wwPDB X-ray Structure Validation Summary Report (i)

Oct 24, 2023 – 07:59 PM EDT

PDB ID	:	3E20
Title	:	Crystal structure of S.pombe eRF1/eRF3 complex
Authors	:	Cheng, Z.; Lim, M.; Kong, C.; Song, H.
Deposited on	:	2008-08-05
Resolution	:	3.50 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

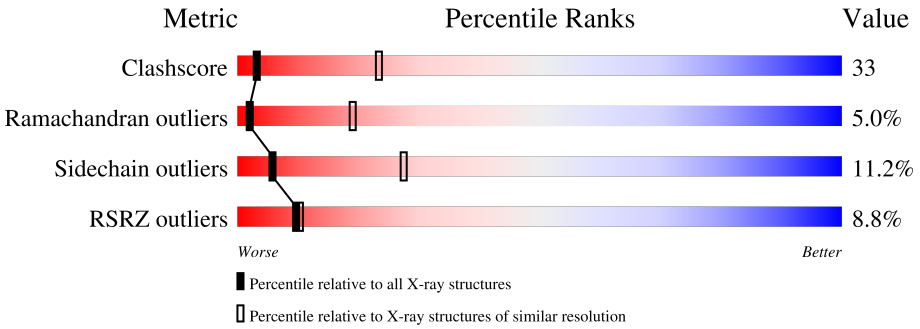
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)
RSRZ outliers	127900	1559 (3.60-3.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	201	11% 53% 38% 6%
1	D	201	12% 51% 39% 6%
1	E	201	5% 42% 43% 12%
1	J	201	6% 43% 44% 10%
2	B	441	4% 32% 21% 5% 41%
2	C	441	4% 33% 20% 41%
2	H	441	5% 22% 14% 60%

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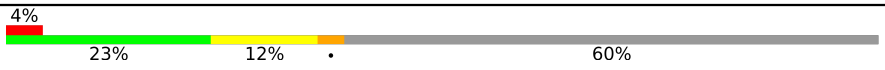
Mol	Chain	Length	Quality of chain
2	K	441	

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 13096 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Eukaryotic peptide chain release factor GTP-binding subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	196	Total	C	N	O	S	0	0	0
			1524	965	256	293	10			
1	D	196	Total	C	N	O	S	0	0	0
			1524	965	256	293	10			
1	E	196	Total	C	N	O	S	0	0	0
			1524	965	256	293	10			
1	J	196	Total	C	N	O	S	0	0	0
			1524	965	256	293	10			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	462	GLY	-	expression tag	UNP O74718
A	463	PRO	-	expression tag	UNP O74718
A	464	LEU	-	expression tag	UNP O74718
A	465	GLY	-	expression tag	UNP O74718
A	466	SER	-	expression tag	UNP O74718
D	462	GLY	-	expression tag	UNP O74718
D	463	PRO	-	expression tag	UNP O74718
D	464	LEU	-	expression tag	UNP O74718
D	465	GLY	-	expression tag	UNP O74718
D	466	SER	-	expression tag	UNP O74718
E	462	GLY	-	expression tag	UNP O74718
E	463	PRO	-	expression tag	UNP O74718
E	464	LEU	-	expression tag	UNP O74718
E	465	GLY	-	expression tag	UNP O74718
E	466	SER	-	expression tag	UNP O74718
J	462	GLY	-	expression tag	UNP O74718
J	463	PRO	-	expression tag	UNP O74718
J	464	LEU	-	expression tag	UNP O74718
J	465	GLY	-	expression tag	UNP O74718
J	466	SER	-	expression tag	UNP O74718

- Molecule 2 is a protein called Eukaryotic peptide chain release factor subunit 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	261	Total	C	N	O	S	0	0	0
			2088	1321	347	405	15			
2	B	261	Total	C	N	O	S	0	0	0
			2088	1321	347	405	15			
2	H	175	Total	C	N	O	S	0	0	0
			1412	900	225	277	10			
2	K	175	Total	C	N	O	S	0	0	0
			1412	900	225	277	10			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-7	MET	-	expression tag	UNP P79063
C	-6	HIS	-	expression tag	UNP P79063
C	-5	HIS	-	expression tag	UNP P79063
C	-4	HIS	-	expression tag	UNP P79063
C	-3	HIS	-	expression tag	UNP P79063
C	-2	HIS	-	expression tag	UNP P79063
C	-1	HIS	-	expression tag	UNP P79063
C	0	MET	-	expression tag	UNP P79063
B	-7	MET	-	expression tag	UNP P79063
B	-6	HIS	-	expression tag	UNP P79063
B	-5	HIS	-	expression tag	UNP P79063
B	-4	HIS	-	expression tag	UNP P79063
B	-3	HIS	-	expression tag	UNP P79063
B	-2	HIS	-	expression tag	UNP P79063
B	-1	HIS	-	expression tag	UNP P79063
B	0	MET	-	expression tag	UNP P79063
H	-7	MET	-	expression tag	UNP P79063
H	-6	HIS	-	expression tag	UNP P79063
H	-5	HIS	-	expression tag	UNP P79063
H	-4	HIS	-	expression tag	UNP P79063
H	-3	HIS	-	expression tag	UNP P79063
H	-2	HIS	-	expression tag	UNP P79063
H	-1	HIS	-	expression tag	UNP P79063
H	0	MET	-	expression tag	UNP P79063
K	-7	MET	-	expression tag	UNP P79063
K	-6	HIS	-	expression tag	UNP P79063
K	-5	HIS	-	expression tag	UNP P79063
K	-4	HIS	-	expression tag	UNP P79063
K	-3	HIS	-	expression tag	UNP P79063
K	-2	HIS	-	expression tag	UNP P79063

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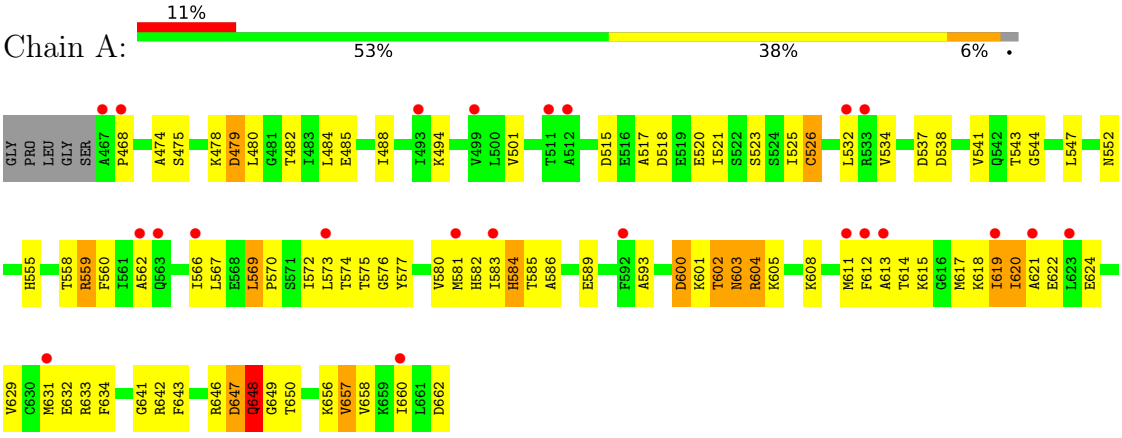
Chain	Residue	Modelled	Actual	Comment	Reference
K	-1	HIS	-	expression tag	UNP P79063
K	0	MET	-	expression tag	UNP P79063

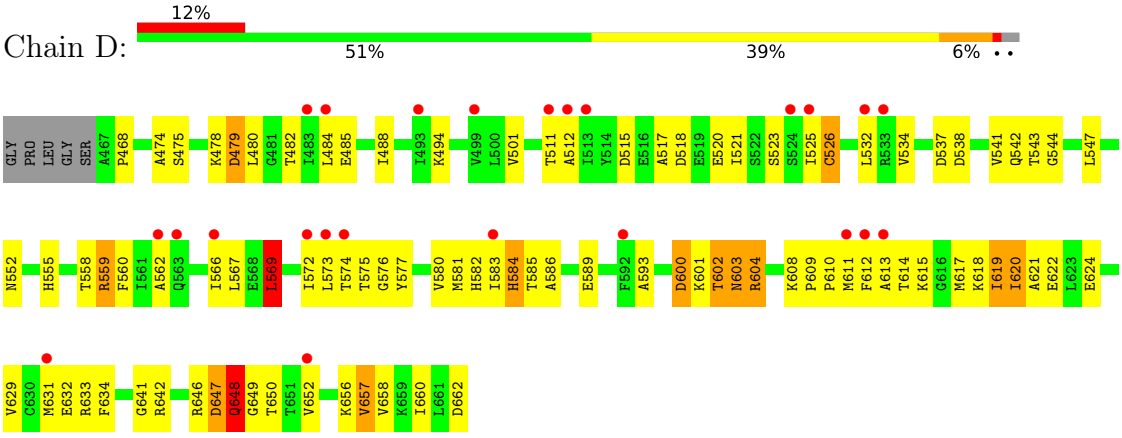
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

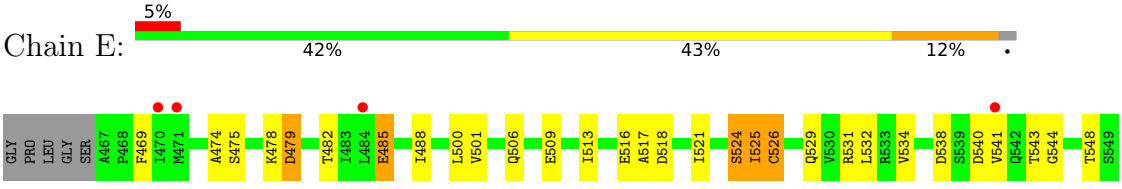
• Molecule 1: Eukaryotic peptide chain release factor GTP-binding subunit

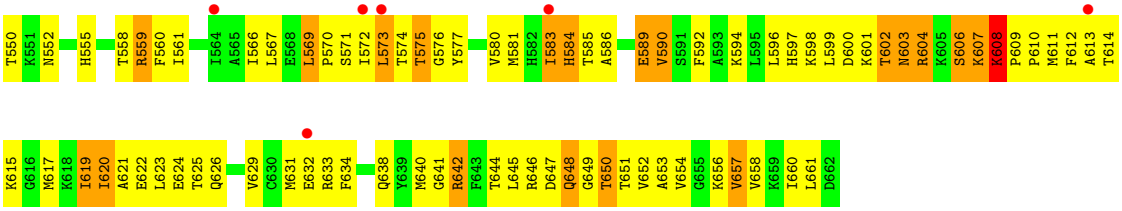


• Molecule 1: Eukaryotic peptide chain release factor GTP-binding subunit



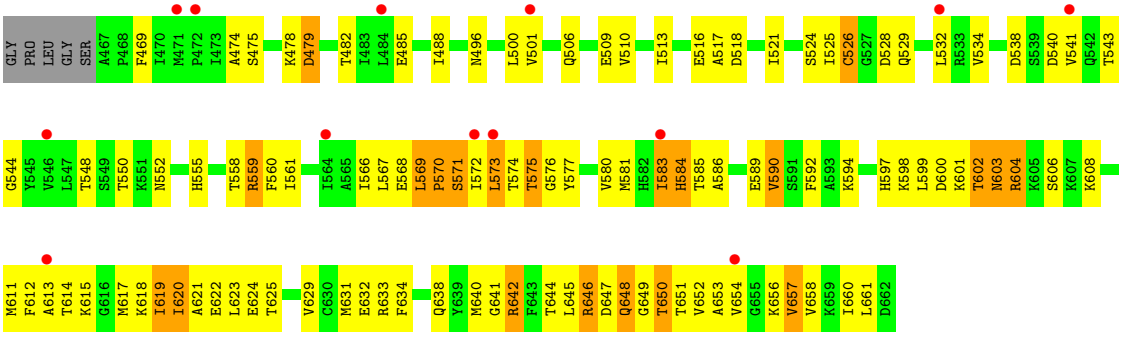
• Molecule 1: Eukaryotic peptide chain release factor GTP-binding subunit





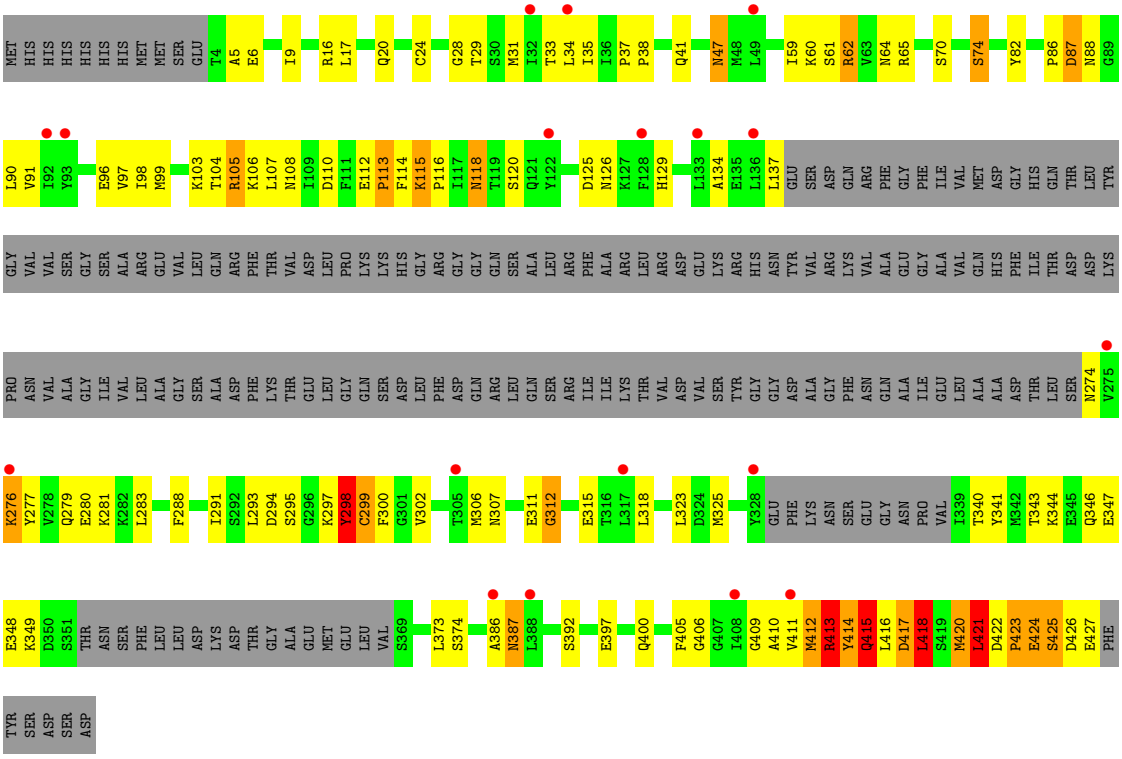
• Molecule 1: Eukaryotic peptide chain release factor GTP-binding subunit

Chain J:



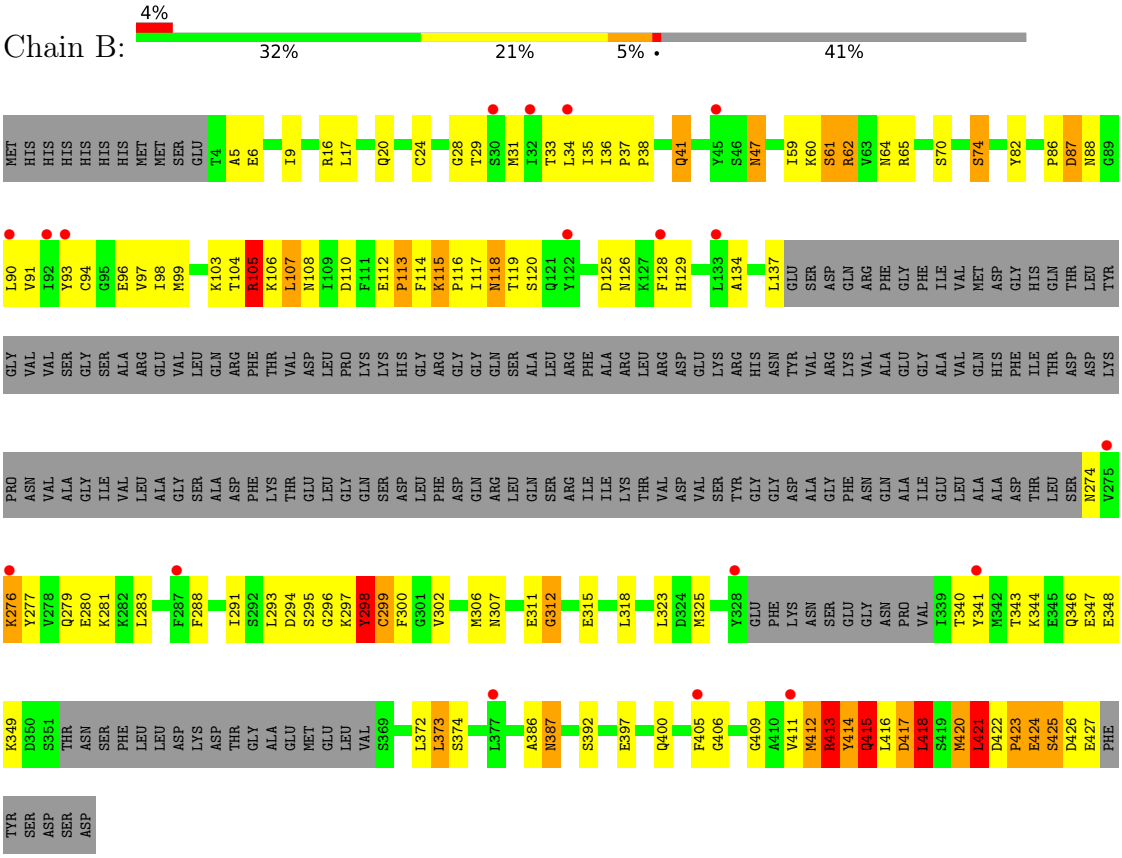
• Molecule 2: Eukaryotic peptide chain release factor subunit 1

Chain C:



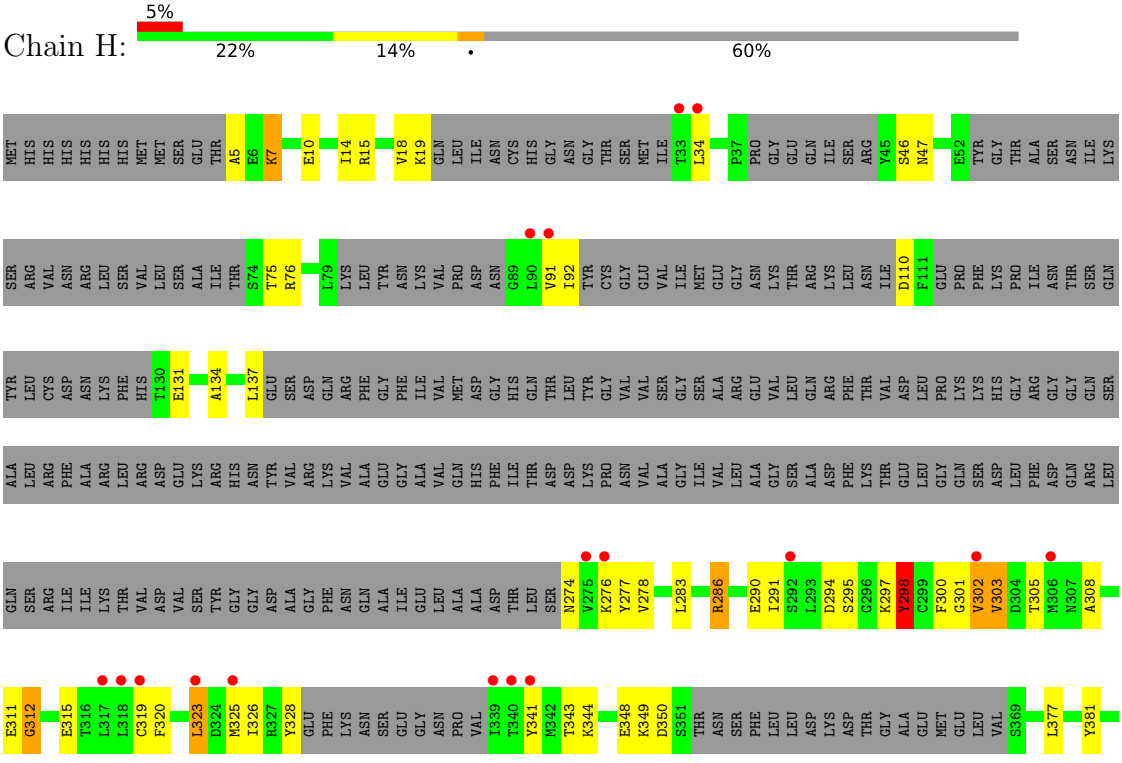
• Molecule 2: Eukaryotic peptide chain release factor subunit 1

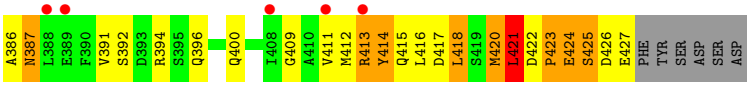
Chain B:



• Molecule 2: Eukaryotic peptide chain release factor subunit 1

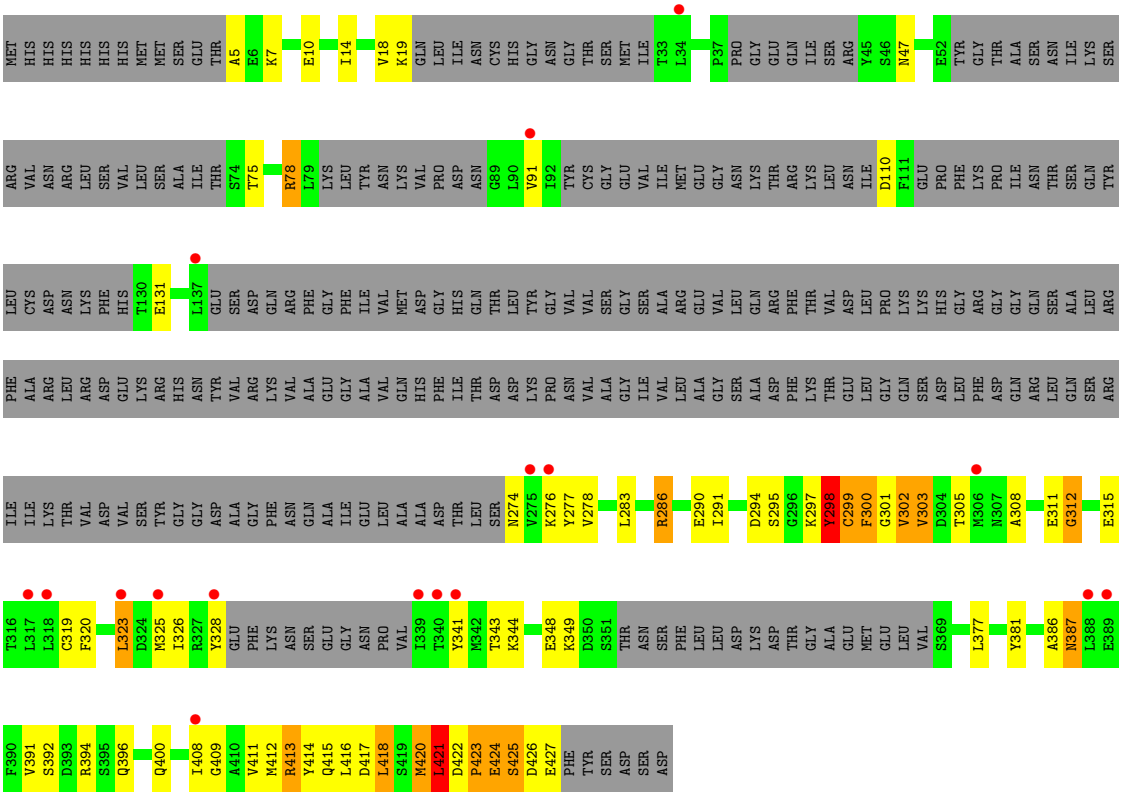
Chain H:





• Molecule 2: Eukaryotic peptide chain release factor subunit 1

Chain K:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α, β, γ	129.85Å 129.85Å 332.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 3.50 88.51 – 3.50	Depositor EDS
% Data completeness (in resolution range)	99.7 (30.00-3.50) 99.7 (88.51-3.50)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.43 (at 3.49Å)	Xtriage
Refinement program	REFMAC 5.4.0077	Depositor
R, R_{free}	0.258 , 0.280 0.283 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	123.7	Xtriage
Anisotropy	0.046	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 115.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	0.439 for h,-k,-l	Xtriage
F_o,F_c correlation	0.88	EDS
Total number of atoms	13096	wwPDB-VP
Average B, all atoms (Å^2)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.25% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.36	0/1547	0.57	1/2089 (0.0%)
1	D	0.36	0/1547	0.55	0/2089
1	E	0.49	0/1547	0.63	1/2089 (0.0%)
1	J	0.48	1/1547 (0.1%)	0.65	1/2089 (0.0%)
2	B	0.34	0/2119	0.61	6/2848 (0.2%)
2	C	0.34	0/2119	0.63	7/2848 (0.2%)
2	H	0.34	0/1425	0.55	1/1901 (0.1%)
2	K	0.34	0/1425	0.56	1/1901 (0.1%)
All	All	0.38	1/13276 (0.0%)	0.60	18/17854 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	D	0	2
1	E	0	3
1	J	0	1
2	B	0	1
2	C	0	1
2	H	0	1
2	K	0	1
All	All	0	12

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	646	ARG	CB-CG	-5.26	1.38	1.52

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	K	413	ARG	NE-CZ-NH2	9.76	125.18	120.30
2	B	105	ARG	CG-CD-NE	8.50	129.65	111.80
2	C	413	ARG	NE-CZ-NH2	-8.02	116.29	120.30
2	C	413	ARG	NE-CZ-NH1	7.61	124.11	120.30
2	B	413	ARG	NE-CZ-NH1	-7.29	116.66	120.30

There are no chirality outliers.

5 of 12 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	569	LEU	Peptide
1	A	647	ASP	Peptide
2	C	413	ARG	Peptide
1	D	569	LEU	Peptide
1	D	647	ASP	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1524	0	1569	89	0
1	D	1524	0	1569	92	0
1	E	1524	0	1569	117	0
1	J	1524	0	1569	104	0
2	B	2088	0	2077	144	0
2	C	2088	0	2077	133	0
2	H	1412	0	1388	117	0
2	K	1412	0	1388	86	0
All	All	13096	0	13206	878	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 33.

The worst 5 of 878 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:425:SER:CB	2:B:426:ASP:HA	1.52	1.38

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:414:TYR:CE2	2:H:416:LEU:HD11	1.60	1.36
2:C:425:SER:CB	2:C:426:ASP:HA	1.52	1.34
2:H:425:SER:CB	2:H:426:ASP:HA	1.51	1.29
2:K:425:SER:CB	2:K:426:ASP:HA	1.52	1.23

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	194/201 (96%)	170 (88%)	20 (10%)	4 (2%)	7	38
1	D	194/201 (96%)	170 (88%)	20 (10%)	4 (2%)	7	38
1	E	194/201 (96%)	164 (84%)	23 (12%)	7 (4%)	3	26
1	J	194/201 (96%)	166 (86%)	23 (12%)	5 (3%)	5	33
2	B	253/441 (57%)	201 (79%)	33 (13%)	19 (8%)	1	11
2	C	253/441 (57%)	203 (80%)	31 (12%)	19 (8%)	1	11
2	H	155/441 (35%)	113 (73%)	30 (19%)	12 (8%)	1	10
2	K	155/441 (35%)	114 (74%)	31 (20%)	10 (6%)	1	14
All	All	1592/2568 (62%)	1301 (82%)	211 (13%)	80 (5%)	2	19

5 of 80 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	479	ASP
1	A	575	THR
1	A	648	GLN
2	C	87	ASP
2	C	299	CYS

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	172/175 (98%)	153 (89%)	19 (11%)	6 29
1	D	172/175 (98%)	151 (88%)	21 (12%)	5 23
1	E	172/175 (98%)	144 (84%)	28 (16%)	2 13
1	J	172/175 (98%)	145 (84%)	27 (16%)	2 15
2	B	232/383 (61%)	208 (90%)	24 (10%)	7 32
2	C	232/383 (61%)	210 (90%)	22 (10%)	8 34
2	H	154/383 (40%)	144 (94%)	10 (6%)	17 50
2	K	154/383 (40%)	141 (92%)	13 (8%)	11 40
All	All	1460/2232 (65%)	1296 (89%)	164 (11%)	6 27

5 of 164 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	286	ARG
1	J	620	ILE
2	H	323	LEU
1	J	559	ARG
1	J	657	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 43 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	310	GLN
1	E	563	GLN
2	B	346	GLN
2	B	415	GLN
2	H	310	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	196/201 (97%)	0.80	23 (11%) 4 5	69, 77, 80, 82	0
1	D	196/201 (97%)	0.86	24 (12%) 4 5	69, 77, 80, 82	0
1	E	196/201 (97%)	0.71	10 (5%) 28 25	49, 58, 67, 72	0
1	J	196/201 (97%)	0.72	13 (6%) 18 17	49, 58, 67, 72	0
2	B	261/441 (59%)	0.51	18 (6%) 16 16	66, 79, 83, 83	0
2	C	261/441 (59%)	0.56	18 (6%) 16 16	66, 79, 83, 83	0
2	H	175/441 (39%)	0.60	22 (12%) 3 5	66, 83, 116, 122	0
2	K	175/441 (39%)	0.56	17 (9%) 7 8	66, 83, 118, 138	0
All	All	1656/2568 (64%)	0.66	145 (8%) 10 10	49, 77, 98, 138	0

The worst 5 of 145 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	K	339	ILE	5.2
2	H	389	GLU	4.5
2	K	388	LEU	3.9
2	K	340	THR	3.9
2	H	388	LEU	3.9

6.2 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.