



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 30, 2016 – 11:25 AM EST

PDB ID : 5IE2  
Title : Crystal structure of a plant enzyme  
Authors : Fan, M.R.; Li, M.; Chang, W.R.  
Deposited on : 2016-02-24  
Resolution : 1.85 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20028320  
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) : rb-20028320

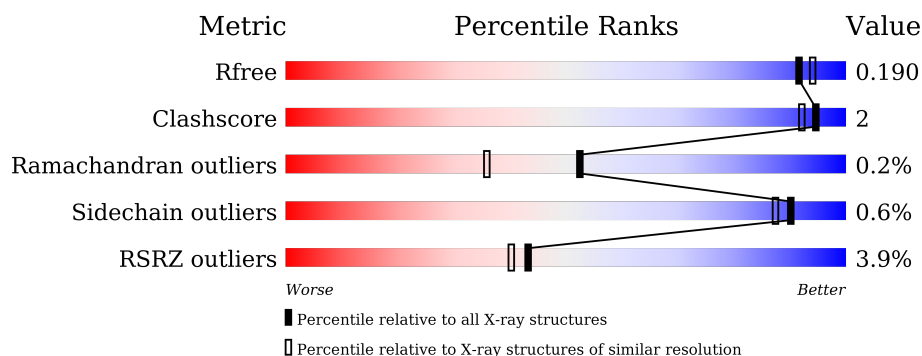
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.85 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	1745 (1.86-1.86)
Clashscore	102246	1898 (1.86-1.86)
Ramachandran outliers	100387	1875 (1.86-1.86)
Sidechain outliers	100360	1875 (1.86-1.86)
RSRZ outliers	91569	1747 (1.86-1.86)

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	514	<div> <div>4%</div> <div> <div></div> <div>94%</div> <div></div> </div> <div>...</div> </div>
1	B	514	<div> <div>4%</div> <div> <div></div> <div>94%</div> <div></div> </div> <div>..</div> </div>

## 2 Entry composition [i](#)

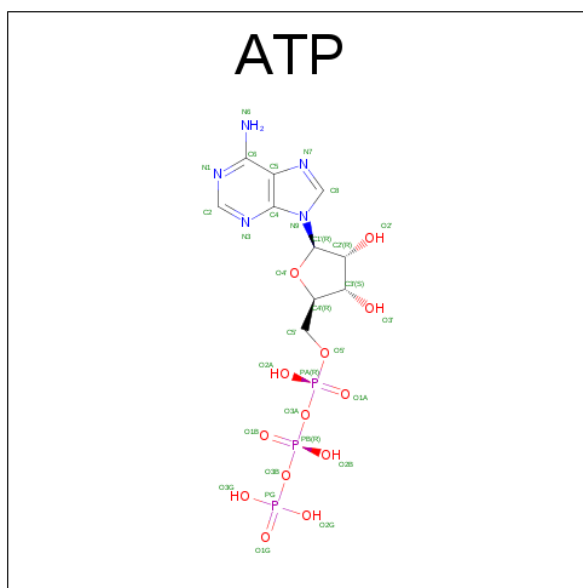
There are 5 unique types of molecules in this entry. The entry contains 8715 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Oxalate-CoA ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	506	Total	C	N	O	S	0	6	0
			3879	2467	664	738	10			
1	B	506	Total	C	N	O	S	0	3	0
			3870	2461	664	735	10			

- Molecule 2 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula:  $C_{10}H_{16}N_5O_{13}P_3$ ).

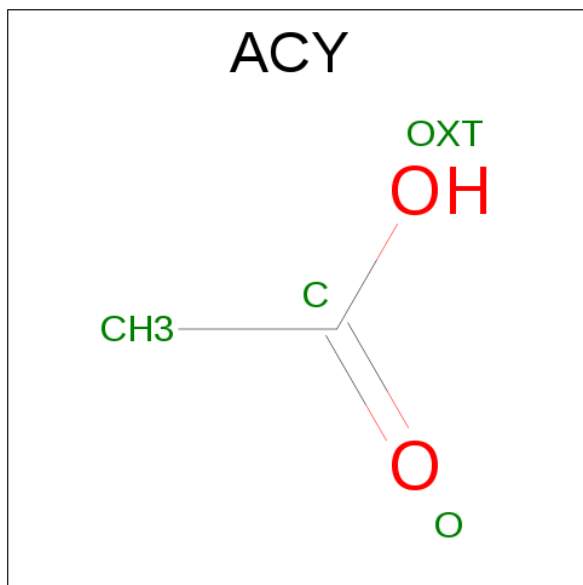


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	B	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Mg 1 1	0	0
3	A	1	Total Mg 1 1	0	0

- Molecule 4 is ACETIC ACID (three-letter code: ACY) (formula: C<sub>2</sub>H<sub>4</sub>O<sub>2</sub>).



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

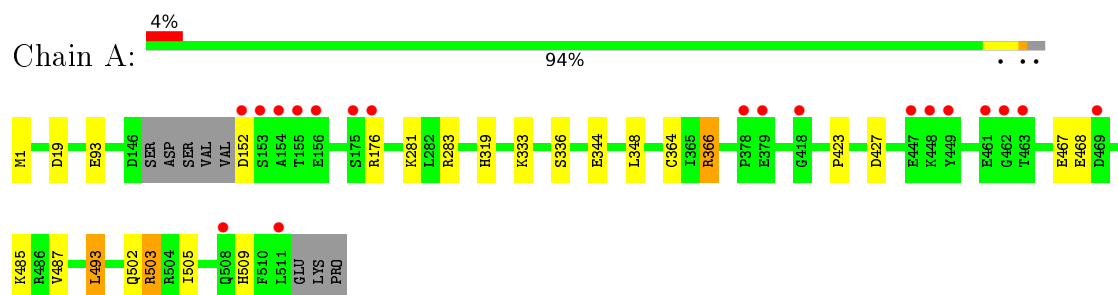
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	448	Total O 448 448	0	0
5	B	446	Total O 446 446	0	0

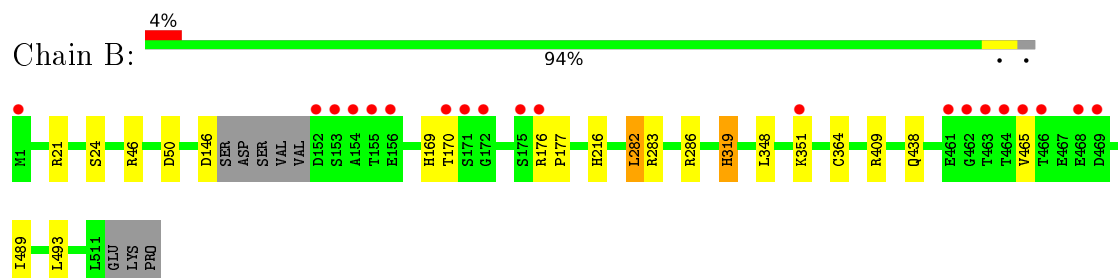
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Oxalate–CoA ligase



#### • Molecule 1: Oxalate–CoA ligase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	71.23Å 117.04Å 72.02Å 90.00° 93.58° 90.00°	Depositor
Resolution (Å)	28.69 – 1.85 45.38 – 1.85	Depositor EDS
% Data completeness (in resolution range)	99.8 (28.69-1.85) 96.0 (45.38-1.85)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.26 (at 1.84Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, $R_{free}$	0.149 , 0.189 0.151 , 0.190	Depositor DCC
$R_{free}$ test set	1943 reflections (2.01%)	DCC
Wilson B-factor (Å <sup>2</sup> )	22.1	Xtriage
Anisotropy	0.276	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 51.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.015 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	8715	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.98% 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

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ACY, ATP

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	0.80	0/3981	0.82	6/5409 (0.1%)
1	B	0.79	0/3963	0.77	4/5384 (0.1%)
All	All	0.79	0/7944	0.79	10/10793 (0.1%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	366	ARG	NE-CZ-NH1	16.15	128.37	120.30
1	A	366	ARG	NE-CZ-NH2	-15.53	112.54	120.30
1	A	493	LEU	CA-CB-CG	7.35	132.21	115.30
1	A	503	ARG	NE-CZ-NH2	-6.83	116.89	120.30
1	A	366	ARG	CD-NE-CZ	5.86	131.81	123.60
1	B	409	ARG	NE-CZ-NH1	-5.73	117.43	120.30
1	B	283	ARG	NE-CZ-NH2	-5.68	117.46	120.30
1	B	282	LEU	CA-CB-CG	5.40	127.72	115.30
1	B	286	ARG	NE-CZ-NH2	-5.39	117.60	120.30
1	A	283	ARG	NE-CZ-NH2	-5.21	117.69	120.30

There are no chirality outliers.

There are no planarity outliers.

### 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	3879	0	3908	15	0
1	B	3870	0	3893	12	0
2	A	31	0	12	0	0
2	B	31	0	12	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	4	0	3	0	0
4	B	4	0	3	0	0
5	A	448	0	0	5	3
5	B	446	0	0	4	3
All	All	8715	0	7831	27	3

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 2.

All (27) 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:A:1:MET:N	5:A:704:HOH:O	2.30	0.65
1:A:468:GLU:OE2	5:A:701:HOH:O	2.16	0.60
1:A:427:ASP:OD2	1:A:503:ARG:NH2	2.36	0.51
1:A:423:PRO:HD2	5:A:881:HOH:O	2.11	0.50
1:B:146:ASP:O	5:B:701:HOH:O	2.19	0.50
1:A:502:GLN:HB2	1:A:505:ILE:HD13	1.95	0.48
1:B:176:ARG:HD2	1:B:176:ARG:N	2.28	0.48
1:B:170:THR:OG1	1:B:177:PRO:HA	2.13	0.47
1:A:344:GLU:OE2	1:A:366:ARG:HD2	2.14	0.47
1:A:467:GLU:HG3	1:A:487:VAL:HB	1.96	0.47
1:A:93:GLU:H	1:A:93:GLU:CD	2.18	0.47
1:A:485:LYS:NZ	5:A:702:HOH:O	2.22	0.46
1:A:348:LEU:HD22	1:A:364:CYS:SG	2.56	0.46
1:B:46:ARG:NH1	1:B:50:ASP:OD2	2.41	0.45
1:B:438:GLN:HG2	5:B:953:HOH:O	2.17	0.44
1:A:176:ARG:HG2	1:A:176:ARG:H	1.59	0.42
1:B:216:HIS:HA	1:B:319:HIS:CE1	2.55	0.42
1:B:169:HIS:HE1	5:B:726:HOH:O	2.02	0.42
1:B:465:VAL:O	1:B:489:ILE:HD13	2.18	0.42
1:B:169:HIS:CE1	5:B:726:HOH:O	2.73	0.42
1:A:509:HIS:ND1	1:A:509:HIS:O	2.53	0.41
1:A:503:ARG:HG3	5:A:746:HOH:O	2.21	0.41
1:B:351:LYS:HE3	1:B:351:LYS:HB2	1.85	0.41
1:A:333:LYS:HB2	1:A:336:SER:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:21:ARG:HD2	1:B:24:SER:OG	2.21	0.41
1:B:348:LEU:HD22	1:B:364:CYS:SG	2.60	0.40
1:A:152:ASP:OD1	1:A:152:ASP:N	2.54	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:1144:HOH:O	5:B:986:HOH:O[1_556]	1.93	0.27
5:A:936:HOH:O	5:B:1143:HOH:O[1_455]	2.10	0.10
5:A:1128:HOH:O	5:B:1133:HOH:O[1_455]	2.13	0.07

## 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	508/514 (99%)	499 (98%)	8 (2%)	1 (0%)	52	36
1	B	505/514 (98%)	497 (98%)	7 (1%)	1 (0%)	52	36
All	All	1013/1028 (98%)	996 (98%)	15 (2%)	2 (0%)	52	36

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	319	HIS
1	B	319	HIS

### 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	422/424 (100%)	419 (99%)	3 (1%)	88	84
1	B	419/424 (99%)	417 (100%)	2 (0%)	92	90
All	All	841/848 (99%)	836 (99%)	5 (1%)	90	87

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	ASP
1	A	281	LYS
1	A	493	LEU
1	B	282	LEU
1	B	493	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 for Mogul analysis.

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	ATP	A	601	3	26,33,33	1.08	2 (7%)	26,52,52	1.99	4 (15%)
4	ACY	A	603	-	0,3,3	0.00	-	0,3,3	0.00	-
2	ATP	B	601	3	26,33,33	0.92	2 (7%)	26,52,52	1.95	6 (23%)
4	ACY	B	603	-	0,3,3	0.00	-	0,3,3	0.00	-

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	ATP	A	601	3	-	0/18/38/38	0/3/3/3
4	ACY	A	603	-	-	0/0/0/0	0/0/0/0
2	ATP	B	601	3	-	0/18/38/38	0/3/3/3
4	ACY	B	603	-	-	0/0/0/0	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	ATP	C5-C4	2.03	1.45	1.40
2	B	601	ATP	C5-C4	2.16	1.45	1.40
2	A	601	ATP	C2-N3	2.31	1.36	1.32
2	B	601	ATP	O4'-C1'	2.49	1.44	1.41

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	ATP	N3-C2-N1	-6.20	124.00	128.87
2	A	601	ATP	C1'-N9-C4	-5.88	120.24	126.81
2	B	601	ATP	C1'-N9-C4	-5.84	120.29	126.81
2	B	601	ATP	N3-C2-N1	-5.55	124.51	128.87
2	B	601	ATP	C4'-O4'-C1'	-2.28	107.23	109.64
2	B	601	ATP	O4'-C1'-N9	-2.07	104.19	108.11
2	B	601	ATP	O3G-PG-O2G	2.10	115.17	107.44
2	A	601	ATP	C2-N1-C6	2.15	122.59	118.77
2	B	601	ATP	N6-C6-N1	2.23	122.25	118.52
2	A	601	ATP	N6-C6-N1	2.82	123.25	118.52

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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	506/514 (98%)	-0.09	19 (3%)	44 41	14, 23, 54, 75	0
1	B	506/514 (98%)	-0.09	20 (3%)	42 39	14, 24, 54, 97	0
All	All	1012/1028 (98%)	-0.09	39 (3%)	43 40	14, 23, 54, 97	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	176	ARG	5.3
1	A	152	ASP	5.3
1	B	152	ASP	5.2
1	B	462	GLY	4.8
1	A	176	ARG	4.2
1	B	154	ALA	4.2
1	B	465	VAL	4.0
1	B	464	THR	4.0
1	A	155	THR	3.8
1	A	154	ALA	3.7
1	B	155	THR	3.5
1	B	463	THR	3.4
1	A	462	GLY	3.3
1	A	447	GLU	3.2
1	A	511	LEU	2.9
1	B	172	GLY	2.8
1	A	156	GLU	2.5
1	B	351	LYS	2.5
1	B	468	GLU	2.5
1	A	448	LYS	2.4
1	A	461	GLU	2.4
1	B	466	THR	2.4
1	B	469	ASP	2.4
1	A	379	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	1	MET	2.4
1	A	153	SER	2.3
1	B	175	SER	2.3
1	A	508	GLN	2.3
1	B	153	SER	2.3
1	B	171	SER	2.3
1	A	449	TYR	2.3
1	A	378	PRO	2.3
1	A	463	THR	2.2
1	B	170	THR	2.1
1	B	461	GLU	2.1
1	A	418	GLY	2.1
1	A	175	SER	2.0
1	A	469	ASP	2.0
1	B	156	GLU	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 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(Å <sup>2</sup> )	Q<0.9
4	ACY	B	603	4/4	0.96	0.15	0.39	22,22,24,24	0
4	ACY	A	603	4/4	0.95	0.13	0.04	20,22,23,24	0
2	ATP	B	601	31/31	0.99	0.12	-0.59	15,19,37,39	7
2	ATP	A	601	31/31	0.99	0.09	-0.71	15,19,33,36	5
3	MG	A	602	1/1	0.96	0.09	-	36,36,36,36	0
3	MG	B	602	1/1	0.96	0.09	-	47,47,47,47	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.