



wwPDB X-ray Structure Validation Summary Report ⓘ

May 21, 2020 – 08:22 pm BST

PDB ID : 4ATQ
Title : GABA-transaminase A1R958 in complex with external aldimine PLP-GABA adduct
Authors : Bruce, H.; Tuan, A.N.; Mangas Sanchez, J.; Hart, S.; Turkenburg, J.P.; Grogan, G.
Deposited on : 2012-05-09
Resolution : 2.75 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) 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	:	2.11
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)	:	2.11

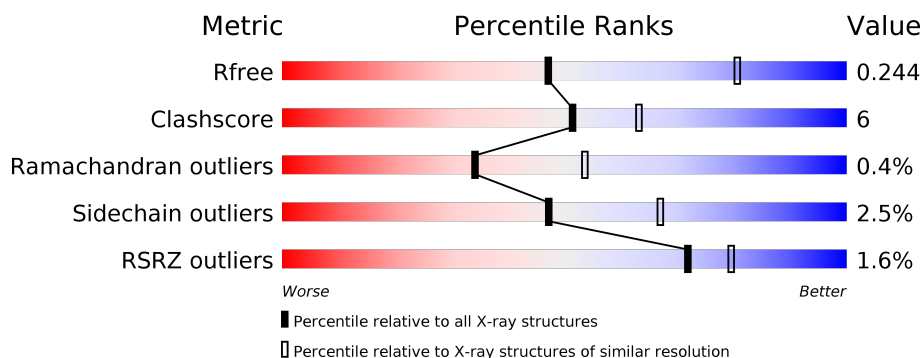
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)
RSRZ outliers	127900	1207 (2.78-2.74)

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 on 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 $\leq 5\%$. 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	456	
1	B	456	
1	C	456	
1	D	456	
1	E	456	
1	F	456	

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Mol	Chain	Length	Quality of chain
1	G	456	<div><div><div></div><div></div><div></div></div><div><div>2%</div><div>83%</div><div>13%</div><div></div><div></div></div><div><div></div><div></div><div></div></div></div>
1	H	456	<div><div><div></div><div></div><div></div></div><div><div>2%</div><div>84%</div><div>11%</div><div></div><div></div></div><div><div></div><div></div><div></div></div></div>
1	I	456	<div><div><div></div><div></div><div></div></div><div><div>2%</div><div>87%</div><div>8%</div><div></div><div></div></div><div><div></div><div></div><div></div></div></div>
1	J	456	<div><div><div></div><div></div><div></div></div><div><div>3%</div><div>83%</div><div>12%</div><div></div><div></div></div><div><div></div><div></div><div></div></div></div>
1	K	456	<div><div><div></div><div></div><div></div></div><div><div>2%</div><div>85%</div><div>10%</div><div></div><div></div></div><div><div></div><div></div><div></div></div></div>
1	L	456	<div><div><div></div><div></div><div></div></div><div><div>7%</div><div>89%</div><div>6%</div><div></div><div></div></div><div><div></div><div></div><div></div></div></div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 38709 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 4-AMINO BUTYRATE TRANSAMINASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	442	Total	C	N	O	S	0	0	0
			3233	2044	562	613	14			
1	B	442	Total	C	N	O	S	0	1	0
			3250	2057	563	615	15			
1	C	442	Total	C	N	O	S	0	0	0
			3237	2049	562	612	14			
1	D	441	Total	C	N	O	S	0	0	0
			3222	2040	562	606	14			
1	E	442	Total	C	N	O	S	0	0	0
			3221	2042	563	602	14			
1	F	444	Total	C	N	O	S	0	1	0
			3241	2051	568	608	14			
1	G	440	Total	C	N	O	S	0	0	0
			3179	2011	554	600	14			
1	H	440	Total	C	N	O	S	0	0	0
			3093	1957	535	587	14			
1	I	440	Total	C	N	O	S	0	0	0
			3136	1979	551	592	14			
1	J	438	Total	C	N	O	S	0	0	0
			3135	1985	546	590	14			
1	K	437	Total	C	N	O	S	0	0	0
			2969	1879	514	563	13			
1	L	436	Total	C	N	O	S	0	0	0
			2983	1870	524	576	13			

There are 12 discrepancies between the modelled and reference sequences:

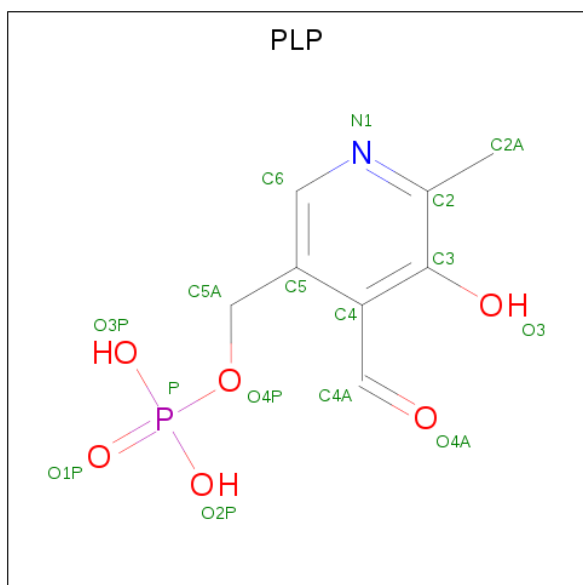
Chain	Residue	Modelled	Actual	Comment	Reference
A	113	THR	ALA	SEE REMARK 999	UNP A1R958
B	113	THR	ALA	SEE REMARK 999	UNP A1R958
C	113	THR	ALA	SEE REMARK 999	UNP A1R958
D	113	THR	ALA	SEE REMARK 999	UNP A1R958
E	113	THR	ALA	SEE REMARK 999	UNP A1R958

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Chain	Residue	Modelled	Actual	Comment	Reference
F	113	THR	ALA	SEE REMARK 999	UNP A1R958
G	113	THR	ALA	SEE REMARK 999	UNP A1R958
H	113	THR	ALA	SEE REMARK 999	UNP A1R958
I	113	THR	ALA	SEE REMARK 999	UNP A1R958
J	113	THR	ALA	SEE REMARK 999	UNP A1R958
K	113	THR	ALA	SEE REMARK 999	UNP A1R958
L	113	THR	ALA	SEE REMARK 999	UNP A1R958

- Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: $C_8H_{10}NO_6P$).



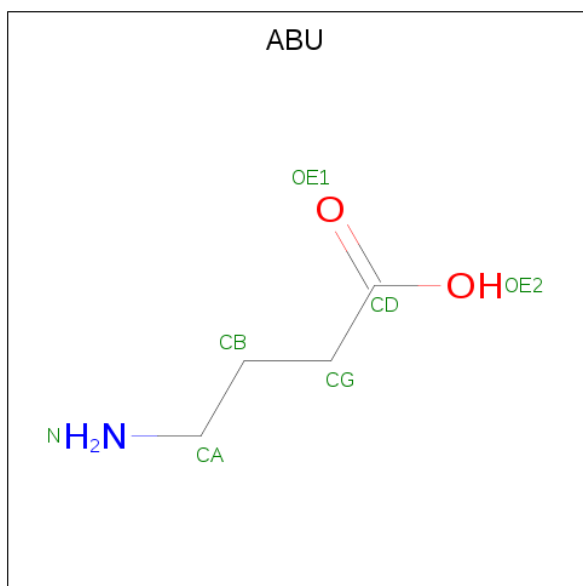
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	B	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	C	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	D	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	E	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	F	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	G	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	H	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	I	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	J	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	K	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	L	1	Total	C	N	O	P	0	0
			15	8	1	5	1		

- Molecule 3 is GAMMA-AMINO-BUTANOIC ACID (three-letter code: ABU) (formula: $C_4H_9NO_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			7	4	1	2		
3	B	1	Total	C	N	O	0	0
			7	4	1	2		
3	C	1	Total	C	N	O	0	0
			7	4	1	2		
3	D	1	Total	C	N	O	0	0
			7	4	1	2		
3	E	1	Total	C	N	O	0	0
			7	4	1	2		
3	F	1	Total	C	N	O	0	0
			7	4	1	2		
3	G	1	Total	C	N	O	0	0
			7	4	1	2		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	H	1	Total	C	N	O	0	0
			7	4	1	2		
3	I	1	Total	C	N	O	0	0
			7	4	1	2		
3	J	1	Total	C	N	O	0	0
			7	4	1	2		
3	K	1	Total	C	N	O	0	0
			7	4	1	2		
3	L	1	Total	C	N	O	0	0
			7	4	1	2		

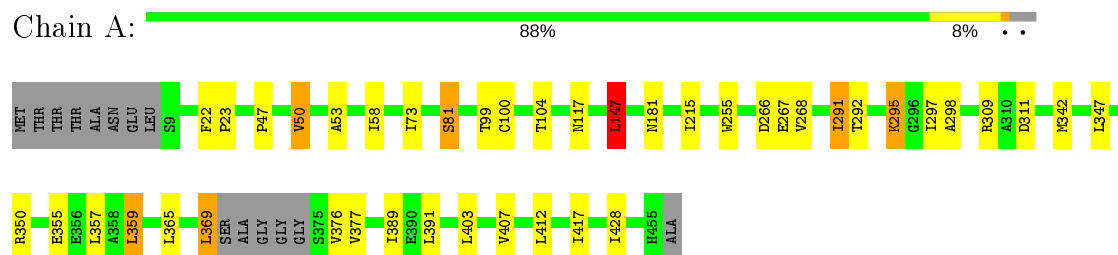
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	101	Total	O	0	0
			101	101		
4	B	96	Total	O	0	0
			96	96		
4	C	55	Total	O	0	0
			55	55		
4	D	37	Total	O	0	0
			37	37		
4	E	79	Total	O	0	0
			79	79		
4	F	75	Total	O	0	0
			75	75		
4	G	35	Total	O	0	0
			35	35		
4	H	9	Total	O	0	0
			9	9		
4	I	18	Total	O	0	0
			18	18		
4	J	14	Total	O	0	0
			14	14		
4	K	12	Total	O	0	0
			12	12		
4	L	15	Total	O	0	0
			15	15		

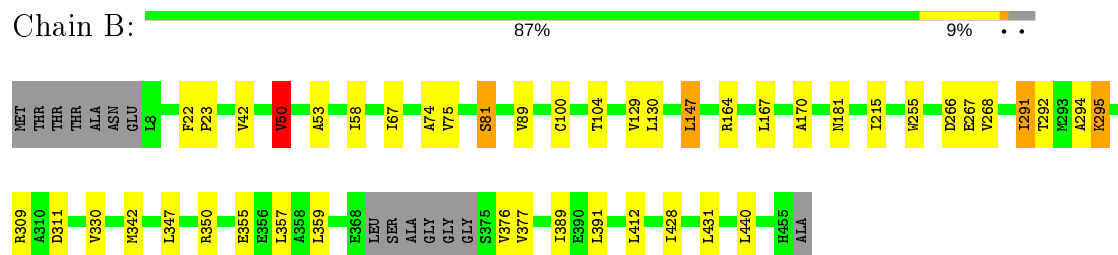
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

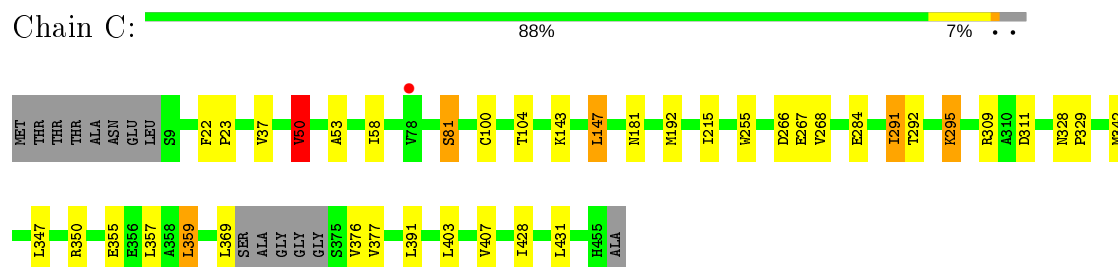
• Molecule 1: 4-AMINO BUTYRATE TRANSAMINASE



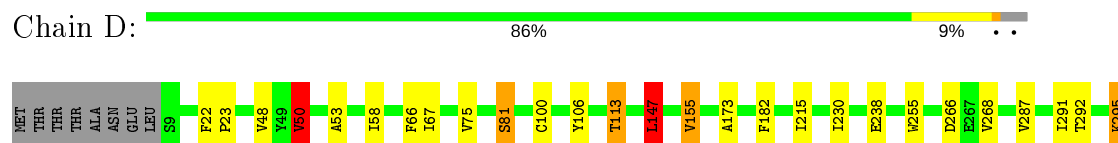
• Molecule 1: 4-AMINO BUTYRATE TRANSAMINASE



• Molecule 1: 4-AMINO BUTYRATE TRANSAMINASE



• Molecule 1: 4-AMINO BUTYRATE TRANSAMINASE





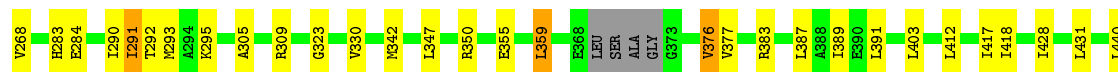
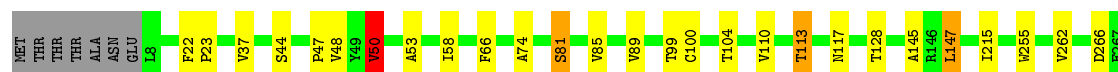
• Molecule 1: 4-AMINO BUTYRATE TRANSAMINASE

Chain E: 85% 10%



• Molecule 1: 4-AMINO BUTYRATE TRANSAMINASE

Chain F: 85% 11%



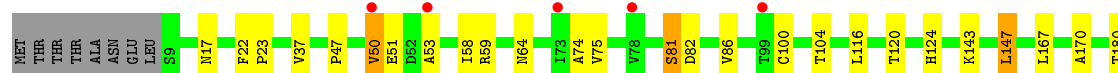
• Molecule 1: 4-AMINO BUTYRATE TRANSAMINASE

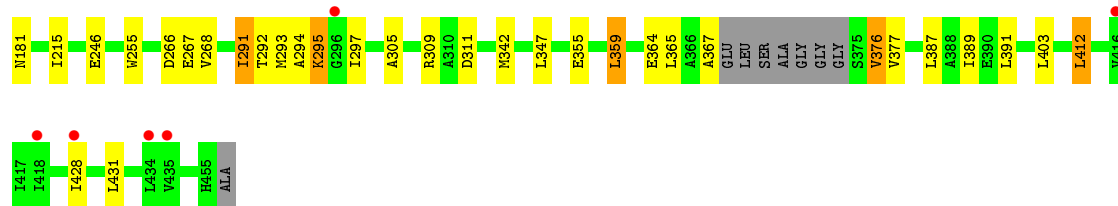
Chain G: 83% 13%



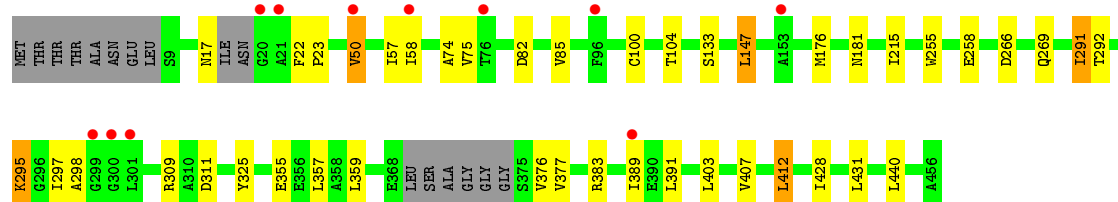
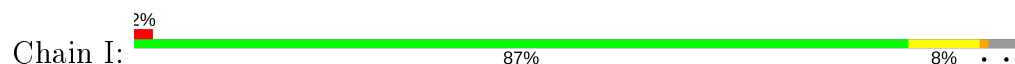
• Molecule 1: 4-AMINO BUTYRATE TRANSAMINASE

Chain H: 84% 11%

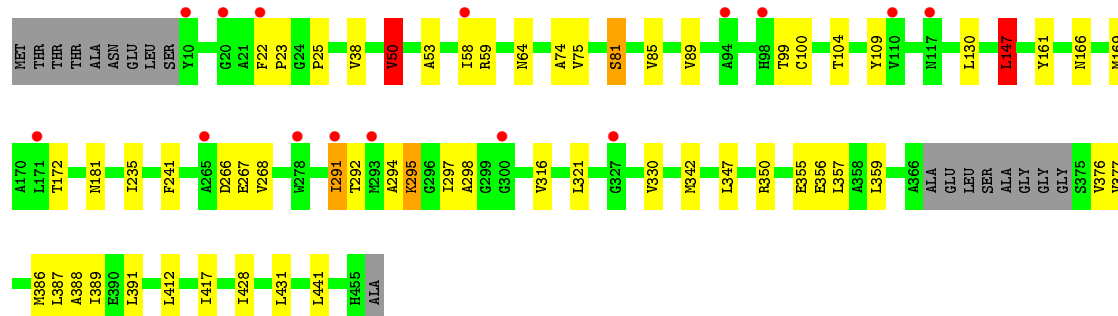
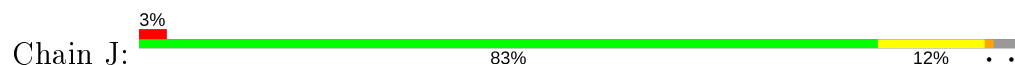




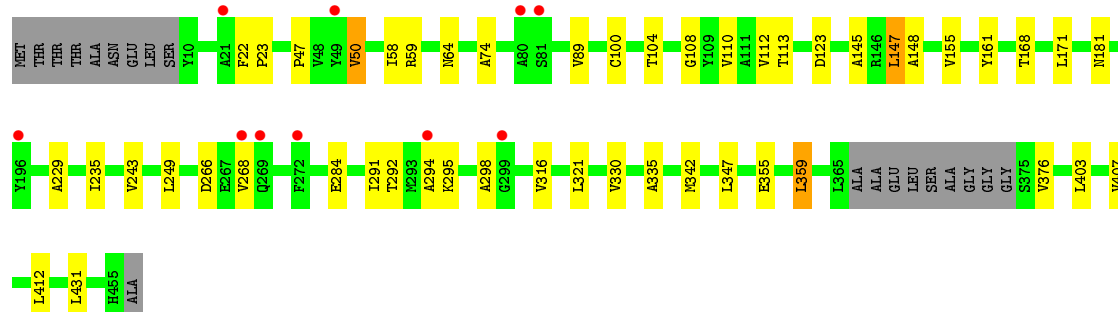
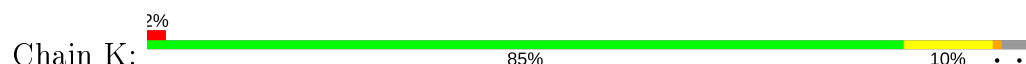
• Molecule 1: 4-AMINO BUTYRATE TRANSAMINASE



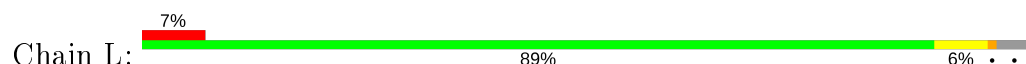
• Molecule 1: 4-AMINO BUTYRATE TRANSAMINASE

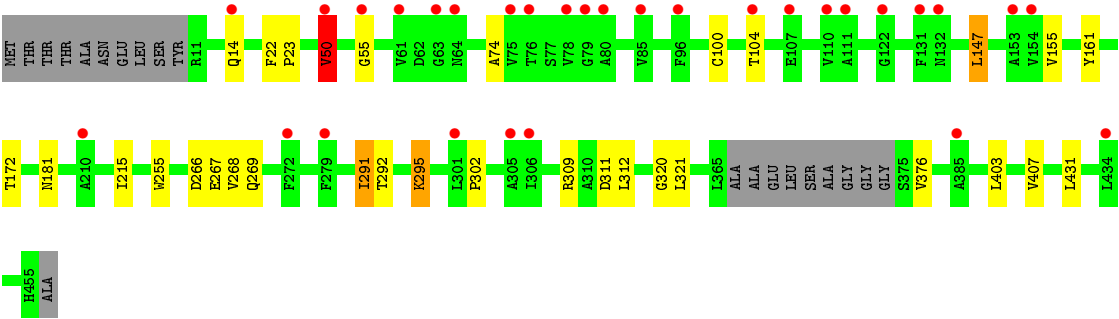


• Molecule 1: 4-AMINO BUTYRATE TRANSAMINASE



• Molecule 1: 4-AMINO BUTYRATE TRANSAMINASE





4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	176.71 Å 292.83 Å 105.96 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	90.87 – 2.75 90.87 – 2.75	Depositor EDS
% Data completeness (in resolution range)	100.0 (90.87-2.75) 100.0 (90.87-2.75)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.50 (at 2.73 Å)	Xtriage
Refinement program	REFMAC 5.6.0119	Depositor
R, R_{free}	0.202 , 0.248 0.201 , 0.244	Depositor DCC
R_{free} test set	7182 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	46.5	Xtriage
Anisotropy	0.301	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 39.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	38709	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.68% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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

Bond lengths and bond angles in the following residue types are not validated in this section: ABU, PLP

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	0.67	0/3292	0.76	1/4479 (0.0%)
1	B	0.68	0/3312	0.79	1/4503 (0.0%)
1	C	0.66	0/3296	0.76	3/4483 (0.1%)
1	D	0.61	0/3281	0.74	3/4462 (0.1%)
1	E	0.64	0/3280	0.73	2/4461 (0.0%)
1	F	0.67	0/3304	0.77	2/4493 (0.0%)
1	G	0.59	0/3238	0.71	1/4411 (0.0%)
1	H	0.56	0/3150	0.70	0/4302
1	I	0.57	0/3194	0.71	0/4350
1	J	0.54	0/3193	0.71	2/4351 (0.0%)
1	K	0.53	0/3025	0.70	0/4141
1	L	0.53	0/3039	0.70	1/4157 (0.0%)
All	All	0.61	0/38604	0.73	16/52593 (0.0%)

There are no bond length outliers.

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	147	LEU	CA-CB-CG	5.93	128.94	115.30
1	D	386	MET	CG-SD-CE	-5.86	90.82	100.20
1	E	147	LEU	CA-CB-CG	5.86	128.78	115.30
1	G	147	LEU	CA-CB-CG	5.71	128.44	115.30
1	C	50	VAL	CB-CA-C	-5.58	100.81	111.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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	3233	0	3216	33	0
1	B	3250	0	3248	30	0
1	C	3237	0	3223	40	0
1	D	3222	0	3214	41	0
1	E	3221	0	3220	48	0
1	F	3241	0	3229	60	0
1	G	3179	0	3132	52	0
1	H	3093	0	2976	43	0
1	I	3136	0	3035	34	0
1	J	3135	0	3077	42	0
1	K	2969	0	2741	40	0
1	L	2983	0	2737	21	0
2	A	15	0	7	1	0
2	B	15	0	6	0	0
2	C	15	0	6	0	0
2	D	15	0	7	1	0
2	E	15	0	7	1	0
2	F	15	0	6	0	0
2	G	15	0	6	0	0
2	H	15	0	6	1	0
2	I	15	0	7	0	0
2	J	15	0	7	1	0
2	K	15	0	6	1	0
2	L	15	0	6	0	0
3	A	7	0	5	1	0
3	B	7	0	5	1	0
3	C	7	0	5	0	0
3	D	7	0	5	1	0
3	E	7	0	5	1	0
3	F	7	0	5	0	0
3	G	7	0	5	0	0
3	H	7	0	5	1	0
3	I	7	0	5	0	0
3	J	7	0	5	1	0
3	K	7	0	5	0	0
3	L	7	0	5	0	0
4	A	101	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	96	0	0	0	0
4	C	55	0	0	1	0
4	D	37	0	0	3	0
4	E	79	0	0	3	0
4	F	75	0	0	3	0
4	G	35	0	0	8	0
4	H	9	0	0	0	0
4	I	18	0	0	2	0
4	J	14	0	0	1	0
4	K	12	0	0	0	0
4	L	15	0	0	1	0
All	All	38709	0	37185	423	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 6.

The worst 5 of 423 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)
1:C:147:LEU:HD12	1:C:147:LEU:O	1.36	1.26
1:F:309:ARG:HD2	4:F:2067:HOH:O	1.58	1.03
1:D:383:ARG:NH2	4:D:2031:HOH:O	2.01	0.93
1:E:117:ASN:HD22	1:F:37:VAL:HG12	1.34	0.91
1:C:147:LEU:HD12	1:C:147:LEU:C	1.90	0.90

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	438/456 (96%)	417 (95%)	19 (4%)	2 (0%)	29 47

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	439/456 (96%)	418 (95%)	18 (4%)	3 (1%)	22	39
1	C	438/456 (96%)	416 (95%)	20 (5%)	2 (0%)	29	47
1	D	437/456 (96%)	414 (95%)	21 (5%)	2 (0%)	29	47
1	E	438/456 (96%)	417 (95%)	19 (4%)	2 (0%)	29	47
1	F	441/456 (97%)	417 (95%)	23 (5%)	1 (0%)	47	69
1	G	436/456 (96%)	414 (95%)	21 (5%)	1 (0%)	47	69
1	H	436/456 (96%)	414 (95%)	20 (5%)	2 (0%)	29	47
1	I	434/456 (95%)	412 (95%)	20 (5%)	2 (0%)	29	47
1	J	434/456 (95%)	413 (95%)	19 (4%)	2 (0%)	29	47
1	K	433/456 (95%)	411 (95%)	20 (5%)	2 (0%)	29	47
1	L	432/456 (95%)	410 (95%)	20 (5%)	2 (0%)	29	47
All	All	5236/5472 (96%)	4973 (95%)	240 (5%)	23 (0%)	34	53

5 of 23 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	100	CYS
1	D	295	LYS
1	A	295	LYS
1	B	100	CYS
1	B	294	ALA

5.3.2 Protein sidechains ⓘ

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	321/336 (96%)	312 (97%)	9 (3%)	43	63
1	B	324/336 (96%)	317 (98%)	7 (2%)	52	70
1	C	320/336 (95%)	312 (98%)	8 (2%)	47	67
1	D	318/336 (95%)	309 (97%)	9 (3%)	43	63
1	E	317/336 (94%)	310 (98%)	7 (2%)	52	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	319/336 (95%)	312 (98%)	7 (2%)	52	70
1	G	309/336 (92%)	302 (98%)	7 (2%)	50	69
1	H	288/336 (86%)	279 (97%)	9 (3%)	40	60
1	I	294/336 (88%)	287 (98%)	7 (2%)	49	68
1	J	301/336 (90%)	293 (97%)	8 (3%)	44	65
1	K	254/336 (76%)	248 (98%)	6 (2%)	49	68
1	L	260/336 (77%)	255 (98%)	5 (2%)	57	73
All	All	3625/4032 (90%)	3536 (98%)	89 (2%)	47	67

5 of 89 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	50	VAL
1	G	117	ASN
1	K	359	LEU
1	F	81	SER
1	F	359	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	181	ASN
1	G	117	ASN
1	H	117	ASN
1	E	269	GLN
1	I	269	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

24 ligands 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
3	ABU	G	1457	2	3,6,6	0.25	0	2,6,6	1.52	1 (50%)
3	ABU	E	1457	2	3,6,6	0.54	0	2,6,6	0.83	0
2	PLP	C	1456	3	15,15,16	2.91	6 (40%)	20,22,23	1.73	5 (25%)
2	PLP	G	1456	3	15,15,16	2.86	6 (40%)	20,22,23	1.59	4 (20%)
2	PLP	F	1456	3	15,15,16	2.33	5 (33%)	20,22,23	1.61	5 (25%)
3	ABU	B	1457	2	3,6,6	0.70	0	2,6,6	1.38	0
3	ABU	L	1457	2	3,6,6	0.52	0	2,6,6	0.81	0
3	ABU	A	1457	2	3,6,6	0.70	0	2,6,6	1.52	1 (50%)
3	ABU	K	1457	2	3,6,6	0.49	0	2,6,6	1.05	0
2	PLP	B	1456	3	15,15,16	2.51	6 (40%)	20,22,23	1.55	3 (15%)
2	PLP	E	1456	3	15,15,16	2.57	7 (46%)	20,22,23	1.50	3 (15%)
2	PLP	D	1456	3	15,15,16	3.08	6 (40%)	20,22,23	1.72	5 (25%)
2	PLP	A	1456	3	15,15,16	2.49	5 (33%)	20,22,23	1.54	4 (20%)
3	ABU	J	1457	2	3,6,6	0.69	0	2,6,6	0.87	0
3	ABU	C	1457	2	3,6,6	0.30	0	2,6,6	1.33	0
2	PLP	I	1457	3	15,15,16	3.04	6 (40%)	20,22,23	1.41	2 (10%)
3	ABU	D	1457	2	3,6,6	0.41	0	2,6,6	1.13	0
2	PLP	J	1456	3	15,15,16	3.05	6 (40%)	20,22,23	1.23	1 (5%)
3	ABU	F	1457	2	3,6,6	0.69	0	2,6,6	1.02	0
3	ABU	I	1458	2	3,6,6	0.33	0	2,6,6	0.97	0
3	ABU	H	1457	2	3,6,6	0.44	0	2,6,6	0.86	0
2	PLP	H	1456	3	15,15,16	3.03	7 (46%)	20,22,23	2.19	6 (30%)
2	PLP	K	1456	3	15,15,16	2.80	6 (40%)	20,22,23	1.88	6 (30%)
2	PLP	L	1456	3	15,15,16	2.69	5 (33%)	20,22,23	1.57	3 (15%)

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
3	ABU	G	1457	2	-	1/2/4/4	-
3	ABU	E	1457	2	-	0/2/4/4	-
2	PLP	C	1456	3	-	0/6/6/8	0/1/1/1
2	PLP	G	1456	3	-	0/6/6/8	0/1/1/1
2	PLP	F	1456	3	-	0/6/6/8	0/1/1/1
3	ABU	B	1457	2	-	2/2/4/4	-
3	ABU	L	1457	2	-	0/2/4/4	-
3	ABU	A	1457	2	-	1/2/4/4	-
3	ABU	K	1457	2	-	1/2/4/4	-
2	PLP	B	1456	3	-	0/6/6/8	0/1/1/1
2	PLP	E	1456	3	-	0/6/6/8	0/1/1/1
2	PLP	D	1456	3	-	1/6/6/8	0/1/1/1
2	PLP	A	1456	3	-	0/6/6/8	0/1/1/1
3	ABU	J	1457	2	-	0/2/4/4	-
3	ABU	C	1457	2	-	1/2/4/4	-
2	PLP	I	1457	3	-	0/6/6/8	0/1/1/1
3	ABU	D	1457	2	-	1/2/4/4	-
2	PLP	J	1456	3	-	2/6/6/8	0/1/1/1
3	ABU	F	1457	2	-	0/2/4/4	-
3	ABU	I	1458	2	-	0/2/4/4	-
3	ABU	H	1457	2	-	0/2/4/4	-
2	PLP	H	1456	3	-	2/6/6/8	0/1/1/1
2	PLP	K	1456	3	-	0/6/6/8	0/1/1/1
2	PLP	L	1456	3	-	0/6/6/8	0/1/1/1

The worst 5 of 71 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1456	PLP	C2A-C2	-8.26	1.36	1.50
2	H	1456	PLP	C2A-C2	-7.10	1.38	1.50
2	G	1456	PLP	C2A-C2	-7.07	1.38	1.50
2	J	1456	PLP	C2A-C2	-7.01	1.38	1.50
2	I	1457	PLP	C2A-C2	-6.85	1.38	1.50

The worst 5 of 49 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	1456	PLP	O2P-P-O1P	-5.05	90.89	110.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1456	PLP	O3P-P-O4P	4.09	117.63	106.73
2	H	1456	PLP	C4-C3-C2	3.99	125.97	120.07
2	I	1457	PLP	O3P-P-O4P	3.93	117.20	106.73
2	F	1456	PLP	C4-C3-C2	3.79	125.67	120.07

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	J	1456	PLP	C5A-O4P-P-O1P
2	H	1456	PLP	C5A-O4P-P-O3P
3	K	1457	ABU	CA-CB-CG-CD
3	D	1457	ABU	CA-CB-CG-CD
2	H	1456	PLP	C5A-O4P-P-O1P

There are no ring outliers.

12 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	1457	ABU	1	0
3	B	1457	ABU	1	0
3	A	1457	ABU	1	0
2	E	1456	PLP	1	0
2	D	1456	PLP	1	0
2	A	1456	PLP	1	0
3	J	1457	ABU	1	0
3	D	1457	ABU	1	0
2	J	1456	PLP	1	0
3	H	1457	ABU	1	0
2	H	1456	PLP	1	0
2	K	1456	PLP	1	0

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, 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	442/456 (96%)	-0.36	0 100 100	15, 27, 47, 68	0
1	B	442/456 (96%)	-0.35	0 100 100	13, 25, 38, 55	0
1	C	442/456 (96%)	-0.22	1 (0%) 95 97	17, 32, 53, 76	0
1	D	441/456 (96%)	-0.20	0 100 100	18, 35, 52, 72	0
1	E	442/456 (96%)	-0.31	1 (0%) 95 97	17, 32, 51, 68	0
1	F	444/456 (97%)	-0.31	0 100 100	19, 29, 47, 76	0
1	G	440/456 (96%)	0.03	8 (1%) 68 76	20, 45, 66, 85	0
1	H	440/456 (96%)	0.03	11 (2%) 57 66	24, 52, 77, 98	0
1	I	440/456 (96%)	0.04	11 (2%) 57 66	26, 51, 77, 105	0
1	J	438/456 (96%)	0.21	15 (3%) 45 53	26, 53, 74, 98	0
1	K	437/456 (95%)	0.19	10 (2%) 60 69	29, 59, 86, 103	0
1	L	436/456 (95%)	0.37	30 (6%) 16 20	33, 62, 84, 98	0
All	All	5284/5472 (96%)	-0.07	87 (1%) 72 79	13, 40, 74, 105	0

The worst 5 of 87 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	55	GLY	4.2
1	H	416	VAL	4.1
1	L	79	GLY	3.8
1	H	434	LEU	3.7
1	H	53	ALA	3.7

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 carbohydrates in this entry.

6.4 Ligands ⓘ

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(\AA^2)	Q<0.9
3	ABU	L	1457	7/7	0.90	0.33	64,66,70,71	0
3	ABU	J	1457	7/7	0.91	0.25	47,54,59,61	0
3	ABU	G	1457	7/7	0.93	0.19	46,48,50,53	0
3	ABU	K	1457	7/7	0.94	0.28	58,65,69,69	0
3	ABU	C	1457	7/7	0.94	0.32	37,38,42,42	0
3	ABU	I	1458	7/7	0.94	0.15	48,59,66,67	0
3	ABU	H	1457	7/7	0.94	0.25	42,49,51,52	0
2	PLP	L	1456	15/16	0.95	0.16	49,64,70,74	0
2	PLP	H	1456	15/16	0.96	0.18	30,33,52,53	0
2	PLP	I	1457	15/16	0.97	0.18	41,45,49,52	0
3	ABU	D	1457	7/7	0.97	0.30	34,40,45,49	0
2	PLP	J	1456	15/16	0.97	0.16	36,39,52,61	0
3	ABU	F	1457	7/7	0.97	0.25	25,27,29,30	0
3	ABU	A	1457	7/7	0.97	0.15	28,30,33,33	0
2	PLP	C	1456	15/16	0.97	0.18	25,28,32,32	0
3	ABU	B	1457	7/7	0.97	0.18	23,26,27,29	0
2	PLP	K	1456	15/16	0.97	0.17	47,59,65,66	0
3	ABU	E	1457	7/7	0.97	0.16	31,32,34,34	0
2	PLP	A	1456	15/16	0.98	0.15	20,23,26,27	0
2	PLP	E	1456	15/16	0.98	0.15	18,23,27,30	0
2	PLP	D	1456	15/16	0.98	0.21	20,24,28,28	0
2	PLP	B	1456	15/16	0.99	0.13	19,23,25,25	0
2	PLP	G	1456	15/16	0.99	0.16	32,35,40,41	0
2	PLP	F	1456	15/16	0.99	0.14	19,21,24,27	0

6.5 Other polymers ⓘ

There are no such residues in this entry.