wwPDB X-ray Structure Validation Summary Report (i)

Aug 28, 2023 – 01:29 AM EDT

PDB ID	:	3KFU
Title	:	Crystal structure of the transamidosome
Authors	:	Blaise, M.; Bailly, M.; Frechin, M.; Thirup, S.; Becker, H.D.; Kern, D.
Deposited on	:	2009-10-28
Resolution	:	3.00 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:

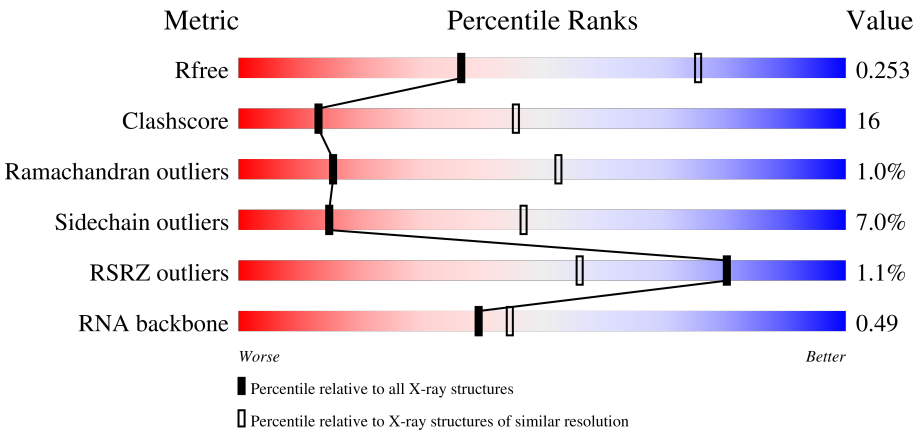
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 3.00 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))
R_{free}	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)
RNA backbone	3102	1173 (3.30-2.70)

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	422	66% 20% • 11%
1	B	422	63% 24% • 11%
1	C	422	2% 65% 22% • 11%
1	D	422	2% 62% 24% • 12%

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Mol	Chain	Length	Quality of chain
2	E	471	% 64% 31% • •
2	H	471	% 63% 31% 5% •
3	F	466	2% 60% 30% 5% •
3	I	466	% 61% 30% 5% 5%
4	G	92	% 70% 21% • 7%
4	J	92	67% 20% • 10%
5	K	76	% 53% 32% 13% •
5	L	76	55% 30% 12% •
5	M	76	4% 36% 30% 25% • 7%
5	N	76	% 34% 33% 24% • 7%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	H2U	M	20	-	-	-	X

2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 33436 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 Non-discriminating and archaeal-type aspartyl-tRNA synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	374	3026	1945	525	549	7	0	0	0
1	B	376	3046	1956	531	552	7	0	0	0
1	C	377	3053	1961	532	553	7	0	0	0
1	D	372	3022	1940	528	548	6	0	0	0

- Molecule 2 is a protein called Glutamyl-tRNA(Gln) amidotransferase subunit A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	E	468	3513	2234	620	652	7	0	1	0
2	H	467	3505	2228	619	651	7	0	1	0

- Molecule 3 is a protein called Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	F	447	3369	2127	612	622	8	0	0	0
3	I	444	3331	2104	608	612	7	0	0	0

- Molecule 4 is a protein called Glutamyl-tRNA(Gln) amidotransferase subunit C.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	G	86	675	428	115	132	0	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
4	J	83	662	421	112	129	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	-1	MET	-	expression tag	UNP Q9LCX4
G	0	PRO	-	expression tag	UNP Q9LCX4
G	1	GLY	-	expression tag	UNP Q9LCX4
J	-1	MET	-	expression tag	UNP Q9LCX4
J	0	PRO	-	expression tag	UNP Q9LCX4
J	1	GLY	-	expression tag	UNP Q9LCX4

- Molecule 5 is a RNA chain called tRNA-Asn.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
5	K	74	1587	706	287	520	74	0	0	0
5	L	74	1587	706	287	520	74	0	0	0
5	M	71	1525	678	276	500	71	0	0	0
5	N	71	1525	678	276	500	71	0	0	0

- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
6	F	1	1	1	0	0
6	I	1	1	1	0	0

- Molecule 7 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
7	F	1	1	1	0	0
7	I	1	1	1	0	0

- Molecule 8 is water.

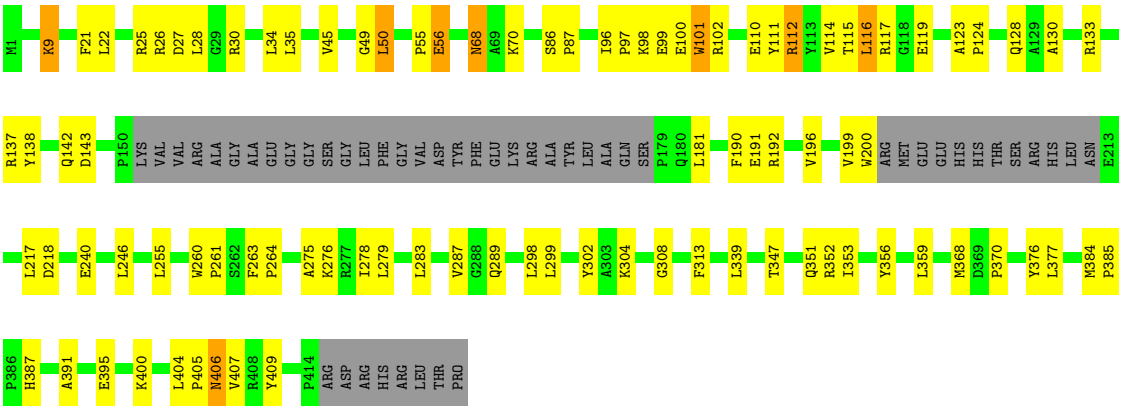
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
8	F	3	3	3	0	0
			Total	O		
8	I	3	3	3	0	0

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.

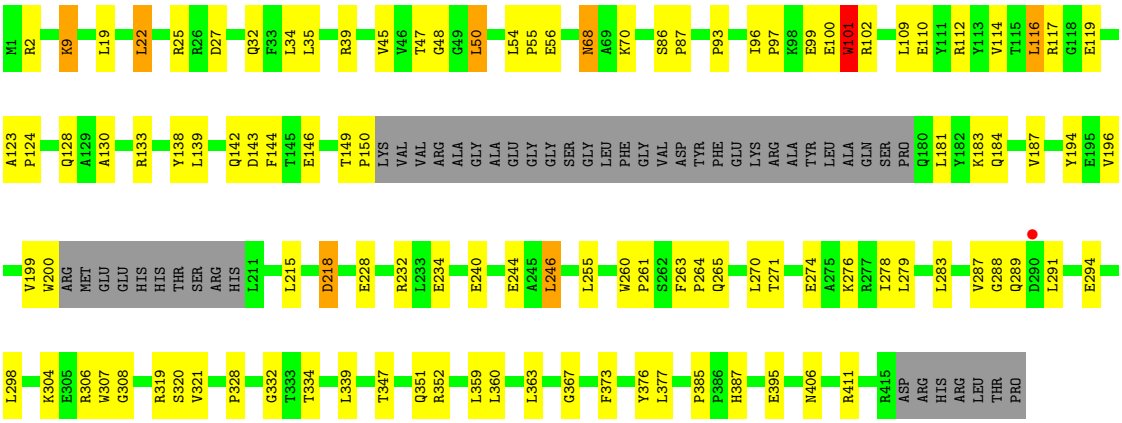
• Molecule 1: Non-discriminating and archaeal-type aspartyl-tRNA synthetase

Chain A: 66% 20% • 11%



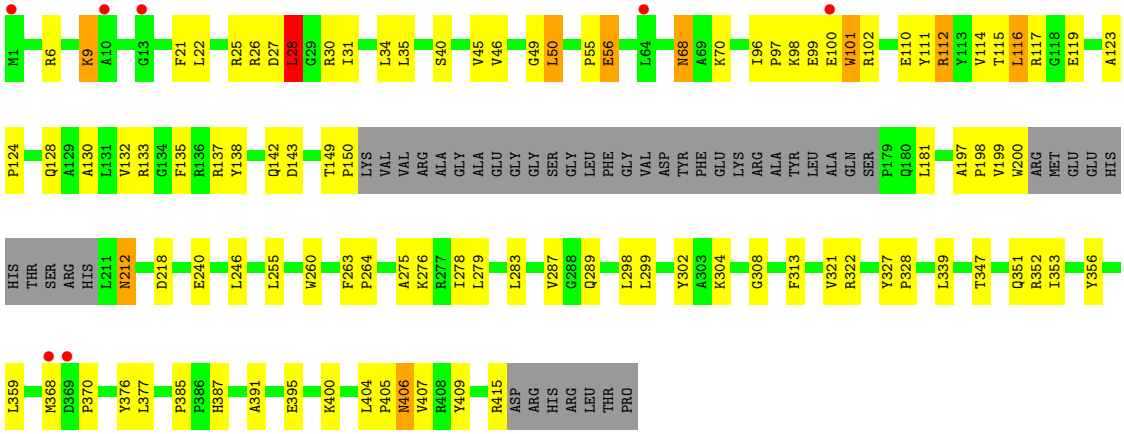
• Molecule 1: Non-discriminating and archaeal-type aspartyl-tRNA synthetase

Chain B: 63% 24% • 11%



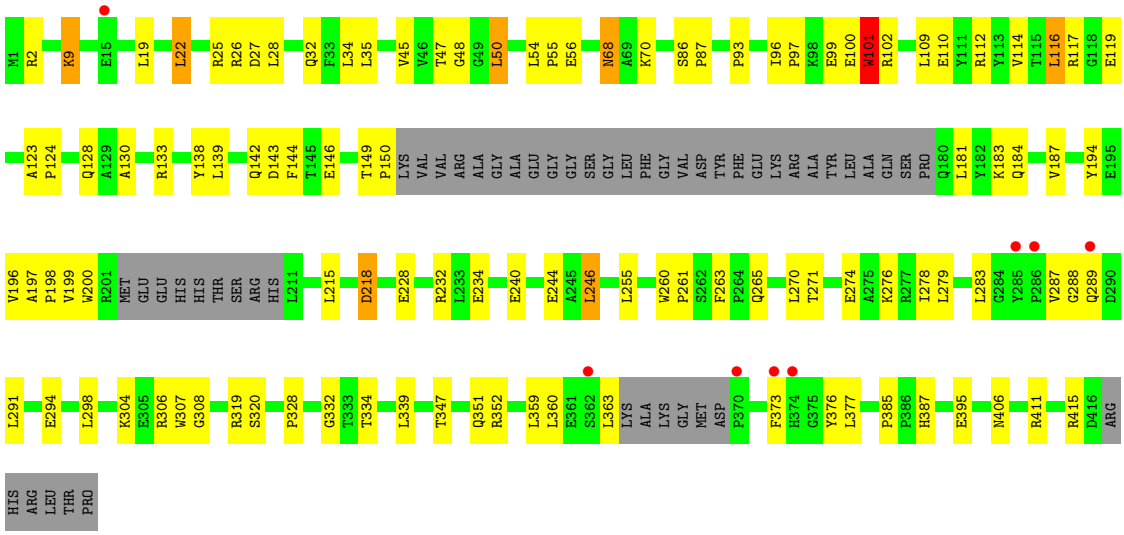
• Molecule 1: Non-discriminating and archaeal-type aspartyl-tRNA synthetase

Chain C: 2% 65% 22% • 11%



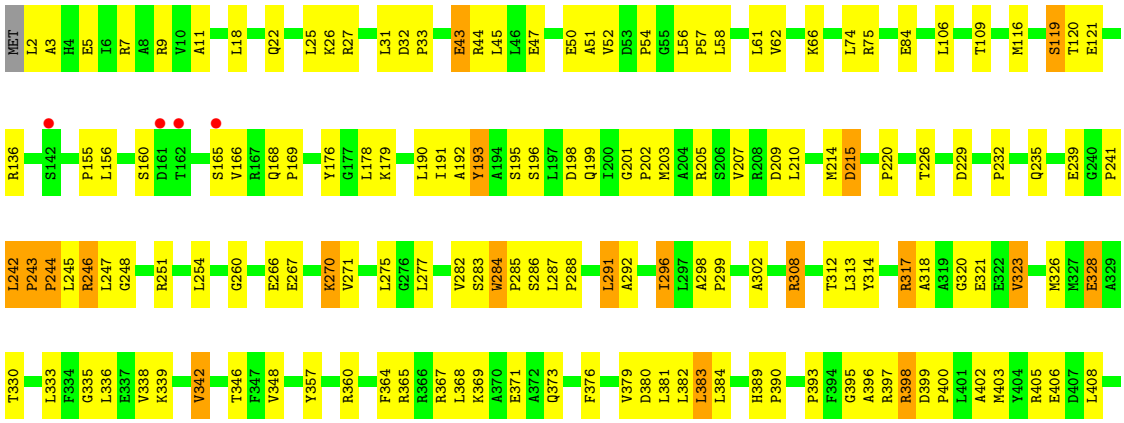
• Molecule 1: Non-discriminating and archaeal-type aspartyl-tRNA synthetase

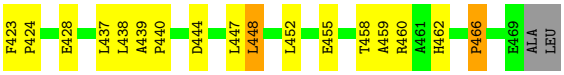
Chain D:



• Molecule 2: Glutamyl-tRNA(Gln) amidotransferase subunit A

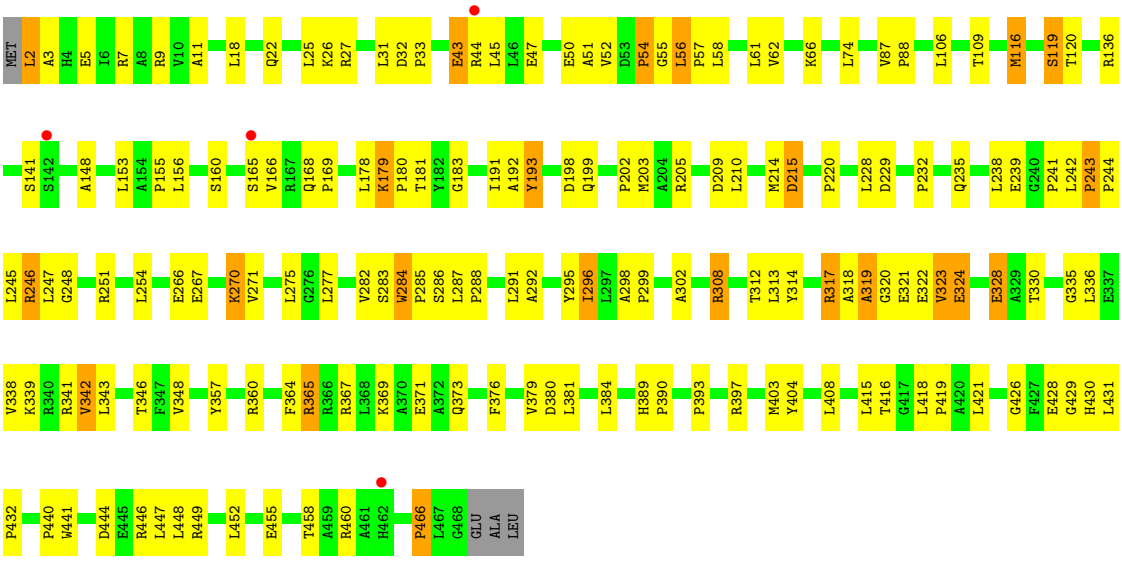
Chain E:





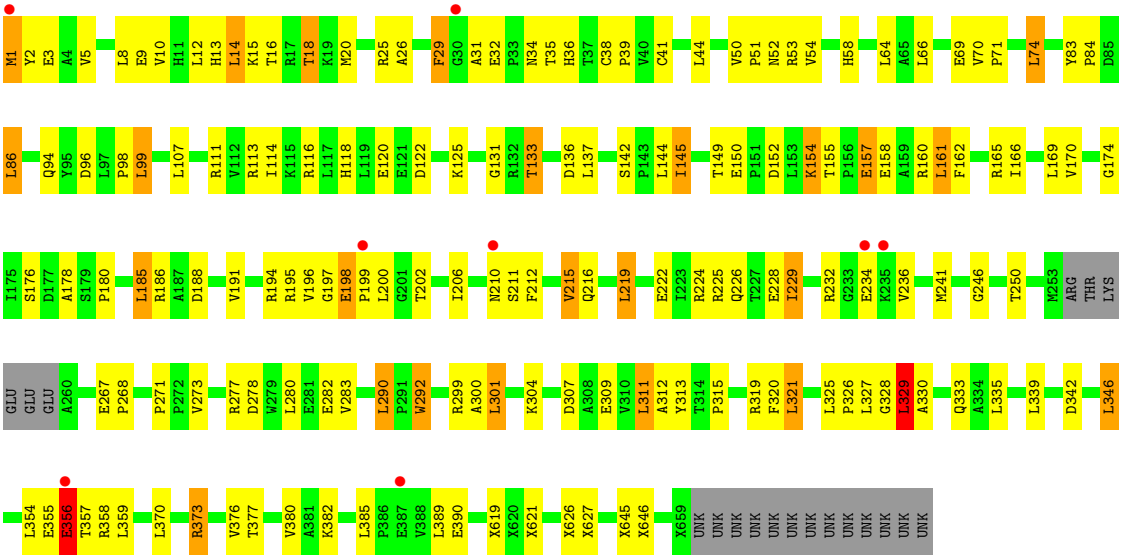
• Molecule 2: Glutamyl-tRNA(Gln) amidotransferase subunit A

Chain H:



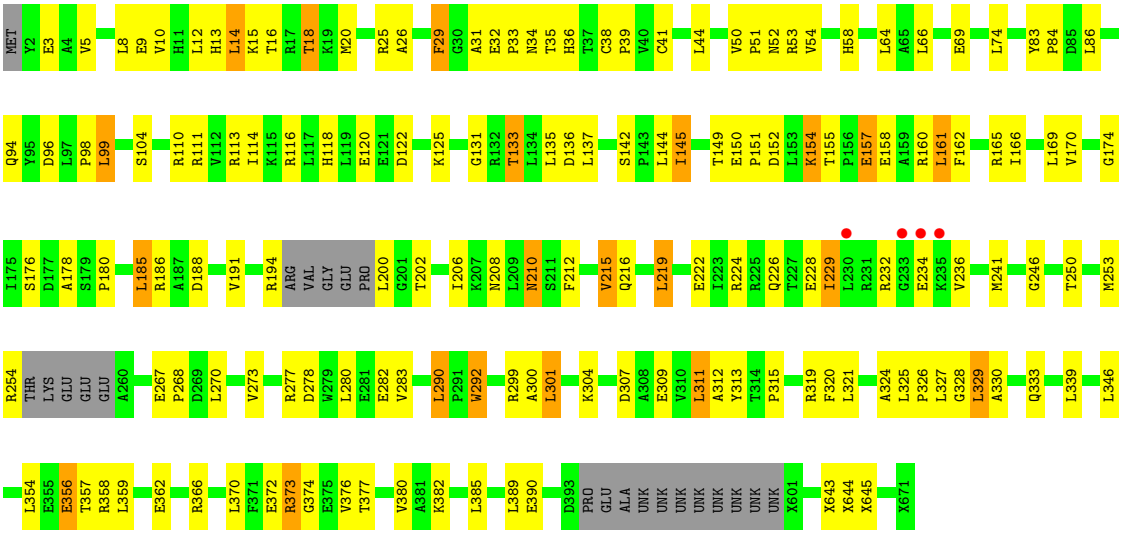
• Molecule 3: Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B

Chain F:



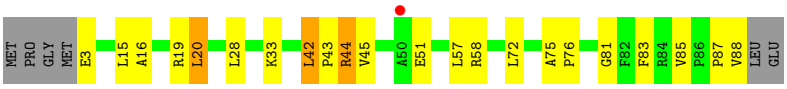
• Molecule 3: Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase subunit B

Chain I:



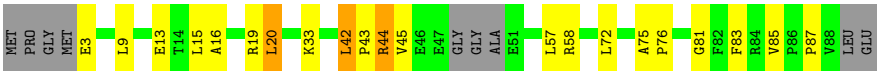
• Molecule 4: Glutamyl-tRNA(Gln) amidotransferase subunit C

Chain G:



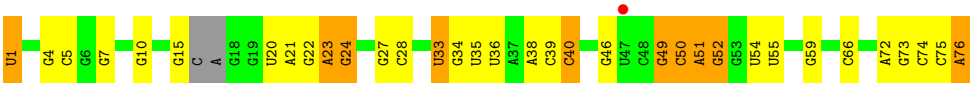
• Molecule 4: Glutamyl-tRNA(Gln) amidotransferase subunit C

Chain J:



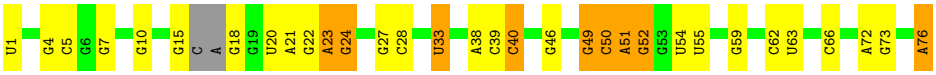
• Molecule 5: tRNA-Asn

Chain K:



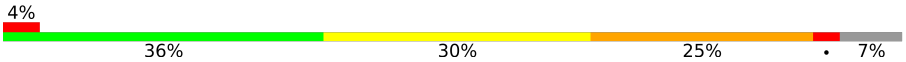
• Molecule 5: tRNA-Asn

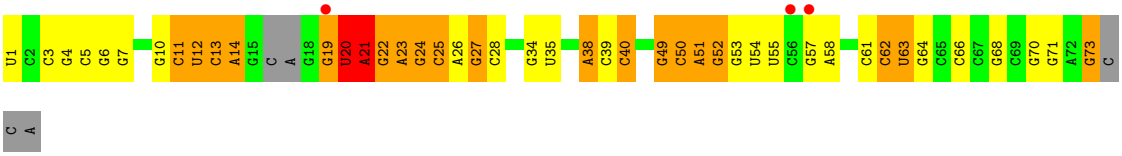
Chain L:



• Molecule 5: tRNA-Asn

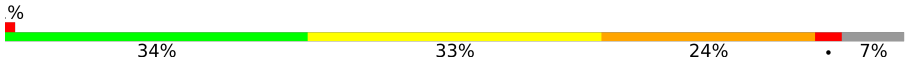
Chain M:

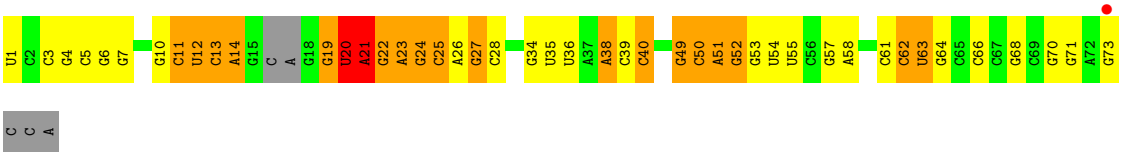




- Molecule 5: tRNA-Asn

Chain N:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	115.92Å 214.00Å 127.84Å 90.00° 93.36° 90.00°	Depositor
Resolution (Å)	39.19 – 3.00 39.19 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.9 (39.19-3.00) 99.9 (39.19-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.42 (at 3.01Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.5_2)	Depositor
R, R_{free}	0.199 , 0.252 0.199 , 0.253	Depositor DCC
R_{free} test set	2487 reflections (2.01%)	wwPDB-VP
Wilson B-factor (Å^2)	62.6	Xtriage
Anisotropy	0.289	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 80.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	33436	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 2.18% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: H2U, MG, 5MU, PSU, ZN

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	0.26	0/3096	0.40	0/4190
1	B	0.23	0/3115	0.40	0/4215
1	C	0.24	0/3123	0.41	1/4226 (0.0%)
1	D	0.22	0/3090	0.39	0/4181
2	E	0.24	0/3593	0.49	1/4887 (0.0%)
2	H	0.29	0/3585	0.50	1/4876 (0.0%)
3	F	0.25	0/3147	0.48	1/4262 (0.0%)
3	I	0.26	0/3081	0.47	0/4170
4	G	0.22	0/686	0.46	0/930
4	J	0.22	0/672	0.44	0/910
5	K	0.34	1/1705 (0.1%)	0.53	0/2655
5	L	0.38	1/1705 (0.1%)	0.56	0/2655
5	M	0.46	3/1636 (0.2%)	0.52	0/2548
5	N	0.47	3/1636 (0.2%)	0.52	0/2548
All	All	0.29	8/33870 (0.0%)	0.47	4/47253 (0.0%)

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	N	1	U	OP3-P	-10.69	1.48	1.61
5	K	1	U	OP3-P	-10.67	1.48	1.61
5	M	1	U	OP3-P	-10.57	1.48	1.61
5	L	1	U	OP3-P	-10.55	1.48	1.61
5	M	21	A	P-OP2	-8.75	1.34	1.49

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	H	466	PRO	N-CA-CB	5.95	110.43	103.30
2	E	466	PRO	N-CA-CB	5.89	110.37	103.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	28	LEU	CA-CB-CG	-5.33	103.05	115.30
3	F	329	LEU	CB-CA-C	-5.22	100.28	110.20

There are no chirality outliers.

There are no planarity outliers.

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	3026	0	3036	69	0
1	B	3046	0	3058	80	0
1	C	3053	0	3066	82	0
1	D	3022	0	3028	76	0
2	E	3513	0	3518	149	0
2	H	3505	0	3507	153	0
3	F	3369	0	3206	147	0
3	I	3331	0	3150	140	0
4	G	675	0	687	35	0
4	J	662	0	675	38	0
5	K	1587	0	807	28	0
5	L	1587	0	807	26	0
5	M	1525	0	774	47	0
5	N	1525	0	774	49	0
6	F	1	0	0	0	0
6	I	1	0	0	0	0
7	F	1	0	0	0	0
7	I	1	0	0	0	0
8	F	3	0	0	1	0
8	I	3	0	0	1	0
All	All	33436	0	30093	1034	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 16.

The worst 5 of 1034 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:H:56:LEU:N	2:H:56:LEU:HD23	1.49	1.18
3:F:329:LEU:HD11	3:F:373:ARG:HH21	1.13	1.14
3:F:329:LEU:HD11	3:F:373:ARG:NH2	1.64	1.13
2:H:323:VAL:CG1	2:H:324:GLU:N	2.09	1.09
3:F:120:GLU:OE2	8:F:675:HOH:O	1.70	1.09

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	368/422 (87%)	343 (93%)	23 (6%)	2 (0%)	29	68
1	B	370/422 (88%)	347 (94%)	22 (6%)	1 (0%)	41	76
1	C	371/422 (88%)	344 (93%)	24 (6%)	3 (1%)	19	57
1	D	364/422 (86%)	342 (94%)	20 (6%)	2 (0%)	29	68
2	E	467/471 (99%)	420 (90%)	39 (8%)	8 (2%)	9	39
2	H	466/471 (99%)	420 (90%)	37 (8%)	9 (2%)	8	36
3	F	386/466 (83%)	354 (92%)	28 (7%)	4 (1%)	15	53
3	I	376/466 (81%)	348 (93%)	25 (7%)	3 (1%)	19	57
4	G	84/92 (91%)	80 (95%)	3 (4%)	1 (1%)	13	48
4	J	79/92 (86%)	77 (98%)	2 (2%)	0	100	100
All	All	3331/3746 (89%)	3075 (92%)	223 (7%)	33 (1%)	15	53

5 of 33 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	415	ARG
2	E	43	GLU
2	E	243	PRO

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Mol	Chain	Res	Type
2	E	466	PRO
2	H	43	GLU

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	316/355 (89%)	302 (96%)	14 (4%)	28	65
1	B	318/355 (90%)	303 (95%)	15 (5%)	26	63
1	C	319/355 (90%)	304 (95%)	15 (5%)	26	63
1	D	316/355 (89%)	302 (96%)	14 (4%)	28	65
2	E	349/354 (99%)	320 (92%)	29 (8%)	11	39
2	H	348/354 (98%)	317 (91%)	31 (9%)	9	35
3	F	328/334 (98%)	294 (90%)	34 (10%)	7	27
3	I	320/334 (96%)	289 (90%)	31 (10%)	8	31
4	G	72/77 (94%)	67 (93%)	5 (7%)	15	48
4	J	72/77 (94%)	68 (94%)	4 (6%)	21	56
All	All	2758/2950 (94%)	2566 (93%)	192 (7%)	15	47

5 of 192 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	F	329	LEU
2	H	291	LEU
3	F	373	ARG
2	H	74	LEU
2	H	336	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
3	F	216	GLN

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Mol	Chain	Res	Type
3	I	216	GLN
3	F	333	GLN
3	I	58	HIS
4	J	68	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
5	K	72/76 (94%)	13 (18%)	0
5	L	72/76 (94%)	13 (18%)	0
5	M	69/76 (90%)	22 (31%)	1 (1%)
5	N	69/76 (90%)	22 (31%)	1 (1%)
All	All	282/304 (92%)	70 (24%)	2 (0%)

5 of 70 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
5	K	10	G
5	K	21	A
5	K	22	G
5	K	23	A
5	K	24	G

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	M	20	H2U
5	N	20	H2U

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

12 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	5MU	N	54	5	19,22,23	2.14	4 (21%)	28,32,35	2.07	6 (21%)
5	PSU	N	55	5	18,21,22	1.07	1 (5%)	22,30,33	1.72	3 (13%)
5	5MU	K	54	5	19,22,23	2.13	4 (21%)	28,32,35	2.05	7 (25%)
5	H2U	M	20	5	18,21,22	3.94	5 (27%)	21,30,33	4.83	7 (33%)
5	PSU	K	55	5	18,21,22	1.12	1 (5%)	22,30,33	1.80	4 (18%)
5	PSU	M	55	5	18,21,22	1.11	1 (5%)	22,30,33	1.74	3 (13%)
5	H2U	K	20	5	18,21,22	3.91	5 (27%)	21,30,33	4.85	7 (33%)
5	5MU	M	54	5	19,22,23	2.14	4 (21%)	28,32,35	2.06	6 (21%)
5	5MU	L	54	5	19,22,23	2.11	4 (21%)	28,32,35	2.03	6 (21%)
5	PSU	L	55	5	18,21,22	1.03	1 (5%)	22,30,33	1.76	3 (13%)
5	H2U	L	20	5	18,21,22	3.89	5 (27%)	21,30,33	4.86	7 (33%)
5	H2U	N	20	5	18,21,22	3.92	5 (27%)	21,30,33	4.84	7 (33%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	5MU	N	54	5	-	0/7/25/26	0/2/2/2
5	PSU	N	55	5	-	0/7/25/26	0/2/2/2
5	5MU	K	54	5	-	0/7/25/26	0/2/2/2
5	H2U	M	20	5	-	3/7/38/39	0/2/2/2
5	PSU	K	55	5	-	2/7/25/26	0/2/2/2
5	PSU	M	55	5	-	0/7/25/26	0/2/2/2
5	H2U	K	20	5	-	0/7/38/39	0/2/2/2
5	5MU	M	54	5	-	0/7/25/26	0/2/2/2
5	5MU	L	54	5	-	0/7/25/26	0/2/2/2
5	PSU	L	55	5	-	0/7/25/26	0/2/2/2
5	H2U	L	20	5	-	0/7/38/39	0/2/2/2
5	H2U	N	20	5	-	3/7/38/39	0/2/2/2

The worst 5 of 40 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	M	20	H2U	O4-C4	9.11	1.41	1.23
5	K	20	H2U	O2-C2	9.06	1.39	1.23
5	K	20	H2U	O4-C4	9.06	1.41	1.23
5	N	20	H2U	O2-C2	9.06	1.39	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	M	20	H2U	O2-C2	9.04	1.39	1.23

The worst 5 of 66 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	N	20	H2U	C4-N3-C2	-15.11	113.26	125.79
5	M	20	H2U	C4-N3-C2	-15.01	113.34	125.79
5	K	20	H2U	C4-N3-C2	-14.89	113.44	125.79
5	L	20	H2U	C4-N3-C2	-14.81	113.50	125.79
5	L	20	H2U	O2-C2-N1	-10.65	109.73	123.11

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	M	20	H2U	C2'-C1'-N1-C2
5	M	20	H2U	C3'-C4'-C5'-O5'
5	N	20	H2U	C3'-C4'-C5'-O5'
5	N	20	H2U	C2'-C1'-N1-C2
5	M	20	H2U	O4'-C4'-C5'-O5'

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	M	20	H2U	1	0
5	N	20	H2U	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
3	I	4
3	F	2

The worst 5 of 6 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	F	396:ALA	C	601:UNK	N	12.21
1	I	609:UNK	C	616:UNK	N	10.53
1	I	656:UNK	C	658:UNK	N	6.43
1	F	643:UNK	C	645:UNK	N	6.30
1	I	639:UNK	C	641:UNK	N	4.45

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

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, 95th 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	374/422 (88%)	-0.49	0	100	100	23, 54, 101, 153	0
1	B	376/422 (89%)	-0.42	1 (0%)	94	84	27, 62, 136, 209	0
1	C	377/422 (89%)	-0.34	7 (1%)	66	37	30, 71, 129, 187	0
1	D	372/422 (88%)	-0.25	8 (2%)	62	33	29, 74, 141, 224	0
2	E	468/471 (99%)	-0.27	4 (0%)	84	63	27, 65, 120, 211	0
2	H	467/471 (99%)	-0.37	4 (0%)	84	63	24, 56, 104, 209	0
3	F	390/466 (83%)	-0.22	8 (2%)	63	34	18, 67, 137, 233	0
3	I	382/466 (81%)	-0.28	4 (1%)	82	59	18, 67, 127, 247	0
4	G	86/92 (93%)	-0.40	1 (1%)	79	54	41, 79, 132, 200	0
4	J	83/92 (90%)	-0.35	0	100	100	36, 64, 113, 147	0
5	K	71/76 (93%)	-0.10	1 (1%)	75	49	48, 82, 120, 161	0
5	L	71/76 (93%)	-0.28	0	100	100	40, 62, 84, 111	0
5	M	68/76 (89%)	0.53	3 (4%)	34	13	69, 101, 175, 190	0
5	N	68/76 (89%)	0.19	1 (1%)	73	46	57, 85, 156, 277	0
All	All	3653/4050 (90%)	-0.30	42 (1%)	80	56	18, 65, 128, 277	0

The worst 5 of 42 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	I	235	LYS	5.4
1	D	370	PRO	3.9
2	H	44	ARG	3.8
2	E	165	SER	3.7
3	I	233	GLY	3.6

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	PSU	M	55	20/21	0.67	0.35	197,203,217,454	0
5	5MU	M	54	21/22	0.74	0.32	183,194,249,494	0
5	H2U	M	20	20/21	0.74	0.49	189,193,344,404	0
5	H2U	N	20	20/21	0.80	0.32	141,145,197,259	0
5	PSU	N	55	20/21	0.84	0.23	100,133,138,254	0
5	5MU	N	54	21/22	0.89	0.28	86,110,113,235	0
5	H2U	K	20	20/21	0.93	0.17	102,107,110,242	0
5	PSU	K	55	20/21	0.95	0.13	75,81,88,201	0
5	5MU	K	54	21/22	0.96	0.15	78,82,86,195	0
5	H2U	L	20	20/21	0.96	0.18	61,63,66,162	0
5	5MU	L	54	21/22	0.97	0.15	55,61,65,151	0
5	PSU	L	55	20/21	0.97	0.16	63,67,68,165	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
7	MG	F	674	1/1	0.85	0.11	46,46,46,46	0
6	ZN	I	467	1/1	0.95	0.20	133,133,133,133	0
7	MG	I	468	1/1	0.96	0.07	46,46,46,46	0
6	ZN	F	673	1/1	0.97	0.22	100,100,100,100	0

6.5 Other polymers (i)

There are no such residues in this entry.