIPYCID LMEGPYLECNEAVIKPFRP GSHHHHHH	
--	---	--

