



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 02:57 am GMT

PDB ID : 1ZMO  
Title : Apo structure of haloalcohol dehalogenase HheA of Arthrobacter sp. AD2  
Authors : de Jong, R.M.; Kalk, K.H.; Tang, L.; Janssen, D.B.; Dijkstra, B.W.  
Deposited on : 2005-05-10  
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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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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
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

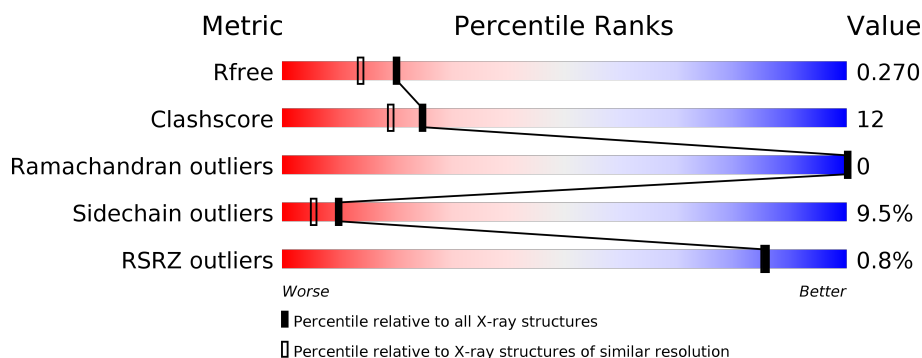
# 1 Overall quality at a glance

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))
$R_{free}$	100719	6609 (2.00-2.00)
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)
RSRZ outliers	101464	6696 (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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	244	<div> <div>75%</div> <div>20%</div> <div>•</div> </div>
1	B	244	<div> <div>78%</div> <div>18%</div> <div>•</div> </div>
1	C	244	<div> <div>2%</div> <div>77%</div> <div>20%</div> <div>•</div> </div>
1	D	244	<div> <div>72%</div> <div>24%</div> <div>•</div> </div>
1	E	244	<div> <div>2%</div> <div>75%</div> <div>21%</div> <div>•</div> </div>
1	F	244	<div> <div>71%</div> <div>23%</div> <div>5%</div> </div>

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Mol	Chain	Length	Quality of chain
1	G	244	<div><div>%</div><div><div></div><div>73%</div><div>23%</div><div></div></div><div></div></div>
1	H	244	<div><div></div><div><div></div><div>76%</div><div>20%</div><div></div></div><div></div></div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 15416 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 halohydrin dehalogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	243	Total	C	N	O	S	0	0	0
			1823	1165	313	341	4			
1	B	243	Total	C	N	O	S	0	0	0
			1825	1167	316	338	4			
1	C	243	Total	C	N	O	S	0	0	0
			1818	1162	313	339	4			
1	D	243	Total	C	N	O	S	0	0	0
			1815	1160	315	336	4			
1	E	243	Total	C	N	O	S	0	0	0
			1822	1162	316	340	4			
1	F	243	Total	C	N	O	S	0	0	0
			1822	1165	315	338	4			
1	G	243	Total	C	N	O	S	0	0	0
			1811	1159	312	336	4			
1	H	243	Total	C	N	O	S	0	0	0
			1818	1163	315	336	4			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	115	Total	O	0	0
			115	115		
2	B	111	Total	O	0	0
			111	111		
2	C	102	Total	O	0	0
			102	102		
2	D	111	Total	O	0	0
			111	111		
2	E	93	Total	O	0	0
			93	93		
2	F	110	Total	O	0	0
			110	110		

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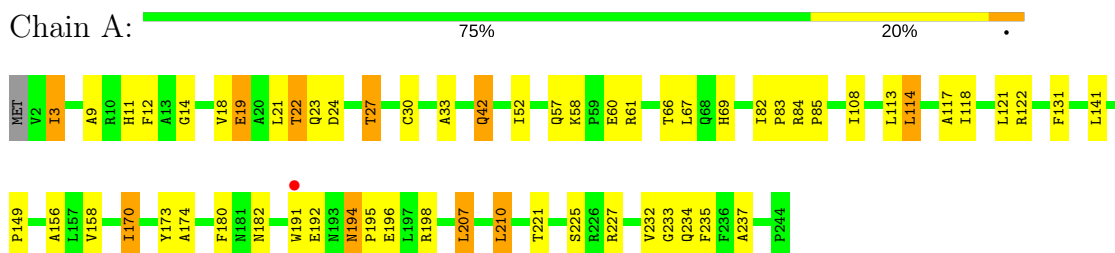
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	G	111	Total 111	O 111	0	0
2	H	109	Total 109	O 109	0	0

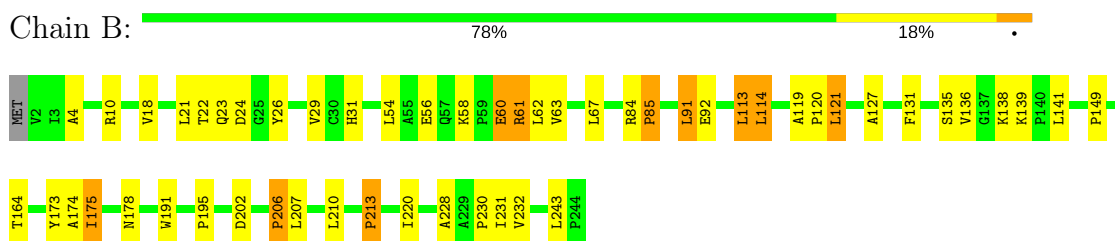
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

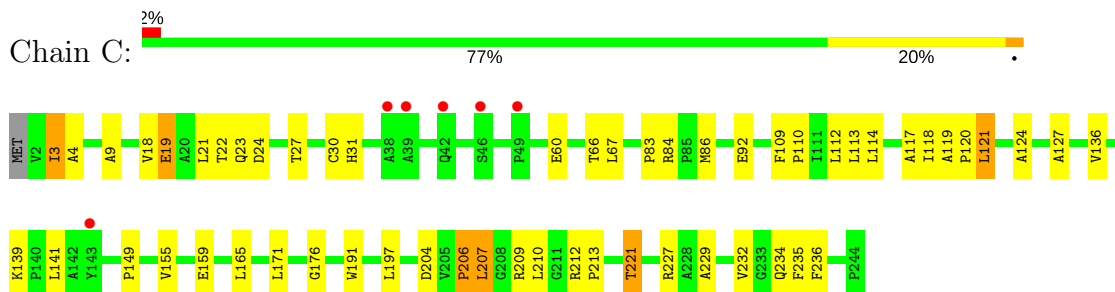
- Molecule 1: halohydrin dehalogenase



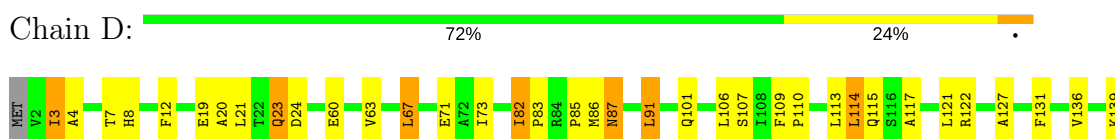
- Molecule 1: halohydrin dehalogenase

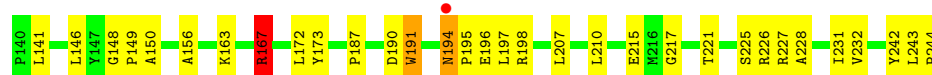


- Molecule 1: halohydrin dehalogenase

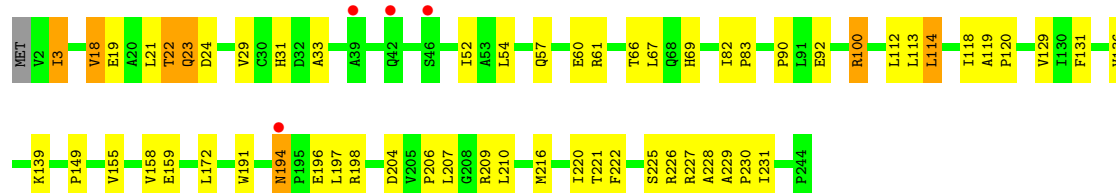
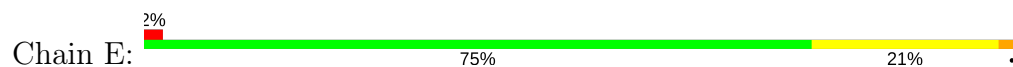


- Molecule 1: halohydrin dehalogenase

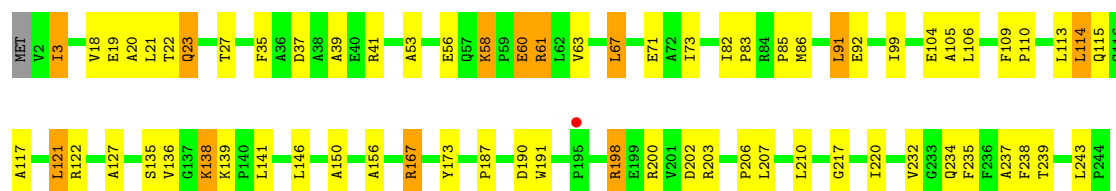




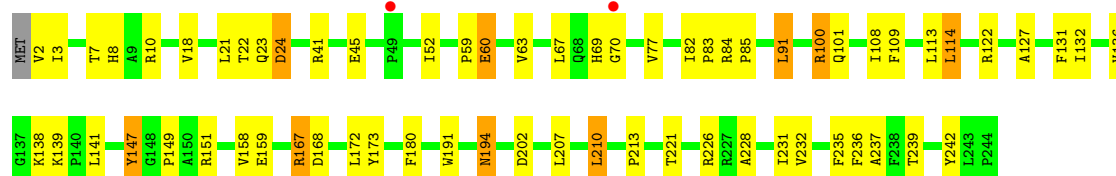
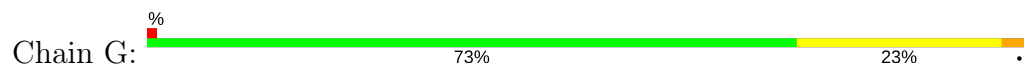
- Molecule 1: halohydrin dehalogenase



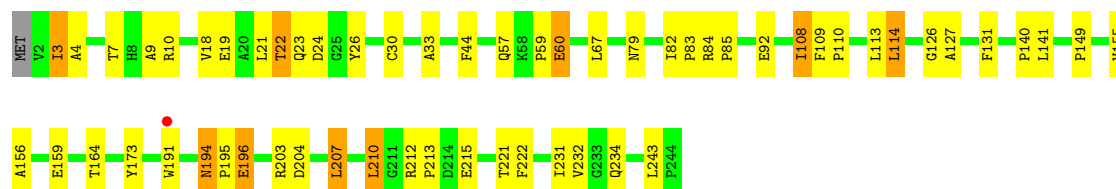
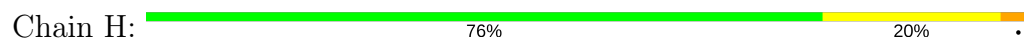
- Molecule 1: halohydrin dehalogenase



- Molecule 1: halohydrin dehalogenase



- Molecule 1: halohydrin dehalogenase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	64.98Å 77.72Å 111.42Å 97.29° 89.97° 112.98°	Depositor
Resolution (Å)	20.05 – 2.00 20.05 – 1.99	Depositor EDS
% Data completeness (in resolution range)	89.3 (20.05-2.00) 84.9 (20.05-1.99)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.72 (at 1.99Å)	Xtriage
Refinement program	CNX	Depositor
R, $R_{free}$	0.218 , 0.273 0.214 , 0.270	Depositor DCC
$R_{free}$ test set	6020 reflections (5.28%)	DCC
Wilson B-factor (Å <sup>2</sup> )	17.0	Xtriage
Anisotropy	0.521	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 58.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.267 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	15416	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.09% 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 ⓘ

### 5.1 Standard geometry ⓘ

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	0.91	0/1867	0.90	1/2552 (0.0%)
1	B	0.88	0/1869	0.92	1/2553 (0.0%)
1	C	0.87	0/1862	0.91	1/2546 (0.0%)
1	D	0.91	0/1859	0.94	2/2541 (0.1%)
1	E	0.90	1/1865 (0.1%)	0.91	0/2548
1	F	0.91	0/1866	0.91	1/2550 (0.0%)
1	G	0.85	0/1855	0.93	1/2537 (0.0%)
1	H	0.88	1/1862 (0.1%)	0.92	0/2545
All	All	0.89	2/14905 (0.0%)	0.92	7/20372 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	G	0	1
1	H	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	44	PHE	CE1-CZ	5.06	1.47	1.37
1	E	18	VAL	CB-CG2	5.03	1.63	1.52

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	167	ARG	NE-CZ-NH1	9.83	125.22	120.30
1	D	167	ARG	NE-CZ-NH2	-9.43	115.58	120.30
1	A	27	THR	N-CA-C	-5.52	96.09	111.00
1	G	210	LEU	CA-CB-CG	5.45	127.83	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	113	LEU	CA-CB-CG	5.44	127.82	115.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	G	147	TYR	Sidechain
1	H	26	TYR	Sidechain

## 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	1823	0	1783	53	0
1	B	1825	0	1795	36	0
1	C	1818	0	1773	52	0
1	D	1815	0	1773	61	0
1	E	1822	0	1787	44	0
1	F	1822	0	1786	59	0
1	G	1811	0	1769	47	0
1	H	1818	0	1782	40	0
2	A	115	0	0	5	0
2	B	111	0	0	6	0
2	C	102	0	0	12	0
2	D	111	0	0	2	0
2	E	93	0	0	0	0
2	F	110	0	0	5	0
2	G	111	0	0	4	0
2	H	109	0	0	5	0
All	All	15416	0	14248	350	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 12.

The worst 5 of 350 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:F:237:ALA:HB1	2:F:297:HOH:O	1.68	0.94
1:F:58:LYS:HB2	1:F:61:ARG:HG3	1.55	0.88
1:G:59:PRO:HG3	1:G:109:PHE:CD2	2.09	0.87
1:D:110:PRO:HA	2:D:343:HOH:O	1.74	0.87
1:D:3:ILE:HD11	1:D:73:ILE:HG12	1.55	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	241/244 (99%)	232 (96%)	9 (4%)	0	100	100
1	B	241/244 (99%)	226 (94%)	15 (6%)	0	100	100
1	C	241/244 (99%)	228 (95%)	13 (5%)	0	100	100
1	D	241/244 (99%)	227 (94%)	14 (6%)	0	100	100
1	E	241/244 (99%)	228 (95%)	13 (5%)	0	100	100
1	F	241/244 (99%)	229 (95%)	12 (5%)	0	100	100
1	G	241/244 (99%)	227 (94%)	14 (6%)	0	100	100
1	H	241/244 (99%)	231 (96%)	10 (4%)	0	100	100
All	All	1928/1952 (99%)	1828 (95%)	100 (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	184/193 (95%)	167 (91%)	17 (9%)	11	6
1	B	184/193 (95%)	163 (89%)	21 (11%)	7	3
1	C	182/193 (94%)	167 (92%)	15 (8%)	13	8
1	D	181/193 (94%)	161 (89%)	20 (11%)	7	4
1	E	184/193 (95%)	168 (91%)	16 (9%)	12	7
1	F	183/193 (95%)	166 (91%)	17 (9%)	10	6
1	G	181/193 (94%)	164 (91%)	17 (9%)	10	6
1	H	182/193 (94%)	166 (91%)	16 (9%)	12	7
All	All	1461/1544 (95%)	1322 (90%)	139 (10%)	10	5

5 of 139 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	91	LEU
1	E	24	ASP
1	H	67	LEU
1	D	113	LEU
1	D	207	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	193	ASN
1	E	42	GLN
1	H	101	GLN
1	E	23	GLN
1	E	69	HIS

### 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 [i](#)

There are no carbohydrates 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 [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	243/244 (99%)	-0.13	1 (0%) 92 92	9, 18, 29, 44	0
1	B	243/244 (99%)	-0.14	0 100 100	8, 18, 31, 41	0
1	C	243/244 (99%)	-0.05	6 (2%) 58 57	9, 19, 33, 42	0
1	D	243/244 (99%)	-0.04	1 (0%) 92 92	10, 18, 33, 45	0
1	E	243/244 (99%)	-0.05	4 (1%) 72 71	9, 18, 34, 46	0
1	F	243/244 (99%)	-0.07	1 (0%) 92 92	9, 18, 32, 47	0
1	G	243/244 (99%)	-0.12	2 (0%) 86 85	9, 18, 32, 38	0
1	H	243/244 (99%)	-0.13	1 (0%) 92 92	9, 18, 29, 40	0
All	All	1944/1952 (99%)	-0.09	16 (0%) 86 85	8, 18, 33, 47	0

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	194	ASN	3.2
1	C	49	PRO	3.0
1	E	42	GLN	3.0
1	C	39	ALA	2.7
1	E	39	ALA	2.7

### 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 carbohydrates 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.