



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 18, 2026 – 10:51 AM UTC

PDB ID : 1FC4 / pdb_00001fc4
Title : 2-AMINO-3-KETOBUTYRATE COA LIGASE
Authors : Schmidt, A.; Matte, A.; Li, Y.; Sivaraman, J.; Larocque, R.; Schrag, J.D.;
Smith, C.; Sauve, V.; Cygler, M.; Montreal-Kingston Bacterial Structural Ge-
nomics Initiative (BSGI)
Deposited on : 2000-07-17
Resolution : 2.00 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 ⓘ 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

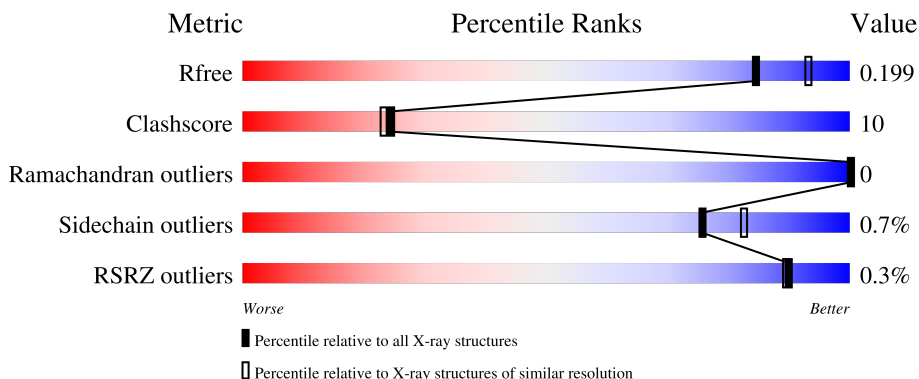
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 2.00 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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	401	 80% 19% .
1	B	401	 81% 18% .

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
2	AKB	A	1200	-	-	X	-
2	AKB	B	1202	-	-	X	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7238 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 2-AMINO-3-KETOBUTYRATE CONENZYME A LIGASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	401	3043	1903	544	578	6	12	0	0	0
1	B	401	3046	1905	545	578	6	12	0	0	0

There are 30 discrepancies between the modelled and reference sequences:

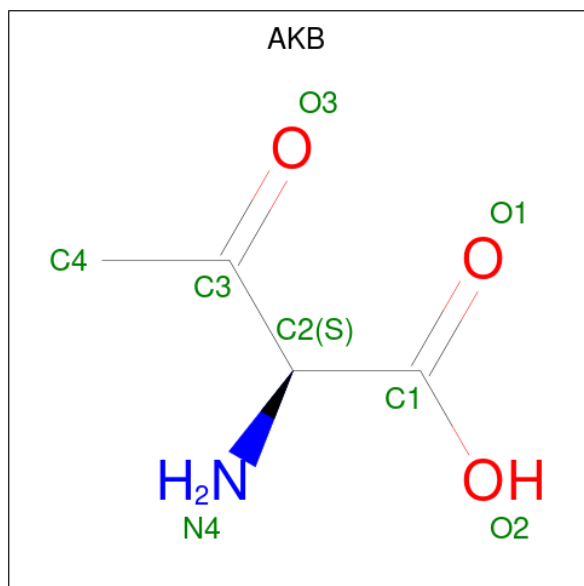
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	cloning artifact	UNP P07912
A	-1	SER	-	cloning artifact	UNP P07912
A	0	HIS	-	cloning artifact	UNP P07912
A	1	MSE	MET	modified residue	UNP P07912
A	69	MSE	MET	modified residue	UNP P07912
A	76	MSE	MET	modified residue	UNP P07912
A	102	MSE	MET	modified residue	UNP P07912
A	158	MSE	MET	modified residue	UNP P07912
A	186	MSE	MET	modified residue	UNP P07912
A	208	MSE	MET	modified residue	UNP P07912
A	232	MSE	MET	modified residue	UNP P07912
A	291	MSE	MET	modified residue	UNP P07912
A	313	MSE	MET	modified residue	UNP P07912
A	331	MSE	MET	modified residue	UNP P07912
A	371	MSE	MET	modified residue	UNP P07912
B	-2	GLY	-	cloning artifact	UNP P07912
B	-1	SER	-	cloning artifact	UNP P07912
B	0	HIS	-	cloning artifact	UNP P07912
B	1	MSE	MET	modified residue	UNP P07912
B	69	MSE	MET	modified residue	UNP P07912
B	76	MSE	MET	modified residue	UNP P07912
B	102	MSE	MET	modified residue	UNP P07912
B	158	MSE	MET	modified residue	UNP P07912
B	186	MSE	MET	modified residue	UNP P07912
B	208	MSE	MET	modified residue	UNP P07912

Continued on next page...

Continued from previous page...

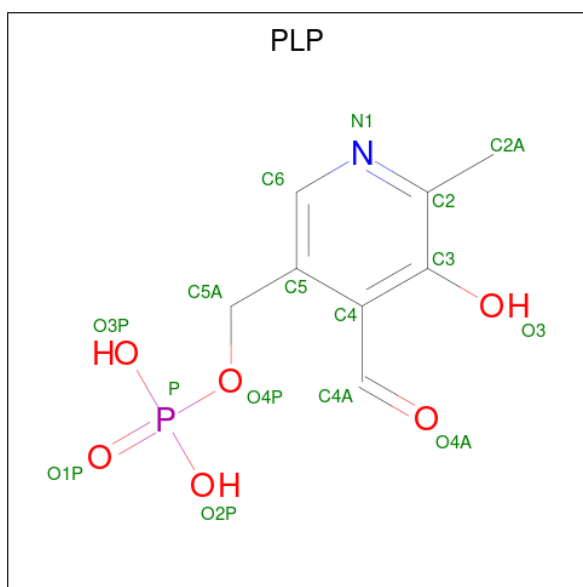
Chain	Residue	Modelled	Actual	Comment	Reference
B	232	MSE	MET	modified residue	UNP P07912
B	291	MSE	MET	modified residue	UNP P07912
B	313	MSE	MET	modified residue	UNP P07912
B	331	MSE	MET	modified residue	UNP P07912
B	371	MSE	MET	modified residue	UNP P07912

- Molecule 2 is 2-AMINO-3-KETOBUTYRIC ACID (CCD ID: AKB) (formula: C₄H₇NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	8	4	1	3	0	0
2	B	1	8	4	1	3	0	0

- Molecule 3 is PYRIDOXAL-5'-PHOSPHATE (CCD ID: PLP) (formula: C₈H₁₀NO₆P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	A	1	15	8	1	5	1	0	0
3	B	1	15	8	1	5	1	0	0

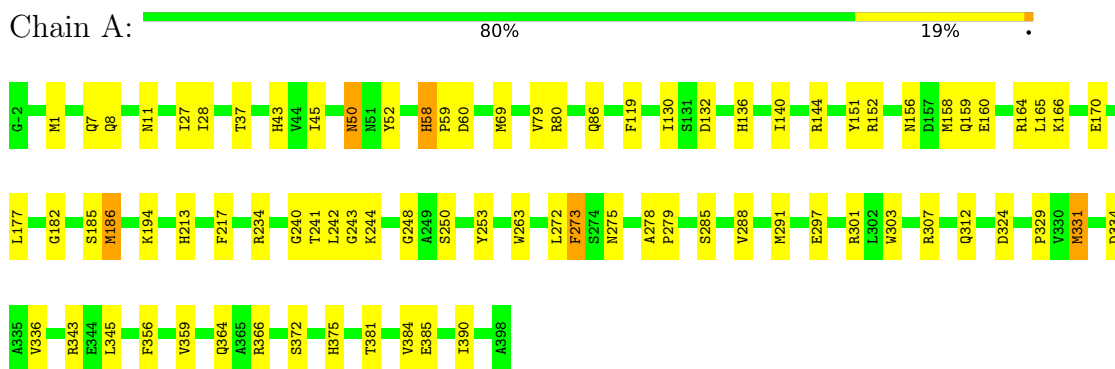
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	535	535	535	0	0
4	B	568	568	568	0	0

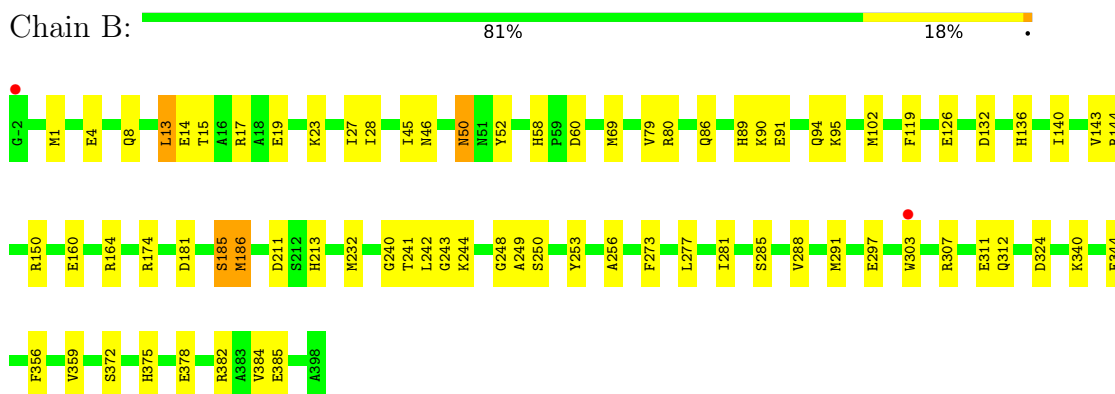
3 Residue-property plots

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: 2-AMINO-3-KETOBUTYRATE CONENZYME A LIGASE



- Molecule 1: 2-AMINO-3-KETOBUTYRATE CONENZYME A LIGASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	63.94Å 98.66Å 118.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	12.00 – 2.00 12.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (12.00-2.00) 98.4 (12.00-2.00)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	10.13 (at 2.00Å)	Xtrriage
Refinement program		Depositor
R, R_{free}	0.151 , 0.212 0.158 , 0.199	Depositor DCC
R_{free} test set	5098 reflections (10.05%)	wwPDB-VP
Wilson B-factor (Å ²)	13.9	Xtrriage
Anisotropy	0.285	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 68.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7238	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 25.07 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.3976e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.54	5/3080 (0.2%)	0.91	13/4133 (0.3%)
1	B	0.53	4/3083 (0.1%)	0.90	10/4137 (0.2%)
All	All	0.54	9/6163 (0.1%)	0.90	23/8270 (0.3%)

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	331	MSE	SE-CE	-7.61	1.72	1.95
1	A	69	MSE	SE-CE	-5.84	1.77	1.95
1	B	186	MSE	SE-CE	-5.73	1.78	1.95
1	B	69	MSE	SE-CE	-5.62	1.78	1.95
1	A	186	MSE	SE-CE	-5.39	1.79	1.95

The worst 5 of 23 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	185	SER	N-CA-C	9.27	123.69	112.38
1	B	80	ARG	N-CA-C	8.04	120.05	111.28
1	A	185	SER	N-CA-C	7.92	122.64	112.34
1	A	80	ARG	N-CA-C	7.60	119.56	111.28
1	A	79	VAL	N-CA-C	-6.61	102.85	110.05

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	3043	0	3004	62	0
1	B	3046	0	3007	65	0
2	A	8	0	5	7	0
2	B	8	0	5	8	0
3	A	15	0	7	0	0
3	B	15	0	7	0	0
4	A	535	0	0	7	0
4	B	568	0	0	7	0
All	All	7238	0	6035	120	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 10.

The worst 5 of 120 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:A:1200:AKB:H41	4:B:1254:HOH:O	1.68	0.92
1:B:126:GLU:HB2	1:B:174:ARG:HH12	1.32	0.90
4:A:1212:HOH:O	2:B:1202:AKB:H41	1.73	0.88
1:B:126:GLU:HB2	1:B:174:ARG:NH1	1.89	0.87
1:B:58:HIS:HD2	1:B:60:ASP:H	1.24	0.86

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	399/401 (100%)	380 (95%)	19 (5%)	0	100	100
1	B	399/401 (100%)	381 (96%)	18 (4%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	798/802 (100%)	761 (95%)	37 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	306/295 (104%)	306 (100%)	0	100	100
1	B	306/295 (104%)	302 (99%)	4 (1%)	61	68
All	All	612/590 (104%)	608 (99%)	4 (1%)	76	82

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	13	LEU
1	B	17	ARG
1	B	160	GLU
1	B	211	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	58	HIS
1	B	159	GLN
1	B	155	ASN
1	B	312	GLN
1	A	308	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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
2	AKB	A	1200	3	5,7,7	2.02	3 (60%)	2,9,9	1.03	0
2	AKB	B	1202	3	5,7,7	1.94	3 (60%)	2,9,9	1.07	0
3	PLP	A	1201	2	15,15,16	3.18	7 (46%)	21,22,23	1.57	5 (23%)
3	PLP	B	1203	2	15,15,16	3.22	8 (53%)	21,22,23	1.57	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
2	AKB	A	1200	3	-	0/6/8/8	-
2	AKB	B	1202	3	-	0/6/8/8	-
3	PLP	A	1201	2	-	3/6/6/8	0/1/1/1
3	PLP	B	1203	2	-	5/6/6/8	0/1/1/1

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1201	PLP	C5-C4	7.30	1.48	1.40

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1203	PLP	C5-C4	7.26	1.48	1.40
3	A	1201	PLP	C2-N1	5.58	1.43	1.33
3	B	1203	PLP	C2-N1	5.53	1.43	1.33
3	B	1203	PLP	C3-C4	4.93	1.49	1.40

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1203	PLP	C5-C6-N1	-3.08	118.82	123.83
3	A	1201	PLP	C5-C6-N1	-3.04	118.88	123.83
3	B	1203	PLP	O4P-C5A-C5	3.03	115.04	109.36
3	A	1201	PLP	O4P-C5A-C5	2.86	114.72	109.36
3	B	1203	PLP	C6-C5-C4	2.67	120.28	118.10

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1201	PLP	C5A-O4P-P-O3P
3	B	1203	PLP	C4-C5-C5A-O4P
3	B	1203	PLP	C5A-O4P-P-O2P
3	B	1203	PLP	C5A-O4P-P-O3P
3	A	1201	PLP	C5A-O4P-P-O1P

There are no ring outliers.

2 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1200	AKB	7	0
2	B	1202	AKB	8	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 [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	389/401 (97%)	-0.55	0 100 100	6, 12, 25, 36	0
1	B	389/401 (97%)	-0.56	2 (0%) 87 87	6, 12, 25, 34	1 (0%)
All	All	778/802 (97%)	-0.55	2 (0%) 90 89	6, 12, 25, 36	1 (0%)

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	-2	GLY	2.7
1	B	303	TRP	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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
2	AKB	A	1200	8/8	0.71	0.22	23,29,31,36	0
2	AKB	B	1202	8/8	0.71	0.18	23,29,31,36	0
3	PLP	A	1201	15/16	0.94	0.14	7,23,27,27	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	PLP	B	1203	15/16	0.95	0.12	7,23,27,27	0

6.5 Other polymers [i](#)

There are no such residues in this entry.