Supplemental Data for:

Identification of Two Structural Elements Important for Ribosome-Dependent GTPase Activity of Elongation Factor 4 (EF4/LepA).

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Supplemental Figures



Figure S1: Structural comparison of EF4 and EF-G. The domain arrangement is represented on the left, the corresponding residues within the domain are indicated above the respective domain. Cartoon representations of EF-G from *Thermus thermophilus* (PDB ID 1FNM¹) and EF4 from *Escherichia coli* (PDB ID 3CB4²) are shown on the right. Domains are labelled as domain I (G-domain and G'-domain), domain II, domain IV, domain V and the CTD. The previously unresolved and likely flexible portion of the CTD (residues 556 to 599) is represented as a helix turn helix cartoon based on the recent X-ray crystallographic structure³.



Figure S2: Amplitude of fluorescence change upon binding of mant-nucleotides to EF4. EF4 wild type (\bullet), EF4 \triangle A494 (\blacksquare), EF4 \triangle P520 (\blacktriangle), EF4 \triangle G555 (\diamond) and EF4 H81A (\bigcirc). Concentration dependence of amplitude 1 (a) and amplitude 2 (b) obtained from fluorescence time courses for mant-GTP and amplitude 1 (c) and amplitude 2 (d) obtained for mant-GDP association.



Figure S3: **Immunodetection of EF4 bound to the ribosome following ultracentrifugation.** (a) EF4 proteins (2 μM) (indicated on top) bound to the 70S (0.1 μM) ribosome in the presence of various guanine nucleotides (GTP, GDPNP, GDP (0.1 mM)) or *apo* indicated on the left. Pellet following ultracentrifugation of EF4 proteins bound to GDPNP in the absence of ribosome is shown (No Rb). (b) EF4 proteins (2 μM) bound to the 50S (0.1 μM) subunit in the presence of various guanine nucleotides (GDPNP, GDP (0.1 mM)) or *apo*. (c) EF4 proteins (2 μM) bound to the 30S (0.1 μM) subunit in the presence of various guanine nucleotides (GDPNP, GDP (0.1 mM)) or *apo*. (d) EF4 H81A (2 μM) bound to the 70S (0.1 μM) in the presence of various guanine nucleotides (GDPNP, GDP (0.1 mM)) or *apo*. (d) EF4 H81A (2 μM) bound to the 70S (0.1 μM) in the presence of various guanine nucleotides (GDPNP, GDP (0.1 mM)) or *apo*. (d) EF4 H81A (2 μM) bound to the 70S (0.1 μM) in the presence of various guanine nucleotides (GDPNP, GDP (0.1 mM)) or *apo*. (d) EF4 H81A (2 μM) bound to the 70S (0.1 μM) in the presence of various guanine nucleotides (GDPNP, GDP (0.1 mM)) or *apo* indicated on top. (e) EF4 ΔG555 protein (10 μM) bound to the 70S, 50S and 30S (0.1 μM) in the presence of GDPNP (0.1 mM)).



Figure S4: Michaelis-Menten titration of 70S ribosome stimulated GTPase activity of EF4 Δ G555. Initial rates of GTP hydrolysis are plotted as a function of increasing 70S ribosome concentration in the presence of (0.01 µM) EF4 Δ G555.



Figure S5: Michaelis-Menten titration of 50S ribosome subunit stimulated GTPase activity of EF4. Initial rates of GTP hydrolysis are plotted as a function of increasing 50S ribosome concentration in the presence of (0.01 μ M) EF4 wild type (\bullet), EF4 Δ A494 (\blacksquare), EF4 Δ P520 (\blacktriangle), EF4 Δ G555 (\diamond).

Supplemental Tables

Table S1: Summary of dissociation rate constants determined for mant-GDP and mant-GTP fromEF4.

	EF4	ΔΑ494	ΔΡ520	ΔG555	H81A
<i>k_{off1(GDP)}</i> y-int (s ⁻¹)	11 ± 2	8 ± 3	13 ± 1	9 ± 2	8 ± 2
$k_{off1(GTP)}$ y-int (s ⁻¹)	32 ± 3	39 ± 3	51 ± 3	76 ± 6	46 ± 6
$k_{off2(GDP)}$ (s ⁻¹)	8 ± 2	4 ± 2	10 ± 2	3 ± 2	4 ± 2
$k_{off2(GTP)}$ (s ⁻¹)	2.4 ± 1.5	1.0 ± 0.5	1.4 ± 0.6	7.2 ± 3.8	0.5 ± 0.4

Table S2: 50S ribosome dependent GTPase activity of EF4 and three truncation variants.

K _M (μΜ)	<i>v_{max}</i> (µM s⁻¹)	k_{cat} (s ⁻¹)	<i>k_{cat}</i> /K _M (s ⁻¹ μM ⁻¹)
0.6 ± 0.1	0.0035 ± 0.0003	0.4 ± 0.1	0.7 ± 0.2
3 ± 2	0.008 ± 0.003	0.8 ± 0.3	0.3 ± 0.2
>1	>0.006	>0.6	NA
>1	>0.001	>0.1	NA
	K _M (μM) 0.6 ± 0.1 3 ± 2 >1 >1	K_{M} (µM) v_{max} (µM s ⁻¹) 0.6 ± 0.1 0.0035 ± 0.0003 3 ± 2 0.008 ± 0.003 >1>0.006>1>0.001	$K_{\rm M}$ (µM) v_{max} (µM s ⁻¹) k_{cat} (s ⁻¹) 0.6 ± 0.1 0.0035 ± 0.0003 0.4 ± 0.1 3 ± 2 0.008 ± 0.003 0.8 ± 0.3 >1>0.006>0.6>1>0.001>0.1

Sequence Alignment

Sequences (SwissProt) and Organisms used in the EF4/LepA multiple sequence alignment

Accession Number	Organism	Seq. identity to <i>E. coli</i> (%)
P60785	Escherichia coli	· · ·
Q9X1V8	Thermotoga maritima	50
Q72KV2	Thermus thermophilus	55
A0RIT7	Bacillus thuringiensis	56
C3P8M5	Bacillus anthracis	55
P37949	Bacillus subtilis	56
Q65H50	Bacillus licheniformis	56
A6QHC7	Staphylococcus aureus	54
C1CKU6	Streptococcus pneumoniae	54
Q5M4M2	Streptococcus thermophilus	56
Q831Z0	Enterococcus faecalis	56
Q03QU8	Lactobacillus brevis	53
Q03FQ4	Pediococcus pentosaceus	53
Q14NN1	Spiroplasma citri	53
A7FXL9	Clostridium botulinum	55
A6L744	Bacteroides vulgatus	53
A6LC18	Parabacteroides distasonis	52
Q2S5I1	Salinibacter ruber	53
A5U598	Mycobacterium tuberculosis	52
I7G5I5	Mycobacterium smegmatis	48
Q82BZ3	Streptomyces avermitilis	48
Q9Z8I4	Chlamydia pneumoniae	50
Q823H7	Chlaymydophila caviae	49
Q9PKX6	Chlamydia muridarum	49
P60788	Shigella flexneri	100
P0A1W5	Salmonella typhi	96
A4TKY0	Yersinia pestis	92
Q6LMS0	Photobacterium profundum	83
Q3IDL4	Pseudoalteromonas haloplanktis	75
Q0VP16	Alcanivorax borkumensis	74
A9KF98	Coxiella burnetii	71
Q87C09	Xylella fastidiosa	67
A91119	Bordetella petrii	66
B9J716	Agrobacterium radiobacter	57
B9JYH0	Agrobacterium vitis	55
Q8UIQ2	Agrobacterium tumefaciens	57
Q6G1F5	Bartonella quintana	56
Q0C5X0	Hyphomonas neptunium	56
Q5NLP5	Zymomonas mobilis	59
Q5FHQ1	Ehrlichia ruminantium	51
A8F140	Rickettsia massiliae	56
C4XND4	Desulfovibrio magneticus	60

Multiple Sequence Alignment of the C-terminal domain of EF4/LepA. Black indicates 100%, dark grey 80 - 100%, light grey 60 - 80% and white < 60% conservation. The start of the *E. coli* CTD is indicated (red arrow).

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		520 *	54	0 *		560	*	580) 	*	600		*	620	*	(640	*	6	60	*	
P60785	: ITYEIP	MAEVVIDFFDRLKS	TSRGYASLD	YNFKRFQASDM		INGERVDALA	LITHRON	SQNRGRE	DVEKM K	DLIPRQQ	FDIAIQA/	AIGTHIIA	RSTVKQLF	R <mark>KNV</mark> LAKC	YGGDISR	KKKLLQKÇ	2K <mark>E</mark> GKKR	MKQIGNV	ELPOEAFI	LAILHV	GKDNK	: 599
Q9X1V8	: IREDAP	AFTTYDFISDRMKA	VSRGYASMD	YEFKEYRRSDL	VKVIII	NKEPVDALS	FIVHRSK	AYQMARI	KIVEKI K	DLIPRHO	POIFIQAE	KAGGRIIA	RADIKALI	RKDVLAKC	YGCDVTR	KMKLLEK(OKEGKKK	IREIGR	TIPQEAFI	AIIKI	GGEDEK	: 621
Q72KV2	: IVYEAP	FAEILYDFHDRLKS	VSRGYASMD	YEQIGYRPGDL	VKVNVL	HGEVVDALI	FIAHREK	AYTMAR	AIVDKIA	EVIPRQI	FEVEIQA	AIG <mark>GKII</mark> A	RATVKALF	R <mark>KDVL</mark> AKC	YGGDVTR	KKKLLEK	OKEGKKR	IKAICKV	EVPQEAF1	AVISA	GRDEPKG	: 610
AORIT7	: LTYEIP	ISEIVYDFFDQLKS	NTKGYASFD	YELIGYKPSKL	VKMDIL	IN <mark>SEQ</mark> VDALS	FIVHRDS	AYDRGK	TAERT R	ELIPRQC	FEVFIQAT	I GNKVVA	RSTIKAME	R <mark>KNV</mark> IAKC	YGGDISR	KRKLLDK(2K <mark>E</mark> GKKR	MKSVGSV	EVPQEAFI	MAVIKM	DDN	: 607
C3P8M5	: LTYEIP	LSEIVYDFFDQLKS	NTKGYASFD	YELIGYKPSKL	VKMDIL	IN <mark>SEQ</mark> VDALS	FIVHRDS	AYDRGK	TAERT KI	ELIPRQ	FEVFIQAT	IGNKVVA	RSTIKAMP	R <mark>KNV</mark> LAKC	YGGDISR	KRKLI <mark>d</mark> k(QK <mark>E</mark> GKKR	MKSVGSV	EVPQEAFI	MAVIKM	DDN	: 607
P37949	: IIYDMP	TAEIVYEFEDQIKS	STKGYASFD	YELIGYKPSKL	VKMDIM	INGEKIDALS	FIVHRDY	AYERGK	TVERLK	ELI PRQ <mark>Ç</mark>	FEVEVQA1	AIG <mark>QKIV</mark> A	RSTIKAME	RKNVLAKC	YGCDISR	KRKLLEK	QKEGKRR	MKQVCSV	EVEQEARI	MAVIKM	DDSPKKQ	: 612
Q65H50	: IVYEIP	TAEIVYEFFDQLKS	NTKGYASFD	YELIGMEPSEL	VKMDIM	INGEKIDALS	FIVHRDY	AYERGK	VIVERIK	ELI PRQ <mark>Ç</mark>	FEVEVQA2	AIGTKIVA	RSTIKAME	R <mark>KNV</mark> LAKC	YGCDISR	KRKLLEK(OKEGKRR	MKQVCSV	EVPQEAFI	MAVIKM	DDSGPKS	: 612
A6QHC7	: IVYELP	LAEVVFDFFDQLKS	NTKGYASFD	YEFIENKESNL	VKMDIL	NGDKVDALS	FIVHRDF	AYERGK	IVEKIK	TLIPRQC	FEVEVQA	AIG <mark>QKIV</mark> A	RTNIKSMO	SKNVLAKC	YGGDISR	KRKLLEK	OKAGKAK	MKAVGNV	(EIPQDAFI	AVIKM	DDE	: 607
CICKU6	: AIXÖID	LADIVFOFFORLKS	STRGYASFD	YELSEYRPSKL	VKMD I III	ING <mark>DR</mark> VDALS	FIVHKDF	AYERGKI	TADETK	KIIPRQC	FEVEIQAA	AIGHKIVA	RTDIKALI	RKNVLAKC	YGCDVSR	KRKLLEK	QKAGKKR	MKSICSV	EVEQEAR	SVISM	DEE	: 607
Q5M4M2	: VIYQIP	LAEIVFDFFDKLKS	STRGYASFD	YELSEYRRSQL	VKMDIII	INGDRVDALS	FIVHREF	AYERGKI	TVDKLK	KII PRQQ	FEVEIQA	AIGQKIVA	RTDIKALF	RKNVLAKC	YGCDVSR	KRKLLEK	QKAGKKR	MKAICSV	EVEQEARI	SVISM	DEDEK	: 610
Q831Z0	: VVYEIP	ISEIVFDFFDKLKS	STKGYASLD	YEMAGYRTSRI	VKMDIL	IN <mark>AEK</mark> VDALS	FIVHRDF	AFERGK	AIVERLK	KLI PRQ <mark>Ç</mark>	IF EVEVQA2	AIG <mark>QKIV</mark> A	RSDIKALF	RKNVLAKC	YGCDVSR	KRKLLEK	OKEGKKR	MKQICSV	EVPOEAFI	MAVIKM	DDQDNAK	: 611
Q03QU8	: IIYNMP	ISELIFDFFDKLKS	NTRGYASLD	YEMNG YQGADL	VKIDIL	NG <mark>DK</mark> VDALS	FIAHRTF	APARGRI	TASRIK	KIIPRQN	FEIFVQAA	AIC <mark>AKII</mark> A	RTTIKAYF	RKDVTAHL	YGGDRTR	RMKLLEK	OKAGKKR	MKAVCKV	DIPQEAFI	MAVIQT	DEDETK	: 610
Q03FQ4	: VKYALP	ISELLEDFEDRIKS	STRGYASLD	YELGEYKVSDL	VKIDIL	INGERVDALS	FISHRDF	AQQRGNI	TASI KI	EIIPRRN	FEIEVQAA	AIG <mark>NKII</mark> A	RTNIRAY	RKDVTSKI	HIGDPDR	RAKLLDK	QKRGKKR	MKSVCKV	EVPQEAFI	TVIKT	DTEGKGGK	: 613
Q14NN1	: LTYEMP	INELVEVEEDRIKS	ISKGYASLD	YDFIGYRPNKL	VKND I III	INNEIIDALS	IIVHRDF	AYGRGK	ALCAKLK	EIIIRQN	FEVEIQA	AT <mark>NHKUTA</mark>	REDIKAME	RKNVLAKC	YGCDITR	KKKLLEK(QKEGKKR	MKAICSV	EVEQEAR	MAVIKI	DD	: 600
A7FXL9	: INYELP	INETIYDFEDALKS	RTRGYASFD	YELIGYKDADI	VKLDIL	N <mark>ADV</mark> VDALS	MIVPRER	AYAKGRI	MAQKLK.	EIIPRQM	FEIFIQA <i>l</i>	AVCARIIA	RETIKAME	RKDVLAKC	YGGDISR	KRKLLEK(QKEGKKR	MRQVCSV	EVPOEAFI	MAVIKI	EE	: 602
A6L744	: IHYKMP	IGEIVIDEYDKLKS	ISKGYASFD	YHQSGFRPSKL	VKLDIL	NGEPVDALS	TITEVDN	AYNLGKI	RMCEKIK.	ELIPRQC	FDIAIQAA	AIGARIIS	RETIKAVE	RKDVTAKC	YGGDVSR	KRKLLEKÇ	RGKKR	MKQIGNV	EVPOKAFI	AVIKL	D	: 593
A6LC18	: IHYDLP	IGEIVIDFYDKLKS	ISKGYASFD	YHLHDFRPSKL	AKIDIII	NGEPVDALS	TTTHVDN	SVTFGRI	RMCEKLK	ELIPRQC	FDIAIQAA	AIGAKIIA	RETIKAVI	RKDVTAKC	YGCDISR	KRKLLEKÇ	REGKKR	MKQICTV	EVPOKAFI	AVIKI	D	: 595
Q2S5I1	: LEYELP	LADIVEDFYDNLKS	ASRGYASFD	YELLEYRESDL	VKLTIL.	DEKPAEPIS	TIVHRDS	AHEVGRI	KLAKKLK.	DVIPRQI	YEVEVQAS	SIGSRIVA	RETIKAQI	RKDVIAKC	YGGDVSR	KKKLLE <mark>E</mark> (QKEGKKR	MKQMGEI	DVPQEAFI	AILSV	DED	: 604
A50598	: LRYIMP	LGELLFDFFDALKS	RTRGYASID	YEEAGEQEAAL	VKVDIL	QGEAVDAFS	AIVHKDT	AYAYCNI	KNTTKLK.	ELLPRQC	FEVEVQAA	AIGSKLLA	RENIRAII	RKDVLSKC	YGGDITR	KRKLLEKÇ	REGKKR	MKTIGRV	EVPOEAF	VAALST	DAAGDKGKK	: 653
17G515	: IRYIMP	IGEIIFDEFDSIKS	RIRGYASID	YEEAGEQEADL	VKVDIL	QGEAVDAFS	AIVHKDG	ASAYCNI	KNTSKIK	ELIPRQC	FEVEVQA	AIG <mark>SRII</mark> A	RENIRAII	RKDVLSKC	YGGDITR	KRKLLEK	REGKKR	MKTIGRV	DVPQEAF	VALIST	DAAGDKPKK	: 658
Q82BZ31	: IRYILP	LAELVEDEEDQLKS	KIRGYASLD	MEPTGEQASSI	VKVDIL.	HGDKVDAFS	ATTERDA	AYAYEVI	KEVAKER.	ELL PRQA	EVPIQAA	ALGSRVIA	RETIRAL	RKDVLAKC	YGGDISR	KRKLLEKÇ	REGKER	MKM VC SV	EVPQEAF.	AVISS	DDSGGSAKGKK	: 622
Q92814	: LAYEL P	INELVSDENDKLKS	VIKGYGSFD	YRLGDYRKGSI	TKTEAT	INEEPIDAFS	CUVHRDK	AESRGR	SICEKIV.	DATEOOT	FKIFIQAA	AT <mark>NKKVI</mark> A	RETIRALS	SKNVIAKC	YGGDITR	KRKLWEKÇ	RKGKKR	MKEFCK	SIPNTAF.	LEVIKI	D	: 602
Q823H71	: LSYDLP	LNEIVSDENDKLKS	VIKGYGSFD	YRLGDYRKGSI	TKTETT	INDEPVDAFS	CUVHRDK	AEARGR	SICEKIIV.	DATEOOT	EKTETŐA4	AT <mark>NKKVI</mark> A	RETIRALS	SKNVIAKC	YGGDITR	KRKLWEKÇ	CKKGKKR	MKEFGKV	SIPNTAF.	LEVIKI	D	: 602
Q9PKX61	: LSYELP	INELVSDENDKLKS	VIKGYGSFD	YRLGDYKPGAI	TRUELL	INDETVDAFS	CLVHRDK	AESKGR	SICERLV.	DATEBÖT	FKIFIQAA	ALNKKLLA	RETIRAL	AKNVIAKC	YGGDITR	KRKLWEKÇ	KKGKKR	MREFCR	SIPNIAR	VEVI KO	E	: 602
P607881	: LIYEIP	MAEVVLDEFDRLKS	ISRGYASLD	YNFKREQASDM	VRVDVL.	INGERVDALA	LITHRDN	SQNRGRI	OLVEKNK	DLIPRQQ	IEDIALQA/	AIG <mark>THII</mark> A	RSTVKQLE	RKNVLAKC	YGGDISR	KKKLLQKÇ	REGKER	WKÖTCN	ELPOPARI	JALLHV	GKDNK	: 599
PUAIW5	: LTYEIP	MAEVVLDEFDRLKS	TSRGYASLD	YNFKREQASDM	VRVDVL.	INNERVDALA	LITHRDN	SQSRGRI	OLVEKNK.		FDIALQA/	AIGTHLIA	RSTVKQLE	RKNVLAKC	YGGDISR	KKKLLQKÇ	CKEGKKR	WKÖTCN	ELPOPARI	ALLHV	GKDNK	: 599
A4TKYU	: LIYELP	MAEVVLLEFDRLKS	TSRGYASLD	YNFKREQTSDM	VRVLVL.	INNERVDALA	LITHRDN	AQYRGRI	LVERMK	PLIPRQC	FDIAIQAA	AIGNHIIA	RSTVKQLE	RKNVLAKC	YGGDVSR	KKKLLQKÇ	KUGKKR	MKQVGNV	ELECEAFI	ALLHV	GKDSK	: 599
QOLMSUI	TITT	MSEVVILLEFLRIKS	TSRGIASLD	INFORTEPSNA	VRVI VM.		TTTHERDE	ANGRGRI		EFIPRON		AIGGMIIA	RATVKOLF	RKNVLAKC	YGGDISR	KKKLLQKQ	AGAAR	MNQIGN	ELFORAFI		GKK	: 597
Q3IDL4	TTYPELP	MAEVVMUFFUKLKS	TSRGFASLD	YNFKHFQTSDA	VRVDIL.	INSERVUALA	MICHINO	AQSEGE	JEADALK.	ELL PROM		AIGGHVIA	RTTIKOME	RKNVIAKC	YCCDVSR	KKKLLKK	CURCERNE	MKQVGNV	EVPOBAF1	ALLKV	GR	: 596
QUVPI6	TTTLP	MAEVVILLFEDRIKS	VSRGPASMD	TAFERTEATRE	VRVDVL.		MICHLDO	SAIRGRA		PLVPRQR		AIGSKIIA	ROTVRAL	RKNVTAKC	IGGDVSR	KERTT DE	NEGRAR		EIFCEAFI		DD	: 599
0970001	· WITLE	TSEVVILLEEDRINS MARVITERENZIZO	MERCYA CLD	NUEL DE ORCOR		NCDRUDALA		ATTRON					RISVIALI	NNVIANC	YCCDICR				ALPOPARI		DNK	. 602
	TIME	TARTUT REPAIRS	VIRGIASLU	HILL EXPOLUTE	VEVIDEL.	NGDRVDALS	VI VIII II O	ADVDADI					ROT VIADI	REN VIANC	VCCDIM				E I POPAFI		DNK	. 602
A91119	· ITTLLP	TAFIVEDFEDRENS	TCKCYACED	TEFLEIRSADV	VEVELL	NGDRVDALA	MUVERAN	ARIKARI	NOFETE			AIGAEVIA	RENVEALE	RENVEACC	VCCDACE	VDVTT DV		MROTON	EIPOEAFI		CDE	. 610
B50710	· IIIDIE	INEVVEDE IDRENS	TCKCYACED	NULDCUKECNI		NCEPUDALE	MAXING MA	AFKRON	MORVIN			TCCNVIA	REI VRALL	RDVIARC	VCCDACR			MROFERN	EIPOEAF.		GDE	. 625
09010021	· IIIEF	INEVVEDE IDALAS	TORCANORD	MILDORREGNI		NCDDUDALS		ADDRCD	NORVIN				REI ISALL	RDVIARC	VCCDAD			MDODOZN	EIPOPAR.		NDE	. 600
0601021	· ITTELP	INEVVEDE IDALAS	TCKCVACED	NITDIREGUL		NCESTDALS		ADRIGIC	MORETE			ALGGRVIA	DETTRAL	REVIARC	VCCDVMP			MPOPCEN	EIFCEAF.		S	. 600
Q0G1F5	· VENELD	INEVVEDENDRUNG	TOPCVACED	A TTTCHPARM	VETOTE	NEEDUDALS	MININT	AFGPCD			TRATETON	TCCPVPA	DETTRAL	PKDUTAKC	VCCDATE	KD KT T DE	AACKER	MPORCEN	TDODARY		DCD	. 604
OSNUDE	• TTYPT	TNEVVEDETDKLAS	TCDCVACEB	NHOTONPECT	VZNUTN	NCEWNDAL	MTUHDUA	AFCPOR	NCOP NE		PRIPION	TCCKVTA	DETTOAM	PKDUTAKC	VCCDICR	KKKTT PK	MECKED	MPOVCC	DIDODAR		CDDS	. 602
058401	- TRYPT D	INCOMPLETING AND A SERVICE AND	TSKCVASTB	NEMDGYMDEET	ARTTIT	INSE DUDALA	CTVHKCK	VEORCE	TCTRIK		VKTATOA	WCCKTIA	BETISEN	REVIANC	VCCDVTR	RMRTTER	REGENER	TRATON	NVEHNAR		TD	. 502
23F121	· TTYRE	T NETWYDEYDE 10A1AS	CSKCVAST	NONDVYEDEET	VELCTI	NAFAVDALA	TTVHPOD	PORCE	AT CURTER		TDTATOA	MCSPTIA	RETISPII RETISPII	RKDVLSKC	VCCDTCP	RENTIER		MROYOM	FTDOSAT		CDF	. 590
C4XND4	· TTYETD	FARTWYDEEDPIKS	ATRCVAST	VETVOVBAGOT	VKTDTM		VIVHREN	AVHYCR	ATATRI	RVTDROT	JE TO TO A	ATCTRTTA	BERNADUC	KNVTAKC	YCCDIER	KRKTIEK	RECKER	MERMONT	FT.DOFAR		GDD	· 6004
CIVUDAI	65 p	F66 dF D 6Ke	3465a8 d		46 6	6 del	6 h	а (1 атитери	6 6	6n a	6 603	a a 66a	R	rK1V akc	VaGD R	4 KT.1 FC	ok GK 4	64 G 6	6Pg AF	Ga T.	000	. 000
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References

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