



# wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 4, 2023 – 07:27 PM EDT

PDB ID : 1MT1  
Title : The Crystal Structure of Pyruvoyl-dependent Arginine Decarboxylase from Methanococcus jannaschii  
Authors : Tolbert, W.D.; Graham, D.E.; White, R.H.; Ealick, S.E.  
Deposited on : 2002-09-20  
Resolution : 2.20 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](mailto: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>.

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

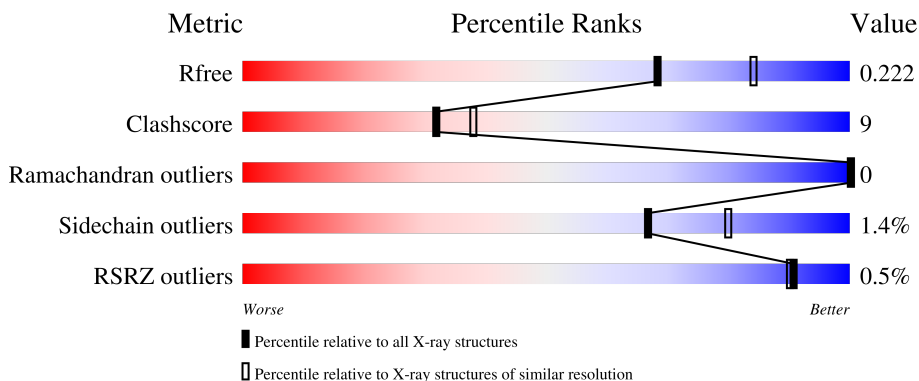
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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  $\geq 3$ , 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	52	 79% 10% 12%
1	C	52	 87% 6% 8%
1	E	52	 69% 25% . .
1	G	52	 63% 15% 21%
1	I	52	 71% 21% . 6%

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Mol	Chain	Length	Quality of chain
1	K	52	
2	B	113	
2	D	113	
2	F	113	
2	H	113	
2	J	113	
2	L	113	

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
3	AG2	C	7004	-	-	-	X

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 7968 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 PYRUVOYL-DEPENDENT ARGININE DECARBOXYLASE BETA CHAIN.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
1	A	46	364	235	60	69	0	3	0
1	C	48	360	230	61	69	0	1	0
1	E	50	397	253	66	78	0	4	0
1	G	41	309	196	52	61	0	2	0
1	I	49	377	241	63	73	0	2	0
1	K	45	344	220	58	66	0	2	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	modified residue	UNP Q57764
C	1	MSE	MET	modified residue	UNP Q57764
E	1	MSE	MET	modified residue	UNP Q57764
G	1	MSE	MET	modified residue	UNP Q57764
I	1	MSE	MET	modified residue	UNP Q57764
K	1	MSE	MET	modified residue	UNP Q57764

- Molecule 2 is a protein called PYRUVOYL-DEPENDENT ARGININE DECARBOXYLASE ALPHA CHAIN.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
2	B	113	872	562	137	165	3	5	0	2	0
2	D	113	911	586	142	174	4	5	0	7	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	N	O	S	Se			
2	F	113	887	573	139	167	3	5	0	4	0
2	H	113	899	581	141	169	3	5	0	5	0
2	J	113	882	569	138	167	3	5	0	3	0
2	L	113	867	561	136	162	3	5	0	1	0

There are 36 discrepancies between the modelled and reference sequences:

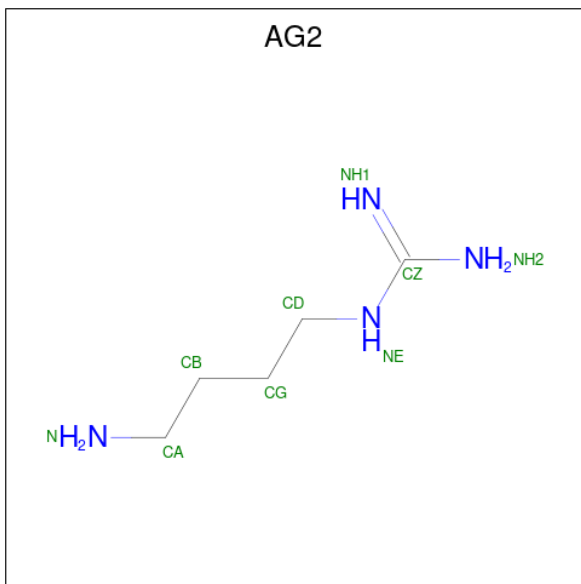
Chain	Residue	Modelled	Actual	Comment	Reference
B	53	PYR	SER	SEE REMARK 999	UNP Q57764
B	55	MSE	MET	modified residue	UNP Q57764
B	69	MSE	MET	modified residue	UNP Q57764
B	108	MSE	MET	modified residue	UNP Q57764
B	126	MSE	MET	modified residue	UNP Q57764
B	133	MSE	MET	modified residue	UNP Q57764
D	53	PYR	SER	SEE REMARK 999	UNP Q57764
D	55	MSE	MET	modified residue	UNP Q57764
D	69	MSE	MET	modified residue	UNP Q57764
D	108	MSE	MET	modified residue	UNP Q57764
D	126	MSE	MET	modified residue	UNP Q57764
D	133	MSE	MET	modified residue	UNP Q57764
F	53	PYR	SER	SEE REMARK 999	UNP Q57764
F	55	MSE	MET	modified residue	UNP Q57764
F	69	MSE	MET	modified residue	UNP Q57764
F	108	MSE	MET	modified residue	UNP Q57764
F	126	MSE	MET	modified residue	UNP Q57764
F	133	MSE	MET	modified residue	UNP Q57764
H	53	PYR	SER	SEE REMARK 999	UNP Q57764
H	55	MSE	MET	modified residue	UNP Q57764
H	69	MSE	MET	modified residue	UNP Q57764
H	108	MSE	MET	modified residue	UNP Q57764
H	126	MSE	MET	modified residue	UNP Q57764
H	133	MSE	MET	modified residue	UNP Q57764
J	53	PYR	SER	SEE REMARK 999	UNP Q57764
J	55	MSE	MET	modified residue	UNP Q57764
J	69	MSE	MET	modified residue	UNP Q57764
J	108	MSE	MET	modified residue	UNP Q57764
J	126	MSE	MET	modified residue	UNP Q57764
J	133	MSE	MET	modified residue	UNP Q57764
L	53	PYR	SER	SEE REMARK 999	UNP Q57764

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Chain	Residue	Modelled	Actual	Comment	Reference
L	55	MSE	MET	modified residue	UNP Q57764
L	69	MSE	MET	modified residue	UNP Q57764
L	108	MSE	MET	modified residue	UNP Q57764
L	126	MSE	MET	modified residue	UNP Q57764
L	133	MSE	MET	modified residue	UNP Q57764

- Molecule 3 is AGMATINE (three-letter code: AG2) (formula: C<sub>5</sub>H<sub>14</sub>N<sub>4</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N 9 5 4	0	0
3	B	1	Total C N 9 5 4	0	0
3	C	1	Total C N 9 5 4	0	0
3	G	1	Total C N 9 5 4	0	0
3	K	1	Total C N 9 5 4	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	25	Total O 25 25	0	0
4	B	52	Total O 52 52	0	0

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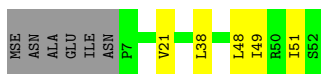
<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>	<b>ZeroOcc</b>	<b>AltConf</b>
4	C	26	Total O 26 26	0	0
4	D	56	Total O 56 56	0	0
4	E	31	Total O 31 31	0	0
4	F	60	Total O 60 60	0	0
4	G	21	Total O 21 21	0	0
4	H	47	Total O 47 47	0	0
4	I	28	Total O 28 28	0	0
4	J	39	Total O 39 39	0	0
4	K	26	Total O 26 26	0	0
4	L	43	Total O 43 43	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.

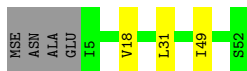
- Molecule 1: PYRUVOYL-DEPENDENT ARGININE DECARBOXYLASE BETA CHAIN

Chain A: 



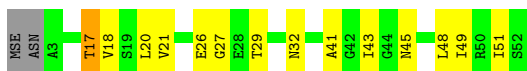
- Molecule 1: PYRUVOYL-DEPENDENT ARGININE DECARBOXYLASE BETA CHAIN

Chain C: 



- Molecule 1: PYRUVOYL-DEPENDENT ARGININE DECARBOXYLASE BETA CHAIN

Chain E: 



- Molecule 1: PYRUVOYL-DEPENDENT ARGININE DECARBOXYLASE BETA CHAIN

Chain G: 



- Molecule 1: PYRUVOYL-DEPENDENT ARGININE DECARBOXYLASE BETA CHAIN

Chain I: 



- Molecule 1: PYRUVOYL-DEPENDENT ARGININE DECARBOXYLASE BETA CHAIN

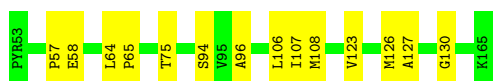
Chain K: 





● Molecule 2: PYRUVOYL-DEPENDENT ARGININE DECARBOXYLASE ALPHA CHAIN

Chain B: 88% 12%



● Molecule 2: PYRUVOYL-DEPENDENT ARGININE DECARBOXYLASE ALPHA CHAIN

Chain D: 84% 16%



● Molecule 2: PYRUVOYL-DEPENDENT ARGININE DECARBOXYLASE ALPHA CHAIN

Chain F: 78% 21%



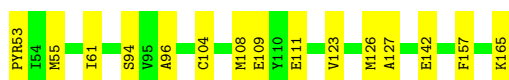
● Molecule 2: PYRUVOYL-DEPENDENT ARGININE DECARBOXYLASE ALPHA CHAIN

Chain H: 84% 16%



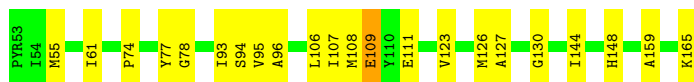
● Molecule 2: PYRUVOYL-DEPENDENT ARGININE DECARBOXYLASE ALPHA CHAIN

Chain J: 87% 13%



● Molecule 2: PYRUVOYL-DEPENDENT ARGININE DECARBOXYLASE ALPHA CHAIN

Chain L: 81% 19%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	56.77Å 92.99Å 87.23Å 90.00° 94.84° 90.00°	Depositor
Resolution (Å)	63.50 – 2.20 63.50 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.7 (63.50-2.20) 99.7 (63.50-2.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.14	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.75 (at 2.00Å)	Xtrriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.190 , 0.229 0.184 , 0.222	Depositor DCC
$R_{free}$ test set	8839 reflections (7.37%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	19.1	Xtrriage
Anisotropy	0.134	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 52.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	7968	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	19.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.16% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: PYR, AG2

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.36	0/371	0.63	0/504
1	C	0.36	0/366	0.59	0/498
1	E	0.39	0/403	0.64	0/549
1	G	0.36	0/312	0.64	0/423
1	I	0.37	0/383	0.63	0/521
1	K	0.40	0/349	0.60	0/474
2	B	0.34	0/880	0.62	0/1181
2	D	0.34	0/918	0.63	0/1231
2	F	0.32	0/895	0.63	0/1203
2	H	0.33	0/906	0.62	0/1213
2	J	0.31	0/889	0.60	0/1191
2	L	0.34	0/875	0.60	0/1174
All	All	0.34	0/7547	0.62	0/10162

There are no bond length outliers.

There are no bond angle outliers.

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	364	0	366	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	360	0	364	4	0
1	E	397	0	396	17	0
1	G	309	0	316	17	0
1	I	377	0	380	14	0
1	K	344	0	348	20	0
2	B	872	0	890	15	0
2	D	911	0	922	20	0
2	F	887	0	909	21	0
2	H	899	0	921	23	0
2	J	882	0	899	12	0
2	L	867	0	890	19	0
3	A	9	0	13	1	0
3	B	9	0	13	1	0
3	C	9	0	13	0	0
3	G	9	0	13	2	0
3	K	9	0	13	2	0
4	A	25	0	0	0	0
4	B	52	0	0	0	0
4	C	26	0	0	0	0
4	D	56	0	0	0	0
4	E	31	0	0	0	0
4	F	60	0	0	2	0
4	G	21	0	0	0	0
4	H	47	0	0	0	0
4	I	28	0	0	0	0
4	J	39	0	0	0	0
4	K	26	0	0	0	0
4	L	43	0	0	0	0
All	All	7968	0	7666	136	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 9.

The worst 5 of 136 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:D:104[B]:CYS:SG	2:F:69:MSE:HB3	1.81	1.21
2:D:134:ARG:HE	1:E:45:ASN:HD21	1.14	0.93
2:D:104[B]:CYS:HG	2:F:69:MSE:HB3	1.26	0.93
2:H:134:ARG:HE	1:K:45:ASN:HD21	1.17	0.91
1:E:21[B]:VAL:HG12	1:E:41:ALA:HB1	1.69	0.75

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	47/52 (90%)	45 (96%)	2 (4%)	0	100	100
1	C	47/52 (90%)	45 (96%)	2 (4%)	0	100	100
1	E	52/52 (100%)	50 (96%)	2 (4%)	0	100	100
1	G	41/52 (79%)	40 (98%)	1 (2%)	0	100	100
1	I	49/52 (94%)	47 (96%)	2 (4%)	0	100	100
1	K	45/52 (86%)	43 (96%)	2 (4%)	0	100	100
2	B	113/113 (100%)	112 (99%)	1 (1%)	0	100	100
2	D	118/113 (104%)	116 (98%)	2 (2%)	0	100	100
2	F	115/113 (102%)	113 (98%)	2 (2%)	0	100	100
2	H	116/113 (103%)	114 (98%)	2 (2%)	0	100	100
2	J	114/113 (101%)	112 (98%)	2 (2%)	0	100	100
2	L	112/113 (99%)	111 (99%)	1 (1%)	0	100	100
All	All	969/990 (98%)	948 (98%)	21 (2%)	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	39/40 (98%)	39 (100%)	0	100	100
1	C	39/40 (98%)	39 (100%)	0	100	100
1	E	43/40 (108%)	42 (98%)	1 (2%)	50	63
1	G	34/40 (85%)	34 (100%)	0	100	100
1	I	41/40 (102%)	40 (98%)	1 (2%)	49	62
1	K	37/40 (92%)	36 (97%)	1 (3%)	44	57
2	B	92/85 (108%)	92 (100%)	0	100	100
2	D	97/85 (114%)	96 (99%)	1 (1%)	76	86
2	F	94/85 (111%)	92 (98%)	2 (2%)	53	67
2	H	95/85 (112%)	94 (99%)	1 (1%)	73	85
2	J	93/85 (109%)	91 (98%)	2 (2%)	52	65
2	L	91/85 (107%)	89 (98%)	2 (2%)	52	65
All	All	795/750 (106%)	784 (99%)	11 (1%)	67	80

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	J	111	GLU
1	K	14	LEU
2	L	111	GLU
2	L	109	GLU
2	H	113	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	32	ASN
1	I	16	ASN
1	K	45	ASN
1	I	32	ASN
1	E	45	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

5 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	AG2	G	7003	-	8,8,8	0.30	0	7,8,8	0.31	0
3	AG2	K	7002	-	8,8,8	0.29	0	7,8,8	0.31	0
3	AG2	A	7005	-	8,8,8	0.29	0	7,8,8	0.34	0
3	AG2	C	7004	-	8,8,8	0.33	0	7,8,8	0.28	0
3	AG2	B	7001	-	8,8,8	0.29	0	7,8,8	0.29	0

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	AG2	G	7003	-	-	0/6/6/6	-
3	AG2	K	7002	-	-	0/6/6/6	-
3	AG2	A	7005	-	-	1/6/6/6	-
3	AG2	C	7004	-	-	0/6/6/6	-
3	AG2	B	7001	-	-	0/6/6/6	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	7005	AG2	CG-CD-NE-CZ

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	7003	AG2	2	0
3	K	7002	AG2	2	0
3	A	7005	AG2	1	0
3	B	7001	AG2	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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	46/52 (88%)	-0.39	0 100 100	7, 14, 27, 51	0
1	C	48/52 (92%)	-0.51	0 100 100	7, 13, 32, 48	0
1	E	50/52 (96%)	-0.50	0 100 100	8, 13, 24, 38	0
1	G	41/52 (78%)	-0.44	0 100 100	7, 13, 27, 44	0
1	I	49/52 (94%)	-0.22	0 100 100	10, 18, 40, 53	0
1	K	45/52 (86%)	0.01	5 (11%) 5 4	8, 14, 55, 71	0
2	B	107/113 (94%)	-0.42	0 100 100	6, 16, 30, 36	0
2	D	107/113 (94%)	-0.46	0 100 100	6, 16, 30, 36	0
2	F	107/113 (94%)	-0.45	0 100 100	5, 14, 28, 41	0
2	H	107/113 (94%)	-0.41	0 100 100	7, 17, 33, 37	0
2	J	107/113 (94%)	-0.34	0 100 100	9, 19, 37, 41	0
2	L	107/113 (94%)	-0.36	0 100 100	7, 18, 32, 37	0
All	All	921/990 (93%)	-0.39	5 (0%) 91 90	5, 16, 34, 71	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	K	8	LEU	6.4
1	K	10	ALA	5.8
1	K	9	HIS	4.4
1	K	12	PHE	3.3
1	K	11	TYR	2.5

### 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 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, 95<sup>th</sup> 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	AG2	C	7004	9/9	0.31	0.55	32,39,41,41	9
3	AG2	A	7005	9/9	0.68	0.31	28,32,40,41	9
3	AG2	K	7002	9/9	0.71	0.34	25,32,37,37	9
3	AG2	G	7003	9/9	0.78	0.27	30,35,40,40	9
3	AG2	B	7001	9/9	0.80	0.25	28,32,38,41	9

### 6.5 Other polymers [i](#)

There are no such residues in this entry.