Supporting Information

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Arabidopsis_thaliana/1-543	1 - MAVSSAFVGC <mark>P</mark> KLETLLNHHNLS <mark>P</mark> SSSSSSSSSSQT <mark>PLGLNG</mark> VRVL <mark>P</mark> KNNRTRR <mark>G</mark> LIQKARCELS ASSDS	69
Triticum_aestivum/1-528	1 - MAGATSATAAAG AFAAGAKARGSSAACP WVVAAGGRRRSG - VVRCDAG GDAQA	52
Hordeum_vulgare/1-527	1 - MAGAISATAAAG AFAA - AKARGPAAACP WU VAAGGRKRSG - VVRCDAG	51
Physcomitrella natens/1=476		5
Chlamydomonas_reinhardtii/1-522	1 - MOTTMOORLOGRNVAGRSVAPSVPAHRSFHSHRAATOTATISAAASSTKLPA	53
Synechococcus/1-425		
Escherichia_coli/1-418		
Methanopyrus_kandleri/1-404		
Archidensis theliese// 6/2		440
Triticum aestivum/1-528	53 ASKLASITALEGERISADATI NE-SITAVIGI SVHTAPVDMERI AVAFFI WDRAISELTSI NHIFFAX	122
Hordeum_vulgare/1-527	52 ASKAASITALEOFKIS-ADRYMKEK-SSIAVIGLSVHTAPVEMREKLAVAEELWPRAISELTSLNHIEEAAV	121
Or/za/1-537	62 VAKAASVAALEQFKIS - ADRYMKER - SSIAVIGLSVHTAPVEMREKLAVAEELWPRAISELTSLNHIEEAAV	131
Physcomitrella_patens/1-476	6 RIKAA <mark>s</mark> lsafqefqnaran <mark>r</mark> ytkv <mark>k - ssvmvlglsih<u>tt</u>pvemrek</mark> laipeaewp <mark>r</mark> aidels <mark>s</mark> onhieeagv	76
Chlamydomonas_reinhardtii/1-522	54 SHLESSKKALDSLKQQAVNRYAGDKKSSIIAIGLTIHNAPVELREKLAVPEAEWPRAIEELCOFPHIEEAAV	125
Synechococcus/1-425	1	46
Methanonyrus kandleri/1-404		40
memanopyrus_render/1-404		
Arabidopsis_thaliana/1-543	141 L ST CNRME I YVL AL SOHROVKEVT EVMSKT SG I PVSE I COHRFLL YNKDATOH I FEVSAGLDSL VL GEGO I L	212
Triticum_aestivum/1-528	123 L <mark>ST CNR</mark> ME I YVVAL SWNRG I REVVDWMSKKSG I PASEL REHL FML RD SDAT RHL FEVS SGLDSL VL GEGQ I L	194
Hordeum_vulgare/1-527	122 L STCNRME I YVVAL SWNRG I REVVDWISKKSG I PASEL REHL FML ROSDATRHL FEVSAGLOSL VL GEGO I L	193
Oryza/1-537	132 L ST CNAME I YVVAL SWNRGTRE V DOWNSR KSGT PASEL REHLFML ROSDATRHLFE VSAGLOSLVLGEGOTL	203
Chlamudomonas reinhardtii/1-522	126 IST CNDMEL YVVGI SWIB GVBEVE EVMISH SSTSCHLEETTTIL RUGHAUMETTISSEL SSTCH BURGEN ST	140
Synechococcus/1-425	47 I STONRLE I YAVVOETE OGVRE I COFLAET GOLOLNRLERYLEFTLLHODA I RHLLRVA AGLESLVLGE GOL	118
Escherichia_coli/1-418	47 L STCNRTELYL SVEEQDNLQEAL I RWLCDYHNLNEEDL RKSLYWHODNDAVSHLMRVASGLDSLVL GEPQIL	118
Methanopyrus_kandleri/1-404	45 LQTCNRVEVYASGARDRAEELGDLIHDDAWVKRGSEAVRHLFRVACGLESMMVGEQEIL	103
Arabidopsis_thaliana/1-543	213 AQVKQVKVGQGVNGFGRNISGLFKHAITVGKRVRTETNIASGAVSVSSAAVELALMKLPQSSNVSARMCVT	284
Hordeum vulgare/1-527	194 A V KO V KI BONS GOL GKNI DAMENDA I TA GKRVR CETNI SA GAVSVSA AVELAMMKI PASECLSA BMILLI	265
Or/za/1-537	204 AQVKQVVRSGQNSGGLGKNIDRMFKDAITAGKRVRCETNISSGAVSVSSAAVELALMKLPKSECLSARMLLI	275
Physcomitrella_patens/1-476	149 AQVKQVLKVGQEVSGFGRNLTGLFKQAITAGKRVRTETNISAGAVSVSSAAVELAVMKLPEGGVSRVNVLIV	220
Chlamydomonas_reinhardtii/1-522	198 AQVRQVYKVGQNCPGFGRHLNGLFKQAITAGKRVRAETSISTGSVSVSSAAVELAOLKLPTHNWSDAKVCII	269
Synechococcus/1-425	119 AQVKAAHKLGQQHKGLGRLLDRMFKRAITAGKRVRSETNIGTGAVSISSAAVELAQMKVKDLSNQKIAII	188
Escherichia_coli/1-418	119 GOVKKAFADSOKGHMKASELERMFOKSFSVAKRVRTETDIGASAVSVAFAACTLARGIFESLS.	188
methanopyrus_kandierv1-404	104 ROVARATORAARLOILDEALKIVFERAINLONKAREEIKISEGAVSIGSAAVELAERELOSLHDKIVLVV	1/3
Arabidopsis_thaliana/1-543	285 GAGKMGKLVIKHLMAKGCTKVVVVNRSEERVSAIREEMPGIEIIYRPLDEMLACASEADVVFTSTASETPLF	356
Triticum_aestivum/1-528	267 GAGKMGKLVVKHLIAKGCKKVVVVNRSVERVDAIREEMKDIEIVYRPLTEMYEAAADANVVFTSTASESLLF	338
Hordeum_vulgare/1-527	266 GAGKMGKLVVKHLIAKGCKKVVVVNRSVERVDAIREEMKDIEIVYRPLTEMYEAAADADVVFTSTASESLLF	337
Oryza/1-537	276 GAGKMGKLVVKHLIAKGCKKVVVVNRSVERVDAIREEMKDIEIVYRPLTEMYEAAAEADVVFTSTASETPLF	347
Physcomitrella_patens/1-476	221 GAGKMSKLLVKHLISKGCTRMTIVNRSEORVLDLOTEFPDANIIYEPLTEMLRCTGESDLVFTSTSSETPLF	292
Chiamydomonas_reinnarduv1-522 Synachococcus/1-425	2/0 GAGMS TLL VALUS KGAEVIVLNKSL VAGALAEE PEVKANINE MPULUG VERADVIVAS OSE TLL	260
Escherichia coli/1-418	189 GAGET I EL VARHEREHKVOKMI I ANR TRERAO I LADEVGAEVIALS DI DERL READI I I SSTASPLPI I	257
Methanopyrus_kandleri/1-404	174 GAGEMGKTVAKSLVDRGVRAVLVANRTYERAVELARDLGGEAVRFD ELVDHLARSDVVVSATAAPHPVI	242
		1
Arabidopsis_thaliana/1-543	357 L KEHVENL PQASPEVGGLRHFVD I SVPRNVGSCVGEVETARVYNVDDL KEVVAANKEDRMRKAMEAOT I I TE	428
Triticum_aestivum/1-528	339 T KEHAEAL PPT SLAMGGVRL FVDT SVPRNVSACL SE VEHARVYNVDDL REVVEANKEDRV RKAMEAQATTT	410
Orrza/1-537		409
Physcomitrella patens/1-476	293 TKENVEPL TPASOTS GOVENFIDIS VPRNVAACLS DLSSTRVYNVDDLKEVVAANKE DREKAADAOVIIDA	364
Chlamydomonas_reinhardtii/1-522	342 H <mark>KEHVEAMSKPS</mark> DVVGSK <mark>R</mark> RFVD I SVPRN I APA I NELEHGI VYNVDDLKEVVAANKEGRAQAAAEAEVLI RE	413
Synechococcus/1-425	261 DRAKLENLDLHTLILIDISVPLNVAADVEEIAGVRLYNVDALKEVVAONQASRRKMAEEAEALLEE	326
Escherichia_coli/1-418	258 GKGMVERALKSR RNOPMLLVDI AVPRDVEPEVGKLANAYLYSVDDLOSI I SHNLAORKAAAVEAETI VAO	327
Methanopyrus_kandleri/1-404	243 HVDDVREALRKRD - RRSPILIIDIANPROVEEGVENIEDVEVRTIDDLRVIARENLERRKEIPKVEKLIEE	313
Arabidopsis thaliana/1-543	429 ESTOFEAWEDSLETVPTIKKL RAYAERIRVAELEKCMSKMG. DDINKKTTRAVDDLSRGIVNRFLHGPMOHL	499
Triticum_aestivum/1-528	411 ELKRFEAWRDSLETVPTIKKLRSYADRIRASELEKCLOKIGEDNLNKKMRRSIEELSTGIVNKLLHGPLOHL	482
Hordeum_vulgare/1-527	410 ELKRFEAW <mark>R</mark> DSLETVPTIKKLRSYADRIRASELEKCLOKIGEDNLNKKMRRSIEELSTGIVNKLLHGPLOHL	481
Oryza/1-537	420 ELKRFEAWRDSLETVPTIKKLRSYADRIRASELEKCLOKIGEDALTKKMRRSIEELSTGIVNKLLHGPLOHL	491
Physcomitrella_patens/1-476	365 E I QN FE AWRDSLETVPT I KKLRSY AERVRQAELEKALSKMP EDLTTKOKRALEDLSRG I VNKLLHGPMOHL	435
Chiamydomonas_reinhardtiv1-522	414 EQRAFEAWROSLETVPTI KALRSKAETI RAAEFEKAVSRLG-EGLSKROL NAVEELSKGI VNKLLHGPMI AL	484
Escherichia coli/1-418	328 ETSEFMAWI RAOSASETI REVESOAEOVROELTAKAI AAI F OGODAOA MODI AWKI TNEL HADTKSI	396
Methanopyrus_kandleri/1-404	314 ELSTVEEELEKLKERRLVADVAKSLHEIKDRELERALRELK TG-DPENVLODFAEAYTKELINVLTSAI	381
		1
Arabidopsis_thaliana/1-543	500 RCDGSDSRTLSETLENMHALNRMYGL EKDILEEKLKAMAEQQQK	543
Hordeum vulgare/1-527	403 NO DOBUSHIL DETLEMMHAL NIMERI DIEKAVLEQKIKAKVEKIQS	528
Or/za/1-537	492 RCDGSDSRTLDETLENMHALNRMFSLDTEKAIIEQKIKAKVEKSQN	537
Physcomitrella_patens/1-476	436 RSDGTDSKTVSETIENMHALERMFDLGSEVLVVETKAKGKK	476
Chlamydomonas_reinhardtii/1-522	485 RCDGTDPDAVGQTLANMEALERMFQLSEVDVAALAGKQ	522
Synechococcus/1-425	398 B AODD I E ARRVCLOSLOML FNLETEEAI	425
Escrieticnia_colv1-418 Methanonyrus_kandleri/1_404		418

Fig. S1. Sequence alignment of Arabidopsis glutamyl-tRNA reductase (GluTR) with Methanopyrus and other homologs. The alignment is colored by conservation.



Fig. S2. Structure comparison of *Methanopyrus kandleri* GluTR (*Mk*GluTR) and *Arabidopsis* GluTR (*At*GluTR). (A) Superposition of the two dimers. (*B*) Superposition of the monomeric halves. *Mk*GluTR is colored gray and *Arabidopsis* GluTR is colored the same as in Fig. 1.



Fig. S3. Alternative conformations of GluTR Arg146. (*A*) Stereo view of the double conformations of Arg146 on chain A of GluTR. The alternative conformation of Arg146 on chain A is displayed together with electron density calculated by using the Fo–Fc coefficient and contoured at 3.0σ as a gray mesh. Arg146 on chain B does not have double conformations. (*B*) Superposition of Arg146 conformations and *Mk*GluTR Arg50. Carbon atoms are colored as indicated, with the glutamate moiety of glutamycin in the *Mk*GluTR structure shown in yellow (O, red; N, blue; S, orange).

	GluTR–GluBP	GluTR-seGluBP*	seGluTR–seGluBP [†]
Data collection			
Space group	P212121	P2 ₁ 2 ₁ 2 ₁	P212121
Cell dimensions			
a, b, c, Å	59.4, 84.8, 360.0	60.0, 84.0, 360.2	60.1, 84.1, 362.0
α, β, γ, °	90, 90, 90	90, 90, 90	90, 90, 90
Wavelength, Å	0.9793	0.9793	0.9793
Resolution, Å [‡]	2.80 (2.90–2.80)	4.20 (4.35–4.20)	3.10 (3.21–3.10)
R _{sym} or R _{merge}	0.104 (0.551)	0.212 (0.529)	0.183 (0.574)
l/σl	17.7 (3.8)	38.7 (15)	12.5 (4.1)
Completeness, %	94.3 (93.4)	100 (100)	99.8 (100)
Redundancy	7.1 (7.5)	25.1 (25.9)	8.4 (8.8)
Refinement			
Resolution, Å	49.56-2.80	—	_
No. reflections	43,245	—	—
R _{work} /R _{free}	0.221/0.272	—	—
No. atoms			
Protein	9,920	—	_
Ligand/ion	0		
Water	47		
β-Factors			
Protein	62.3		
Ligand/ion	None		
Water	31.7		
rmsds			
Bond lengths, Å	0.003		
Bond angles, °	0.969		

Table S1. Data collection, phasing, and refinement statistics for GluTR-GluBP structures

GluBP, glutamyl-tRNA reductase binding protein.

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*Methionines were replaced by selenomethionines in GluBP only. [†]Methionines were replaced by selenomethionines in GluTR and GluBP.

^{*}Values in parentheses are for highest-resolution shell.