



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 01:47 PM UTC

PDB ID : 4ATQ / pdb_00004atq
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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

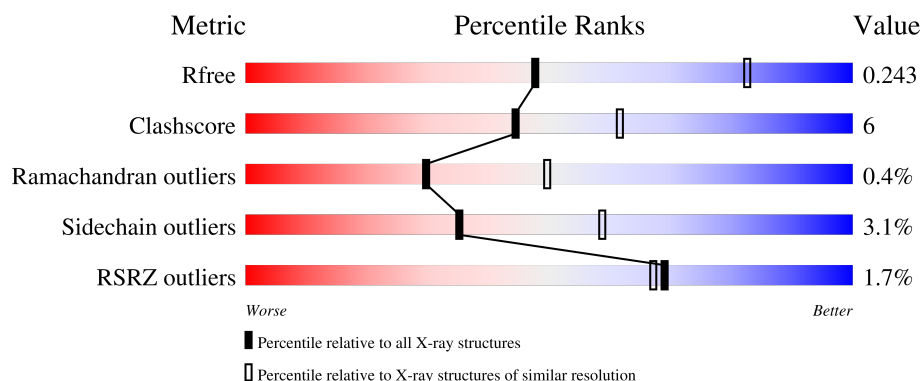
1 Overall quality at a glance

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}	180053	1009 (2.76-2.76)
Clashscore	190562	1044 (2.76-2.76)
Ramachandran outliers	187476	1024 (2.76-2.76)
Sidechain outliers	187428	1024 (2.76-2.76)
RSRZ outliers	180081	1009 (2.76-2.76)

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 $\leq 5\%$. 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	85% 11% ..
1	B	456	85% 11% ..
1	C	456	87% 8% ..
1	D	456	85% 10% ..
1	E	456	83% 12% ..

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Mol	Chain	Length	Quality of chain
1	F	456	83%13%
1	G	456	81%14%
1	H	456	4% 83%12%
1	I	456	2% 86%9%
1	J	456	2% 82%12%
1	K	456	6% 85%11%
1	L	456	4% 87%7%

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:

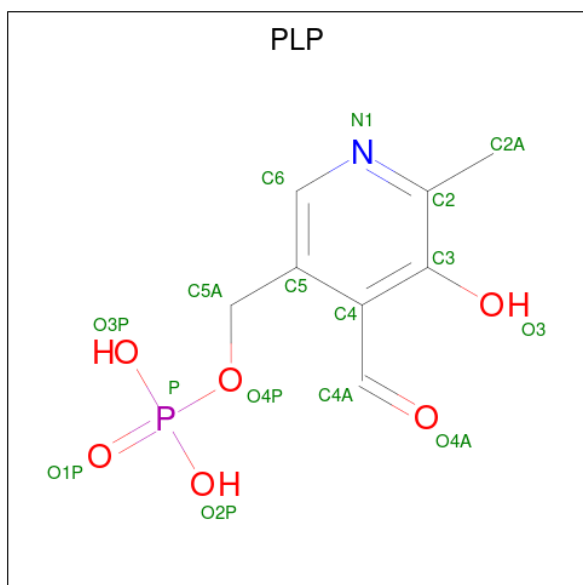
Chain	Residue	Modelled	Actual	Comment	Reference
A	113	THR	ALA	SEE REMARK 999	UNP A1R958
B	113	THR	ALA	SEE REMARK 999	UNP A1R958
C	113	THR	ALA	SEE REMARK 999	UNP A1R958
D	113	THR	ALA	SEE REMARK 999	UNP A1R958
E	113	THR	ALA	SEE REMARK 999	UNP A1R958

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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 (CCD ID: PLP) (formula: $C_8H_{10}NO_6P$).



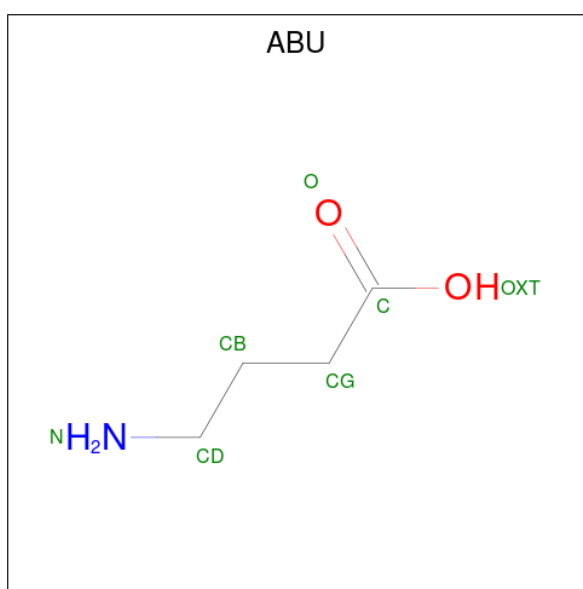
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	B	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	C	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	D	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	E	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	F	1	Total	C	N	O	P	0	0
			15	8	1	5	1		
2	G	1	Total	C	N	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 (CCD ID: ABU) (formula: C₄H₉NO₂).



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		

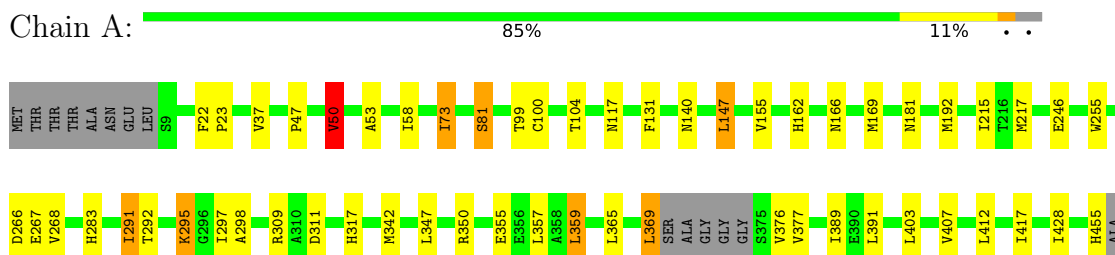
- Molecule 4 is water.

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		

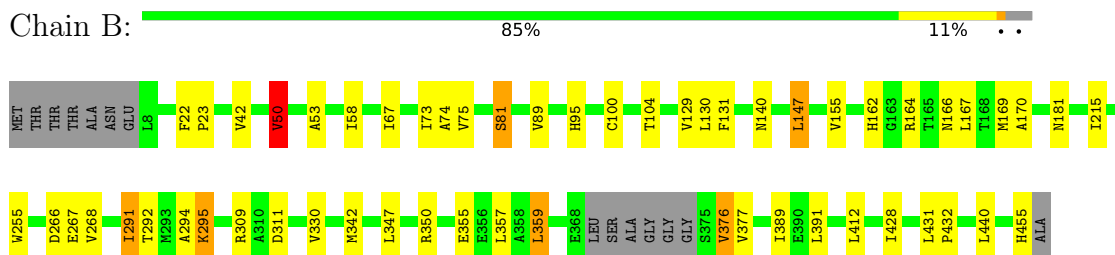
3 Residue-property plots

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.

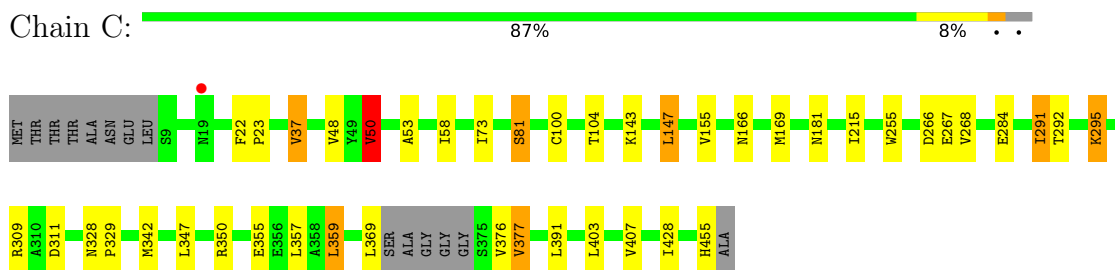
• Molecule 1: 4-AMINOBUTYRATE TRANSAMINASE



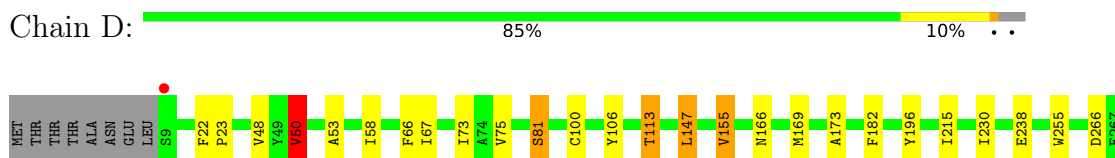
• Molecule 1: 4-AMINOBUTYRATE TRANSAMINASE

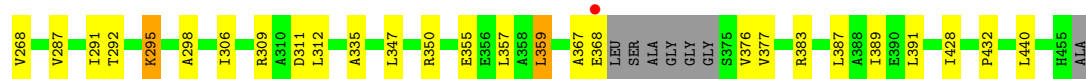


• Molecule 1: 4-AMINOBUTYRATE TRANSAMINASE



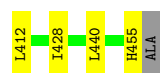
• Molecule 1: 4-AMINOBUTYRATE TRANSAMINASE





• Molecule 1: 4-AMINO BUTYRATE TRANSAMINASE

Chain E: 83% 12% ..



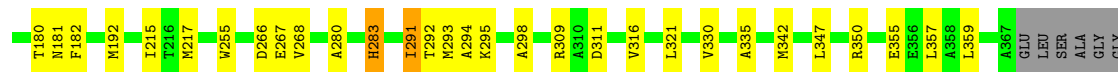
• Molecule 1: 4-AMINO BUTYRATE TRANSAMINASE

Chain F: 83% 13% :: ..



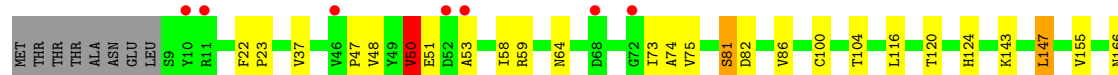
• Molecule 1: 4-AMINO BUTYRATE TRANSAMINASE

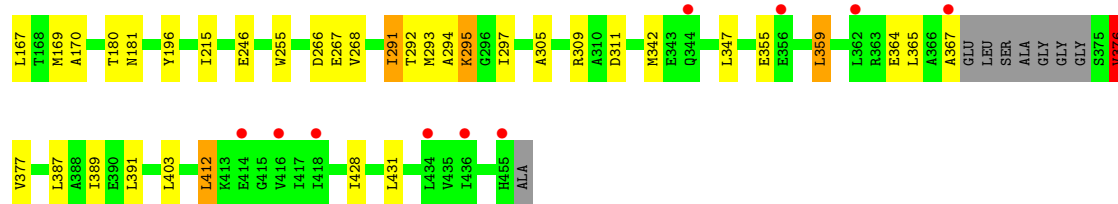
Chain G: 81% 14% . .



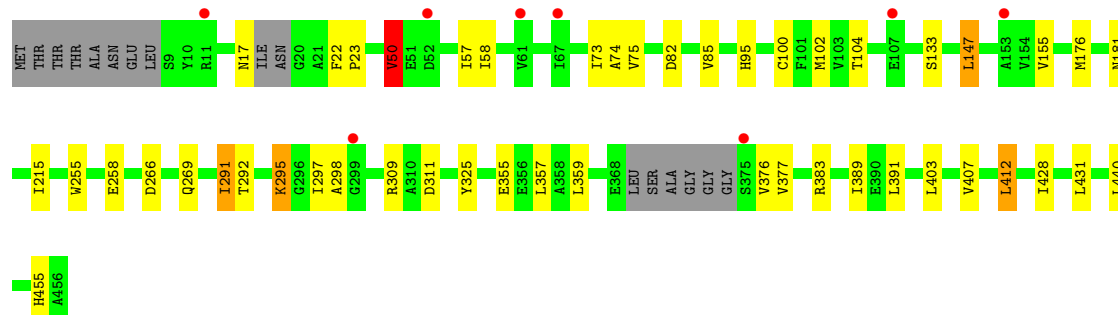
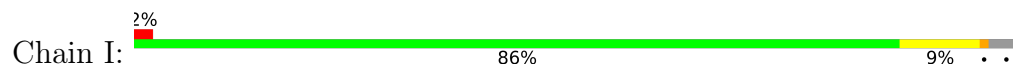
• Molecule 1: 4-AMINO BUTYRATE TRANSAMINASE

Chain H: 4% 83% 12% ..

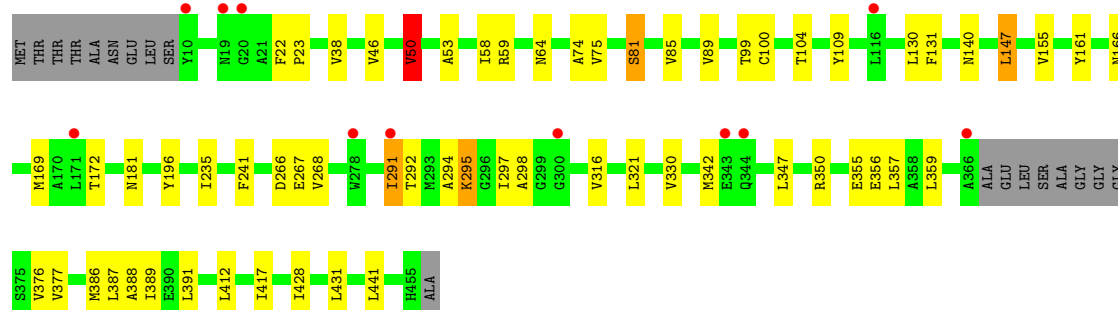
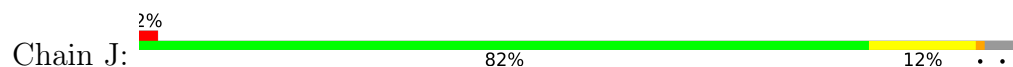




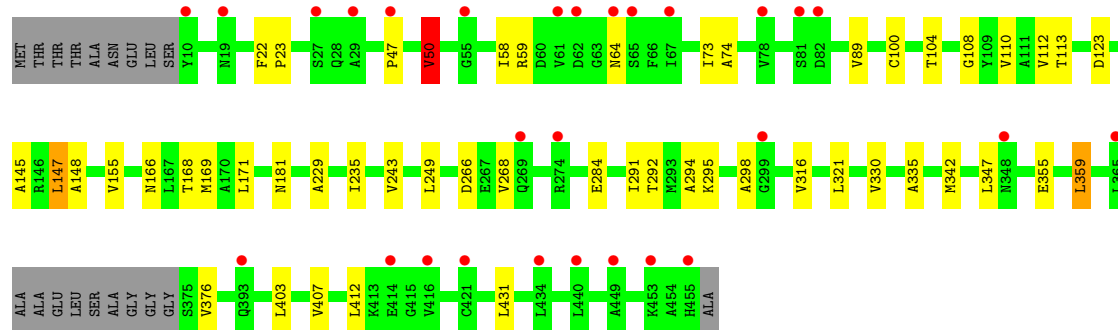
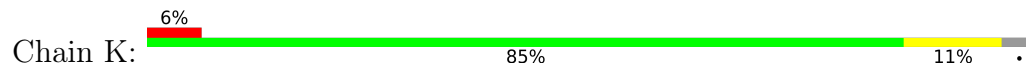
• Molecule 1: 4-AMINO BUTYRATE TRANSAMINASE



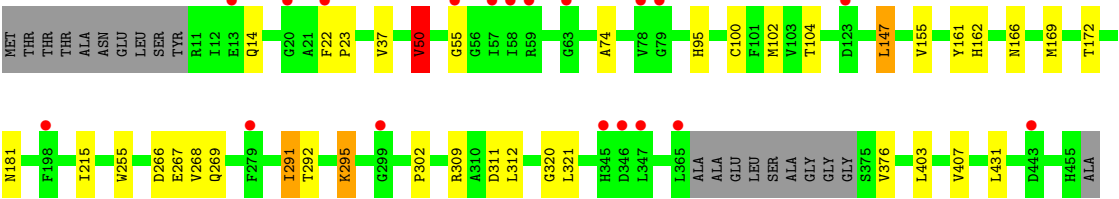
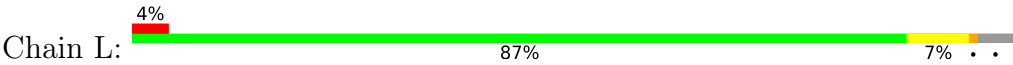
• Molecule 1: 4-AMINO BUTYRATE TRANSAMINASE



• Molecule 1: 4-AMINO BUTYRATE TRANSAMINASE



• Molecule 1: 4-AMINO BUTYRATE TRANSAMINASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	176.71Å 292.83Å 105.96Å 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 2.73Å)	Xtriage
Refinement program	REFMAC 5.6.0119	Depositor
R, R_{free}	0.202 , 0.248 0.201 , 0.243	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)	0.34 , 47.8	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	0.93	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: PLP, ABU

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	0.96	4/3292 (0.1%)	0.93	2/4479 (0.0%)
1	B	0.96	3/3312 (0.1%)	0.94	3/4503 (0.1%)
1	C	0.94	2/3296 (0.1%)	0.93	2/4483 (0.0%)
1	D	0.87	0/3281	0.91	4/4462 (0.1%)
1	E	0.92	4/3280 (0.1%)	0.93	3/4461 (0.1%)
1	F	0.96	6/3304 (0.2%)	0.93	3/4493 (0.1%)
1	G	0.87	1/3238 (0.0%)	0.89	1/4411 (0.0%)
1	H	0.84	0/3150	0.89	4/4302 (0.1%)
1	I	0.85	3/3194 (0.1%)	0.88	1/4350 (0.0%)
1	J	0.80	0/3193	0.89	3/4351 (0.1%)
1	K	0.81	0/3025	0.90	1/4141 (0.0%)
1	L	0.81	2/3039 (0.1%)	0.90	2/4157 (0.0%)
All	All	0.89	25/38604 (0.1%)	0.91	29/52593 (0.1%)

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	317	HIS	ND1-CE1	6.42	1.39	1.32
1	B	162	HIS	CG-CD2	6.31	1.42	1.35
1	F	455	HIS	ND1-CE1	6.15	1.38	1.32
1	E	254	GLU	CA-CB	6.13	1.62	1.53
1	F	455	HIS	CG-CD2	6.04	1.42	1.35

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	50	VAL	CB-CA-C	-7.25	101.28	111.28
1	C	50	VAL	CB-CA-C	-6.88	100.81	111.26
1	B	50	VAL	CB-CA-C	-6.77	100.97	111.26
1	L	50	VAL	CB-CA-C	-6.57	101.28	111.26
1	E	50	VAL	CB-CA-C	-6.41	101.51	111.26

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	38	0
1	B	3250	0	3248	32	0
1	C	3237	0	3223	41	0
1	D	3222	0	3214	42	0
1	E	3221	0	3220	50	0
1	F	3241	0	3229	64	0
1	G	3179	0	3132	57	0
1	H	3093	0	2976	44	0
1	I	3136	0	3035	36	0
1	J	3135	0	3077	45	0
1	K	2969	0	2741	40	0
1	L	2983	0	2737	24	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	0	0
2	L	15	0	6	0	0
3	A	7	0	0	2	0
3	B	7	0	0	1	0
3	C	7	0	0	0	0
3	D	7	0	0	1	0
3	E	7	0	0	1	0
3	F	7	0	0	0	0
3	G	7	0	0	0	0
3	H	7	0	0	1	0
3	I	7	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	J	7	0	0	1	0
3	K	7	0	0	0	0
3	L	7	0	0	0	0
4	A	101	0	0	0	0
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	37125	452	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 452 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:C:147:LEU:HD12	1:C:147:LEU:C	1.90	0.94
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

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%)	24	43
1	B	439/456 (96%)	418 (95%)	18 (4%)	3 (1%)	18	34
1	C	438/456 (96%)	416 (95%)	20 (5%)	2 (0%)	24	43
1	D	437/456 (96%)	414 (95%)	21 (5%)	2 (0%)	24	43
1	E	438/456 (96%)	417 (95%)	19 (4%)	2 (0%)	24	43
1	F	441/456 (97%)	417 (95%)	23 (5%)	1 (0%)	43	64
1	G	436/456 (96%)	414 (95%)	21 (5%)	1 (0%)	43	64
1	H	436/456 (96%)	414 (95%)	20 (5%)	2 (0%)	24	43
1	I	434/456 (95%)	412 (95%)	20 (5%)	2 (0%)	24	43
1	J	434/456 (95%)	413 (95%)	19 (4%)	2 (0%)	24	43
1	K	433/456 (95%)	411 (95%)	20 (5%)	2 (0%)	24	43
1	L	432/456 (95%)	410 (95%)	20 (5%)	2 (0%)	24	43
All	All	5236/5472 (96%)	4973 (95%)	240 (5%)	23 (0%)	30	50

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%)	309 (96%)	12 (4%)	30	54
1	B	324/336 (96%)	314 (97%)	10 (3%)	35	59
1	C	320/336 (95%)	308 (96%)	12 (4%)	29	52
1	D	318/336 (95%)	308 (97%)	10 (3%)	35	59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	317/336 (94%)	307 (97%)	10 (3%)	34	58
1	F	319/336 (95%)	310 (97%)	9 (3%)	38	61
1	G	309/336 (92%)	299 (97%)	10 (3%)	34	58
1	H	288/336 (86%)	277 (96%)	11 (4%)	29	52
1	I	294/336 (88%)	285 (97%)	9 (3%)	35	59
1	J	301/336 (90%)	292 (97%)	9 (3%)	36	60
1	K	254/336 (76%)	247 (97%)	7 (3%)	38	61
1	L	260/336 (77%)	255 (98%)	5 (2%)	50	70
All	All	3625/4032 (90%)	3511 (97%)	114 (3%)	35	59

5 of 114 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	113	THR
1	L	147	LEU
1	G	357	LEU
1	L	50	VAL
1	J	357	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 53 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	345	HIS
1	H	17	ASN
1	L	181	ASN
1	F	393	GLN
1	G	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 oligosaccharides 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	C	1457	2	6,6,6	0.61	0	6,6,6	1.87	2 (33%)
2	PLP	J	1456	3	15,15,16	3.21	6 (40%)	21,22,23	1.27	1 (4%)
2	PLP	G	1456	3	15,15,16	3.00	6 (40%)	21,22,23	1.61	4 (19%)
3	ABU	F	1457	2	6,6,6	1.02	0	6,6,6	1.37	1 (16%)
2	PLP	K	1456	3	15,15,16	2.95	6 (40%)	21,22,23	1.89	6 (28%)
3	ABU	B	1457	2	6,6,6	1.15	0	6,6,6	1.02	0
2	PLP	F	1456	3	15,15,16	2.44	5 (33%)	21,22,23	1.60	5 (23%)
2	PLP	C	1456	3	15,15,16	3.05	6 (40%)	21,22,23	1.73	5 (23%)
3	ABU	E	1457	2	6,6,6	0.76	0	6,6,6	1.44	1 (16%)
3	ABU	D	1457	2	6,6,6	1.16	1 (16%)	6,6,6	1.45	1 (16%)
2	PLP	H	1456	3	15,15,16	3.19	7 (46%)	21,22,23	2.19	6 (28%)
2	PLP	A	1456	3	15,15,16	2.61	5 (33%)	21,22,23	1.47	4 (19%)
3	ABU	J	1457	2	6,6,6	1.22	1 (16%)	6,6,6	1.53	1 (16%)
2	PLP	E	1456	3	15,15,16	2.68	7 (46%)	21,22,23	1.53	4 (19%)
3	ABU	K	1457	2	6,6,6	0.70	0	6,6,6	1.78	2 (33%)
2	PLP	I	1457	3	15,15,16	3.20	6 (40%)	21,22,23	1.41	2 (9%)
3	ABU	G	1457	2	6,6,6	1.16	0	6,6,6	1.24	1 (16%)
3	ABU	H	1457	2	6,6,6	0.80	0	6,6,6	1.60	1 (16%)
3	ABU	I	1458	2	6,6,6	0.82	0	6,6,6	1.64	2 (33%)
3	ABU	A	1457	2	6,6,6	0.83	0	6,6,6	1.28	1 (16%)
3	ABU	L	1457	2	6,6,6	1.15	0	6,6,6	1.25	1 (16%)
2	PLP	D	1456	3	15,15,16	3.25	6 (40%)	21,22,23	1.73	5 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PLP	L	1456	3	15,15,16	2.83	5 (33%)	21,22,23	1.57	4 (19%)
2	PLP	B	1456	3	15,15,16	2.62	6 (40%)	21,22,23	1.60	4 (19%)

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

The worst 5 of 73 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1456	PLP	C2A-C2	-8.86	1.36	1.50
2	H	1456	PLP	C2A-C2	-7.62	1.38	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	1456	PLP	C2A-C2	-7.59	1.38	1.50
2	J	1456	PLP	C2A-C2	-7.52	1.38	1.50
2	I	1457	PLP	C2A-C2	-7.35	1.38	1.50

The worst 5 of 64 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	1456	PLP	O2P-P-O1P	-5.12	90.89	110.83
2	D	1456	PLP	O3P-P-O4P	4.20	117.63	106.67
2	H	1456	PLP	C4-C3-C2	4.07	125.97	119.89
2	I	1457	PLP	O3P-P-O4P	4.04	117.20	106.67
2	E	1456	PLP	O4P-P-O1P	3.90	116.97	106.44

There are no chirality outliers.

5 of 29 torsion outliers are listed below:

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

There are no ring outliers.

12 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	J	1456	PLP	1	0
3	B	1457	ABU	1	0
3	E	1457	ABU	1	0
3	D	1457	ABU	1	0
2	H	1456	PLP	1	0
2	A	1456	PLP	1	0
3	J	1457	ABU	1	0
2	E	1456	PLP	1	0
3	H	1457	ABU	1	0
3	I	1458	ABU	1	0
3	A	1457	ABU	2	0
2	D	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%)	-0.53	0 100 100	15, 27, 47, 68	0
1	B	442/456 (96%)	-0.60	0 100 100	13, 25, 38, 55	1 (0%)
1	C	442/456 (96%)	-0.33	1 (0%) 91 92	17, 32, 53, 76	0
1	D	441/456 (96%)	-0.32	2 (0%) 87 87	18, 35, 52, 72	0
1	E	442/456 (96%)	-0.39	1 (0%) 91 92	17, 32, 51, 68	0
1	F	444/456 (97%)	-0.43	2 (0%) 87 87	17, 29, 47, 76	1 (0%)
1	G	440/456 (96%)	0.06	0 100 100	20, 45, 66, 85	0
1	H	440/456 (96%)	0.26	17 (3%) 43 40	24, 52, 77, 98	0
1	I	440/456 (96%)	0.19	8 (1%) 67 65	26, 51, 77, 105	0
1	J	438/456 (96%)	0.30	11 (2%) 58 56	26, 53, 74, 98	0
1	K	437/456 (95%)	0.65	28 (6%) 25 25	29, 59, 86, 103	0
1	L	436/456 (95%)	0.59	19 (4%) 39 38	33, 62, 84, 98	0
All	All	5284/5472 (96%)	-0.05	89 (1%) 69 67	13, 40, 74, 105	2 (0%)

The worst 5 of 89 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	68	ASP	4.6
1	K	416	VAL	4.5
1	H	434	LEU	4.3
1	L	365	LEU	4.0
1	J	10	TYR	3.8

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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
3	ABU	J	1457	7/7	0.88	0.14	47,54,59,61	0
3	ABU	I	1458	7/7	0.89	0.11	48,59,66,67	0
3	ABU	L	1457	7/7	0.89	0.14	64,66,70,71	0
3	ABU	K	1457	7/7	0.90	0.12	58,65,69,69	0
3	ABU	C	1457	7/7	0.91	0.14	37,38,42,42	0
3	ABU	G	1457	7/7	0.91	0.10	46,48,50,53	0
3	ABU	H	1457	7/7	0.93	0.12	42,49,51,52	0
3	ABU	D	1457	7/7	0.94	0.15	34,40,45,49	0
3	ABU	F	1457	7/7	0.94	0.14	25,27,29,30	0
2	PLP	K	1456	15/16	0.94	0.11	47,59,65,66	0
2	PLP	H	1456	15/16	0.94	0.08	30,33,52,53	0
2	PLP	L	1456	15/16	0.95	0.10	49,64,70,74	0
3	ABU	A	1457	7/7	0.95	0.07	28,30,33,33	0
3	ABU	B	1457	7/7	0.95	0.10	23,26,27,29	0
2	PLP	I	1457	15/16	0.95	0.07	41,45,49,52	0
3	ABU	E	1457	7/7	0.96	0.08	31,32,34,34	0
2	PLP	J	1456	15/16	0.96	0.07	36,39,52,61	0
2	PLP	E	1456	15/16	0.97	0.07	18,23,27,30	0
2	PLP	C	1456	15/16	0.97	0.07	25,28,32,32	0
2	PLP	D	1456	15/16	0.98	0.09	20,24,28,28	0
2	PLP	B	1456	15/16	0.98	0.05	19,23,25,25	0
2	PLP	G	1456	15/16	0.98	0.05	32,35,40,41	0
2	PLP	A	1456	15/16	0.98	0.06	20,23,26,27	0
2	PLP	F	1456	15/16	0.99	0.04	19,21,24,27	0

6.5 Other polymers ⓘ

There are no such residues in this entry.