



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 10, 2026 – 02:09 PM EDT

PDB ID : 35WD / pdb\_000035wd  
Title : 3-bromopropiolate treated pyr5 from Streptomyces pyridomyceticus  
Authors : Melkonian, T.R.; Stephenson, R.; Katz, B.W.; Zhang, Y.; Whitman, C.P.  
Deposited on : 2026-05-20  
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 : 4-5-2 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

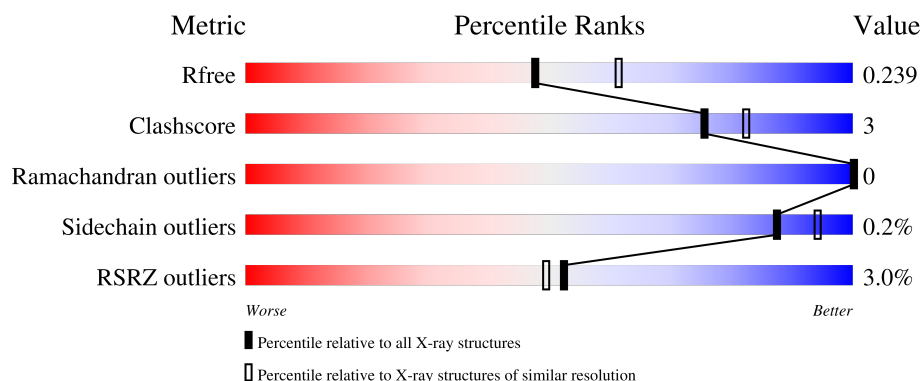
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.20 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))
$R_{free}$	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (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	71	<div> <div>75%</div> <div>7%</div> <div>17%</div> </div>
1	B	71	<div> <div>73%</div> <div>8%</div> <div>17%</div> </div>
1	C	71	<div> <div>3%</div> <div>77%</div> <div>17%</div> </div>
1	D	71	<div> <div>70%</div> <div>13%</div> <div>17%</div> </div>
1	E	71	<div> <div>7%</div> <div>79%</div> <div>17%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	71	<div><div><div>%</div><div><div></div><div></div><div></div></div><div>79%</div><div>•</div><div>17%</div></div></div>
1	G	71	<div><div><div>%</div><div><div></div><div></div><div></div></div><div>73%</div><div>10%</div><div>17%</div></div></div>
1	H	71	<div><div><div>%</div><div><div></div><div></div><div></div></div><div>77%</div><div>•</div><div>18%</div></div></div>
1	I	71	<div><div><div>%</div><div><div></div><div></div><div></div></div><div>77%</div><div>6%</div><div>17%</div></div></div>
1	K	71	<div><div><div>6%</div><div><div></div><div></div><div></div></div><div>80%</div><div>••</div><div>17%</div></div></div>
1	L	71	<div><div><div>3%</div><div><div></div><div></div><div></div></div><div>77%</div><div>6%</div><div>17%</div></div></div>
2	J	71	<div><div><div>%</div><div><div></div><div></div><div></div></div><div>82%</div><div></div><div>18%</div></div></div>

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 11770 atoms, of which 5688 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-oxalocrotonate tautomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	G	59	Total	C	H	N	O	0	0	0
			964	310	476	85	93			
1	H	58	Total	C	H	N	O	0	0	0
			947	304	469	82	92			
1	I	59	Total	C	H	N	O	0	0	0
			954	308	470	84	92			
1	K	59	Total	C	H	N	O	0	0	0
			964	310	476	85	93			
1	L	59	Total	C	H	N	O	0	0	0
			964	310	476	85	93			
1	A	59	Total	C	H	N	O	0	0	0
			964	310	476	85	93			
1	B	59	Total	C	H	N	O	0	0	0
			964	310	476	85	93			
1	C	59	Total	C	H	N	O	0	0	0
			964	310	476	85	93			
1	D	59	Total	C	H	N	O	0	0	0
			954	308	470	84	92			
1	E	59	Total	C	H	N	O	0	0	0
			964	310	476	85	93			
1	F	59	Total	C	H	N	O	0	0	0
			964	310	476	85	93			

- Molecule 2 is a protein called 4-oxalocrotonate tautomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	J	58	Total	C	H	N	O	0	0	0
			943	301	471	82	89			

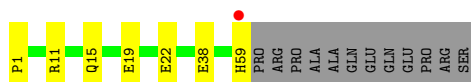
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	G	25	Total 25	O 25	0	0
3	H	20	Total 20	O 20	0	0
3	I	17	Total 17	O 17	0	0
3	J	25	Total 25	O 25	0	0
3	K	23	Total 23	O 23	0	0
3	L	17	Total 17	O 17	0	0
3	A	21	Total 21	O 21	0	0
3	B	27	Total 27	O 27	0	0
3	C	22	Total 22	O 22	0	0
3	D	24	Total 24	O 24	0	0
3	E	17	Total 17	O 17	0	0
3	F	22	Total 22	O 22	0	0

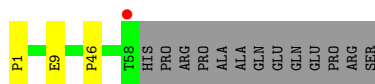
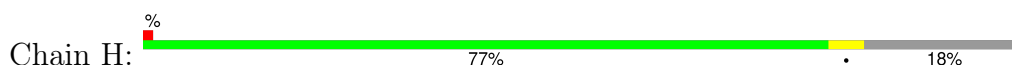
### 3 Residue-property plots [i](#)

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.

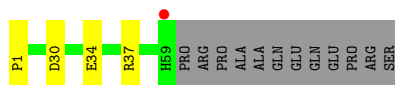
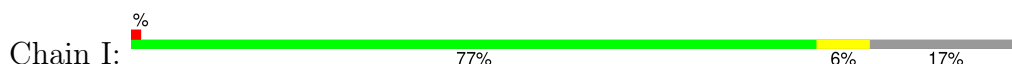
- Molecule 1: 4-oxalocrotonate tautomerase



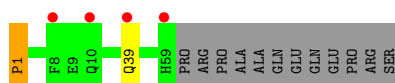
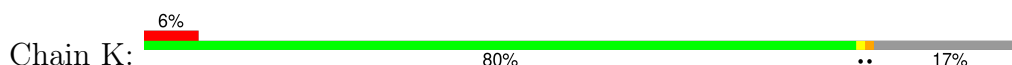
- Molecule 1: 4-oxalocrotonate tautomerase



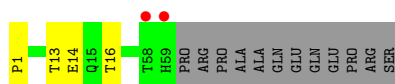
- Molecule 1: 4-oxalocrotonate tautomerase



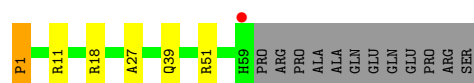
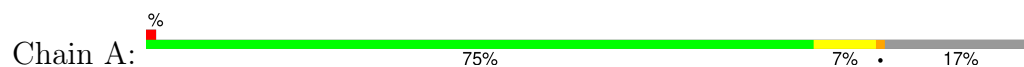
- Molecule 1: 4-oxalocrotonate tautomerase



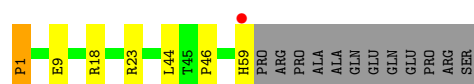
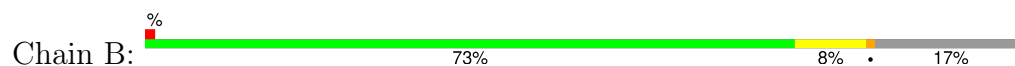
- Molecule 1: 4-oxalocrotonate tautomerase



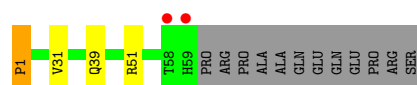
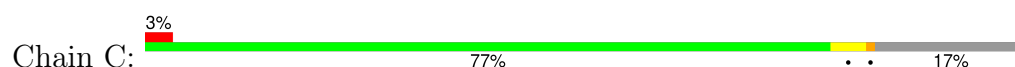
- Molecule 1: 4-oxalocrotonate tautomerase



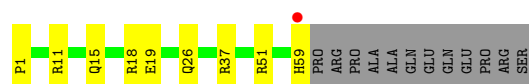
- Molecule 1: 4-oxalocrotonate tautomerase



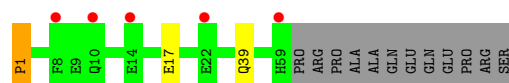
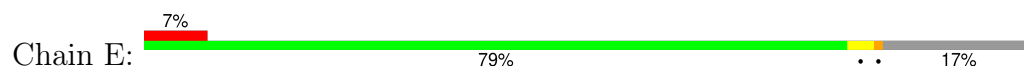
- Molecule 1: 4-oxalocrotonate tautomerase



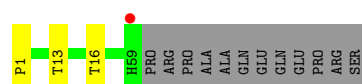
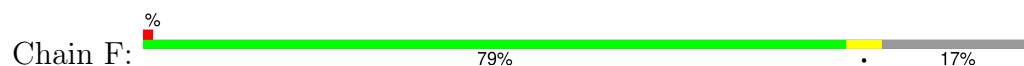
- Molecule 1: 4-oxalocrotonate tautomerase



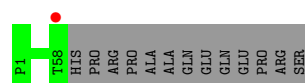
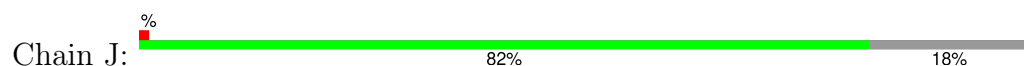
- Molecule 1: 4-oxalocrotonate tautomerase



- Molecule 1: 4-oxalocrotonate tautomerase



- Molecule 2: 4-oxalocrotonate tautomerase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	48.91Å 75.34Å 180.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	90.22 – 2.20 90.22 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.4 (90.22-2.20) 99.6 (90.22-2.20)	Depositor EDS
$R_{merge}$	0.15	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.07 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.21.1_5286	Depositor
R, $R_{free}$	0.191 , 0.239 0.192 , 0.239	Depositor DCC
$R_{free}$ test set	1750 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	20.8	Xtriage
Anisotropy	0.519	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.45 , 42.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.53$ , $\langle L^2 \rangle = 0.37$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	11770	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 39.04 % 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 3.3674e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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: ZIO

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	0.10	0/485	0.29	0/659
1	B	0.10	0/485	0.25	0/659
1	C	0.11	0/485	0.28	0/659
1	D	0.10	0/481	0.25	0/654
1	E	0.10	0/485	0.27	0/659
1	F	0.10	0/485	0.30	0/659
1	G	0.13	0/485	0.30	0/659
1	H	0.13	0/474	0.28	0/644
1	I	0.10	0/481	0.26	0/654
1	K	0.11	0/485	0.28	0/659
1	L	0.11	0/485	0.30	0/659
2	J	0.10	0/482	0.26	0/655
All	All	0.11	0/5798	0.28	0/7879

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	488	476	469	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	488	476	469	6	0
1	C	488	476	469	4	0
1	D	484	470	463	8	0
1	E	488	476	469	2	0
1	F	488	476	469	1	0
1	G	488	476	469	6	0
1	H	478	469	462	2	0
1	I	484	470	463	2	0
1	K	488	476	469	1	0
1	L	488	476	469	2	0
2	J	472	471	471	0	0
3	A	21	0	0	1	0
3	B	27	0	0	2	0
3	C	22	0	0	0	0
3	D	24	0	0	2	0
3	E	17	0	0	0	0
3	F	22	0	0	0	0
3	G	25	0	0	3	0
3	H	20	0	0	1	0
3	I	17	0	0	1	0
3	J	25	0	0	0	0
3	K	23	0	0	0	0
3	L	17	0	0	1	0
All	All	6082	5688	5611	34	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 3.

The worst 5 of 34 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:H:9:GLU:OE1	3:H:101:HOH:O	1.96	0.83
1:G:22:GLU:OE1	3:G:101:HOH:O	1.97	0.81
1:I:30:ASP:OD2	3:I:101:HOH:O	2.05	0.75
1:L:14:GLU:OE1	3:L:101:HOH:O	2.07	0.73
1:A:18:ARG:HG2	1:A:18:ARG:HH11	1.55	0.71

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	57/71 (80%)	57 (100%)	0	0	100	100
1	B	57/71 (80%)	57 (100%)	0	0	100	100
1	C	57/71 (80%)	57 (100%)	0	0	100	100
1	D	57/71 (80%)	57 (100%)	0	0	100	100
1	E	57/71 (80%)	57 (100%)	0	0	100	100
1	F	57/71 (80%)	57 (100%)	0	0	100	100
1	G	57/71 (80%)	57 (100%)	0	0	100	100
1	H	56/71 (79%)	56 (100%)	0	0	100	100
1	I	57/71 (80%)	57 (100%)	0	0	100	100
1	K	57/71 (80%)	56 (98%)	1 (2%)	0	100	100
1	L	57/71 (80%)	57 (100%)	0	0	100	100
2	J	56/71 (79%)	56 (100%)	0	0	100	100
All	All	682/852 (80%)	681 (100%)	1 (0%)	0	100	100

There are no Ramachandran outliers to report.

### 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	52/62 (84%)	52 (100%)	0	100	100
1	B	52/62 (84%)	52 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	52/62 (84%)	52 (100%)	0	100	100
1	D	51/62 (82%)	51 (100%)	0	100	100
1	E	52/62 (84%)	52 (100%)	0	100	100
1	F	52/62 (84%)	52 (100%)	0	100	100
1	G	52/62 (84%)	51 (98%)	1 (2%)	50	66
1	H	51/62 (82%)	51 (100%)	0	100	100
1	I	51/62 (82%)	51 (100%)	0	100	100
1	K	52/62 (84%)	52 (100%)	0	100	100
1	L	52/62 (84%)	52 (100%)	0	100	100
2	J	52/63 (82%)	52 (100%)	0	100	100
All	All	621/745 (83%)	620 (100%)	1 (0%)	87	94

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	59	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	G	15	GLN
1	B	59	HIS
1	F	15	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
1	ZI0	F	1	1	12,13,14	2.06	3 (25%)	12,17,19	1.84	4 (33%)
1	ZI0	H	1	1	12,13,14	2.15	3 (25%)	12,17,19	1.70	3 (25%)
1	ZI0	I	1	1	12,13,14	2.08	3 (25%)	12,17,19	1.96	4 (33%)
1	ZI0	B	1	1	12,13,14	2.01	3 (25%)	12,17,19	1.81	3 (25%)
1	ZI0	E	1	1	12,13,14	1.94	3 (25%)	12,17,19	1.97	4 (33%)
1	ZI0	K	1	1	12,13,14	2.14	4 (33%)	12,17,19	1.97	3 (25%)
1	ZI0	L	1	1	12,13,14	2.21	4 (33%)	12,17,19	2.12	5 (41%)
1	ZI0	D	1	1	12,13,14	2.23	4 (33%)	12,17,19	2.00	5 (41%)
1	ZI0	C	1	1	12,13,14	1.89	4 (33%)	12,17,19	1.82	4 (33%)
1	ZI0	G	1	1	12,13,14	2.23	3 (25%)	12,17,19	1.92	4 (33%)
1	ZI0	A	1	1	12,13,14	1.90	3 (25%)	12,17,19	2.02	5 (41%)

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
1	ZI0	F	1	1	-	0/8/20/22	0/1/1/1
1	ZI0	H	1	1	-	0/8/20/22	0/1/1/1
1	ZI0	I	1	1	-	0/8/20/22	0/1/1/1
1	ZI0	B	1	1	-	0/8/20/22	0/1/1/1
1	ZI0	E	1	1	-	2/8/20/22	0/1/1/1
1	ZI0	K	1	1	-	0/8/20/22	0/1/1/1
1	ZI0	L	1	1	-	1/8/20/22	0/1/1/1
1	ZI0	D	1	1	-	0/8/20/22	0/1/1/1
1	ZI0	C	1	1	-	0/8/20/22	0/1/1/1
1	ZI0	G	1	1	-	0/8/20/22	0/1/1/1
1	ZI0	A	1	1	-	0/8/20/22	0/1/1/1

The worst 5 of 37 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	1	ZI0	C2-C1	5.88	1.60	1.51
1	H	1	ZI0	C2-C1	5.85	1.60	1.51
1	L	1	ZI0	C2-C1	5.60	1.59	1.51
1	D	1	ZI0	C2-C1	5.57	1.59	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	K	1	ZI0	C2-C1	5.47	1.59	1.51

The worst 5 of 44 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1	ZI0	CB-CA-C	-4.70	106.21	112.66
1	L	1	ZI0	CB-CA-C	-4.57	106.39	112.66
1	K	1	ZI0	CB-CA-C	-4.48	106.51	112.66
1	G	1	ZI0	CB-CA-C	-4.30	106.75	112.66
1	E	1	ZI0	CB-CA-C	-4.20	106.89	112.66

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	E	1	ZI0	O1-C1-C2-C3
1	E	1	ZI0	O2-C1-C2-C3
1	L	1	ZI0	C1-C2-C3-O3

There are no ring outliers.

5 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	1	ZI0	1	0
1	E	1	ZI0	1	0
1	K	1	ZI0	1	0
1	C	1	ZI0	2	0
1	A	1	ZI0	1	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 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, 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	58/71 (81%)	0.02	1 (1%) 69 66	15, 24, 43, 68	0
1	B	58/71 (81%)	-0.00	1 (1%) 69 66	14, 23, 45, 73	0
1	C	58/71 (81%)	0.06	2 (3%) 48 45	14, 25, 44, 65	0
1	D	58/71 (81%)	0.07	1 (1%) 69 66	14, 26, 44, 67	0
1	E	58/71 (81%)	0.10	5 (8%) 16 14	15, 24, 47, 62	0
1	F	58/71 (81%)	-0.23	1 (1%) 69 66	13, 23, 40, 70	0
1	G	58/71 (81%)	-0.00	1 (1%) 69 66	13, 23, 40, 70	0
1	H	57/71 (80%)	-0.17	1 (1%) 67 64	13, 22, 39, 50	0
1	I	58/71 (81%)	0.03	1 (1%) 69 66	15, 27, 43, 63	0
1	K	58/71 (81%)	0.04	4 (6%) 23 20	15, 23, 48, 69	0
1	L	58/71 (81%)	0.05	2 (3%) 48 45	13, 23, 41, 72	0
2	J	58/71 (81%)	-0.00	1 (1%) 69 66	14, 26, 43, 51	0
All	All	695/852 (81%)	-0.00	21 (3%) 52 49	13, 24, 44, 73	0

The worst 5 of 21 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	59	HIS	5.5
1	C	59	HIS	4.3
1	B	59	HIS	3.9
1	F	59	HIS	3.9
1	L	59	HIS	3.8

### 6.2 Non-standard residues in protein, DNA, RNA chains

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(Å <sup>2</sup> )	Q<0.9
1	ZI0	E	1	13/14	0.81	0.17	16,27,39,47	0
1	ZI0	K	1	13/14	0.82	0.16	12,24,42,51	0
1	ZI0	L	1	13/14	0.85	0.13	17,26,48,52	0
1	ZI0	H	1	13/14	0.86	0.16	14,21,38,44	0
1	ZI0	B	1	13/14	0.87	0.17	13,23,45,57	0
1	ZI0	A	1	13/14	0.89	0.11	18,23,38,41	0
1	ZI0	G	1	13/14	0.89	0.10	13,26,33,42	0
1	ZI0	C	1	13/14	0.89	0.12	15,28,45,46	0
1	ZI0	I	1	13/14	0.89	0.12	17,26,39,47	0
1	ZI0	F	1	13/14	0.89	0.12	14,23,39,49	0
1	ZI0	D	1	13/14	0.92	0.09	15,24,31,35	0

### 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

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

There are no such residues in this entry.