



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 02:23 PM GMT

PDB ID : 3X2E  
Title : A thermophilic hydrolase  
Authors : Zheng, Y.; Ko, T.P.; Huang, C.H.  
Deposited on : 2014-12-21  
Resolution : 2.85 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  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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) : trunk26865

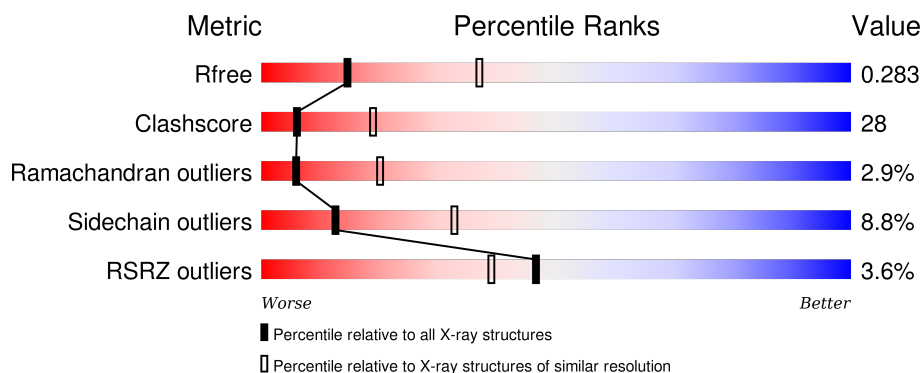
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.85 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))
$R_{free}$	91344	2228 (2.90-2.82)
Clashscore	102246	2499 (2.90-2.82)
Ramachandran outliers	100387	2439 (2.90-2.82)
Sidechain outliers	100360	2442 (2.90-2.82)
RSRZ outliers	91569	2236 (2.90-2.82)

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	411	<div> <div>5%</div> <div> <div></div> <div>50%</div> <div>41%</div> <div>6% •</div> </div> </div>
1	B	411	<div> <div>2%</div> <div> <div></div> <div>48%</div> <div>44%</div> <div>6% •</div> </div> </div>
1	C	411	<div> <div>2%</div> <div> <div></div> <div>52%</div> <div>39%</div> <div>6% •</div> </div> </div>
1	D	411	<div> <div>4%</div> <div> <div></div> <div>49%</div> <div>42%</div> <div>5% •</div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12993 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 Adenosylhomocysteinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	401	Total	C	N	O	S	0	0	0
			3116	1970	539	593	14			
1	B	401	Total	C	N	O	S	0	0	0
			3116	1970	539	593	14			
1	C	401	Total	C	N	O	S	0	0	0
			3116	1970	539	593	14			
1	D	401	Total	C	N	O	S	0	0	0
			3116	1970	539	593	14			

There are 32 discrepancies between the modelled and reference sequences:

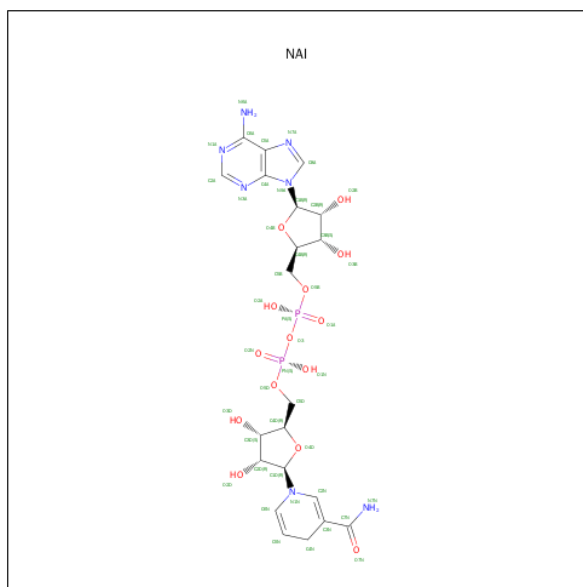
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	EXPRESSION TAG	UNP O51933
A	2	ALA	-	EXPRESSION TAG	UNP O51933
A	406	HIS	-	EXPRESSION TAG	UNP O51933
A	407	HIS	-	EXPRESSION TAG	UNP O51933
A	408	HIS	-	EXPRESSION TAG	UNP O51933
A	409	HIS	-	EXPRESSION TAG	UNP O51933
A	410	HIS	-	EXPRESSION TAG	UNP O51933
A	411	HIS	-	EXPRESSION TAG	UNP O51933
B	1	MET	-	EXPRESSION TAG	UNP O51933
B	2	ALA	-	EXPRESSION TAG	UNP O51933
B	406	HIS	-	EXPRESSION TAG	UNP O51933
B	407	HIS	-	EXPRESSION TAG	UNP O51933
B	408	HIS	-	EXPRESSION TAG	UNP O51933
B	409	HIS	-	EXPRESSION TAG	UNP O51933
B	410	HIS	-	EXPRESSION TAG	UNP O51933
B	411	HIS	-	EXPRESSION TAG	UNP O51933
C	1	MET	-	EXPRESSION TAG	UNP O51933
C	2	ALA	-	EXPRESSION TAG	UNP O51933
C	406	HIS	-	EXPRESSION TAG	UNP O51933
C	407	HIS	-	EXPRESSION TAG	UNP O51933
C	408	HIS	-	EXPRESSION TAG	UNP O51933

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Chain	Residue	Modelled	Actual	Comment	Reference
C	409	HIS	-	EXPRESSION TAG	UNP O51933
C	410	HIS	-	EXPRESSION TAG	UNP O51933
C	411	HIS	-	EXPRESSION TAG	UNP O51933
D	1	MET	-	EXPRESSION TAG	UNP O51933
D	2	ALA	-	EXPRESSION TAG	UNP O51933
D	406	HIS	-	EXPRESSION TAG	UNP O51933
D	407	HIS	-	EXPRESSION TAG	UNP O51933
D	408	HIS	-	EXPRESSION TAG	UNP O51933
D	409	HIS	-	EXPRESSION TAG	UNP O51933
D	410	HIS	-	EXPRESSION TAG	UNP O51933
D	411	HIS	-	EXPRESSION TAG	UNP O51933

- Molecule 2 is 1,4-DIHYDRONICOTINAMIDE ADENINE DINUCLEOTIDE (three-letter code: NAI) (formula: C<sub>21</sub>H<sub>29</sub>N<sub>7</sub>O<sub>14</sub>P<sub>2</sub>).

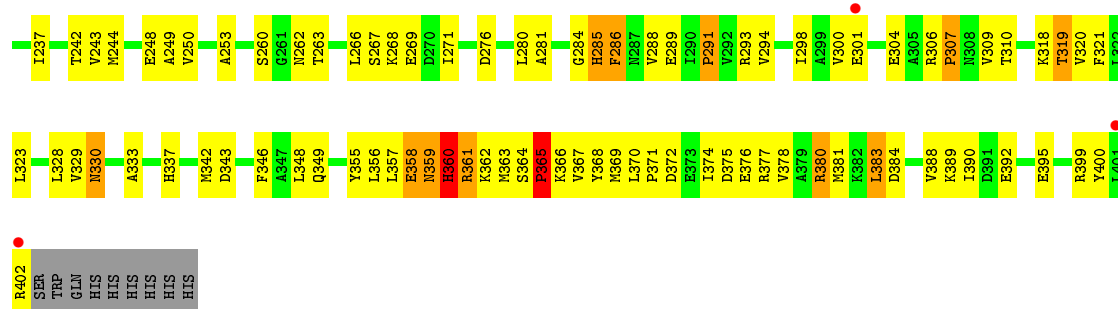


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	B	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	C	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	D	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	89	Total 89	O 89	0	0
3	B	98	Total 98	O 98	0	0
3	C	75	Total 75	O 75	0	0
3	D	91	Total 91	O 91	0	0

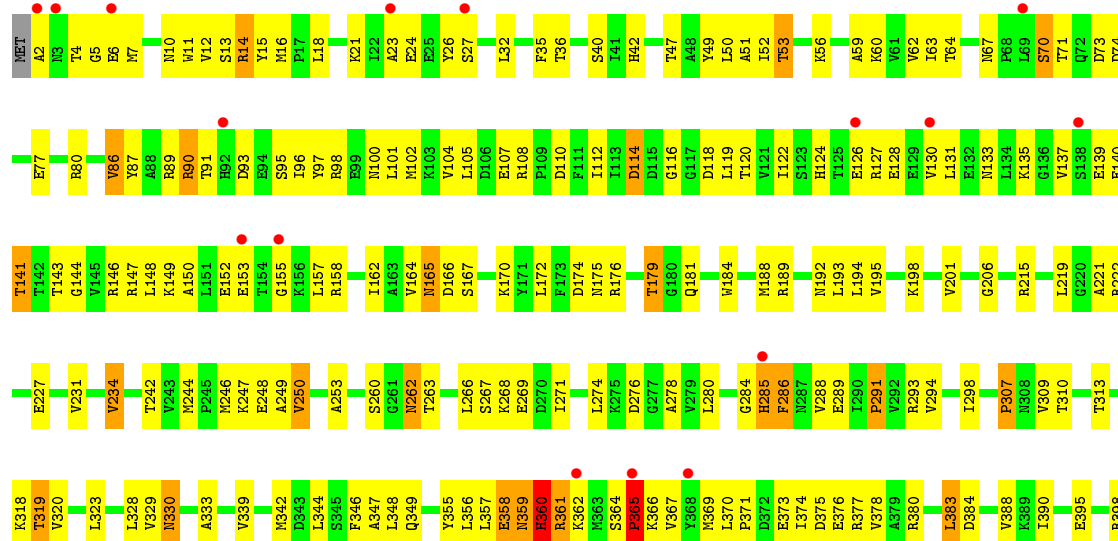




• Molecule 1: Adenosylhomocysteinase



• Molecule 1: Adenosylhomocysteinase



R399	Y400	L401	R402	SER	TRP	GLN	HIS	HIS	HIS	HIS	HIS	HIS
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## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	106.33Å 112.00Å 164.89Å 90.00° 103.50° 90.00°	Depositor
Resolution (Å)	25.00 – 2.85 24.80 – 2.85	Depositor EDS
% Data completeness (in resolution range)	(Not available) (25.00-2.85) 93.2 (24.80-2.85)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.22 (at 2.84Å)	Xtriage
Refinement program	CNS 1.21	Depositor
R, $R_{free}$	0.229 , 0.282 0.230 , 0.283	Depositor DCC
$R_{free}$ test set	2043 reflections (5.01%)	DCC
Wilson B-factor (Å <sup>2</sup> )	54.2	Xtriage
Anisotropy	0.856	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 67.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	1 of 40772 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	12993	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	78.0	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 46.82 % 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 1.0846e-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, 0.375 respectively for untwinned datasets, and 0.333, 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: NAI

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	0.43	0/3161	0.68	0/4273
1	B	0.47	0/3161	0.72	0/4273
1	C	0.45	0/3161	0.70	1/4273 (0.0%)
1	D	0.46	0/3161	0.70	0/4273
All	All	0.46	0/12644	0.70	1/17092 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	222	ARG	N-CA-C	-5.01	97.48	111.00

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	3116	0	3190	193	0
1	B	3116	0	3190	195	0
1	C	3116	0	3190	177	0
1	D	3116	0	3190	192	0
2	A	44	0	27	2	0
2	B	44	0	27	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	44	0	27	2	0
2	D	44	0	27	2	0
3	A	89	0	0	2	0
3	B	98	0	0	4	0
3	C	75	0	0	3	0
3	D	91	0	0	1	0
All	All	12993	0	12868	724	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 28.

The worst 5 of 724 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:67:ASN:HD22	1:C:70:SER:HB2	1.09	1.10
1:C:108:ARG:HH21	1:C:129:GLU:HB3	1.10	1.07
1:A:245:PRO:HG2	1:B:389:LYS:HE3	1.36	1.06
1:A:67:ASN:HD22	1:A:70:SER:HB2	1.22	1.00
1:B:361:ARG:HH11	1:B:361:ARG:HB3	1.25	0.99

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	399/411 (97%)	345 (86%)	41 (10%)	13 (3%)	5	17
1	B	399/411 (97%)	350 (88%)	39 (10%)	10 (2%)	7	24
1	C	399/411 (97%)	348 (87%)	39 (10%)	12 (3%)	5	19
1	D	399/411 (97%)	346 (87%)	41 (10%)	12 (3%)	5	19
All	All	1596/1644 (97%)	1389 (87%)	160 (10%)	47 (3%)	6	20

5 of 47 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	141	THR
1	A	285	HIS
1	A	286	PHE
1	A	365	PRO
1	B	141	THR

### 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	337/347 (97%)	309 (92%)	28 (8%)	14	36
1	B	337/347 (97%)	304 (90%)	33 (10%)	10	27
1	C	337/347 (97%)	308 (91%)	29 (9%)	13	34
1	D	337/347 (97%)	309 (92%)	28 (8%)	14	36
All	All	1348/1388 (97%)	1230 (91%)	118 (9%)	12	33

5 of 118 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	359	ASN
1	C	60	LYS
1	D	330	ASN
1	B	360	HIS
1	B	380	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	359	ASN
1	C	181	GLN
1	D	330	ASN
1	C	10	ASN
1	C	100	ASN

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

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	NAI	A	500	-	38,48,48	1.01	1 (2%)	48,73,73	1.97	6 (12%)
2	NAI	B	500	-	38,48,48	1.07	2 (5%)	48,73,73	1.96	6 (12%)
2	NAI	C	500	-	38,48,48	1.01	2 (5%)	48,73,73	2.10	7 (14%)
2	NAI	D	500	-	38,48,48	1.01	2 (5%)	48,73,73	2.09	7 (14%)

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	NAI	A	500	-	-	0/25/72/72	0/5/5/5
2	NAI	B	500	-	-	0/25/72/72	0/5/5/5
2	NAI	C	500	-	-	0/25/72/72	0/5/5/5
2	NAI	D	500	-	-	0/25/72/72	0/5/5/5

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	500	NAI	C8A-N7A	-2.12	1.30	1.34
2	C	500	NAI	C8A-N7A	-2.02	1.30	1.34
2	A	500	NAI	O4B-C1B	2.05	1.43	1.41
2	B	500	NAI	C4N-C5N	2.12	1.53	1.49
2	C	500	NAI	O4B-C1B	2.48	1.44	1.41

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	500	NAI	N3A-C2A-N1A	-9.88	121.33	128.89
2	C	500	NAI	N3A-C2A-N1A	-9.88	121.33	128.89
2	B	500	NAI	N3A-C2A-N1A	-9.39	121.71	128.89
2	A	500	NAI	N3A-C2A-N1A	-9.25	121.81	128.89
2	C	500	NAI	PN-O3-PA	-7.59	111.41	132.73

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	500	NAI	2	0
2	B	500	NAI	2	0
2	C	500	NAI	2	0
2	D	500	NAI	2	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	401/411 (97%)	0.17	21 (5%) 31 24	29, 83, 127, 140	0
1	B	401/411 (97%)	-0.05	10 (2%) 61 56	32, 68, 100, 120	0
1	C	401/411 (97%)	0.06	10 (2%) 61 56	38, 80, 121, 135	0
1	D	401/411 (97%)	0.01	16 (3%) 42 34	35, 74, 112, 121	0
All	All	1604/1644 (97%)	0.05	57 (3%) 46 39	29, 76, 118, 140	0

The worst 5 of 57 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	ALA	10.8
1	C	70	SER	6.3
1	B	2	ALA	5.1
1	A	137	VAL	5.1
1	C	92	HIS	4.8

### 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](#)

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	NAI	A	500	44/44	0.96	0.14	-0.63	58,75,86,86	0
2	NAI	C	500	44/44	0.96	0.15	-0.76	55,74,88,94	0
2	NAI	B	500	44/44	0.96	0.14	-0.90	65,72,86,89	0
2	NAI	D	500	44/44	0.95	0.14	-0.91	58,69,78,81	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.