wwPDB X-ray Structure Validation Summary Report (i)

Aug 7, 2020 – 12:57 PM BST

PDB ID	:	6UAM
Title	:	Apo-form Dimer of Y77A Mutant Putative Ryanodine Receptor from Bacteroides thetaiotaomicron VPI-5482
Authors	:	Wu, R.; Joachimiak, A.; Jedrzejczak, R.; Midwest Center for Structural Genomics (MCSG)
Deposited on	:	2019-09-11
Resolution	:	2.80 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*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

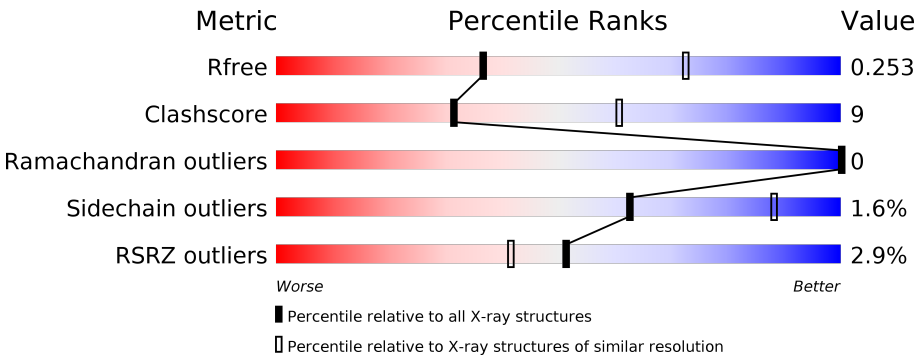
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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 >=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 <=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	100	% 70% 22% • 7%
1	B	100	6% 70% 25% • •
1	C	100	4% 79% 13% 8%
1	D	100	% 79% 14% • 6%
1	E	100	4% 71% 23% • 5%
1	F	100	78% 16% 6%

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
2	CIT	A	301	-	-	-	X
2	CIT	B	301	-	-	-	X

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4768 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.

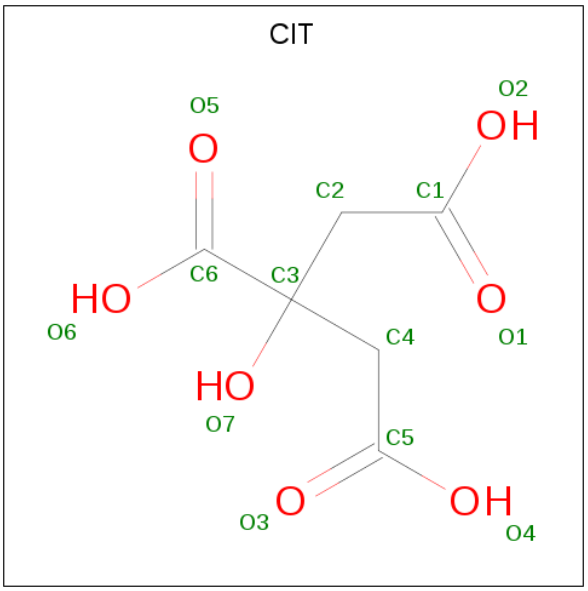
- Molecule 1 is a protein called Putative ryanodine receptor.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	93	767	484	129	150	1	3	1	0	0
1	B	96	792	500	134	154	1	3	1	0	0
1	C	92	757	476	126	151	1	3	0	0	0
1	D	94	775	488	130	153	1	3	1	0	0
1	E	95	783	494	131	154	1	3	0	0	0
1	F	94	775	488	130	153	1	3	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

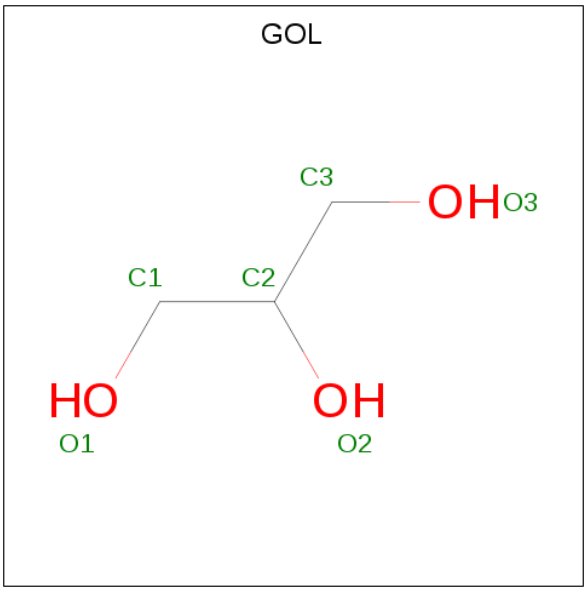
Chain	Residue	Modelled	Actual	Comment	Reference
A	77	ALA	TYR	engineered mutation	UNP Q8A5J2
B	77	ALA	TYR	engineered mutation	UNP Q8A5J2
C	77	ALA	TYR	engineered mutation	UNP Q8A5J2
D	77	ALA	TYR	engineered mutation	UNP Q8A5J2
E	77	ALA	TYR	engineered mutation	UNP Q8A5J2
F	77	ALA	TYR	engineered mutation	UNP Q8A5J2

- Molecule 2 is CITRIC ACID (three-letter code: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O		0	0
			13	6	7			
2	B	1	Total	C	O		0	0
			13	6	7			
2	B	1	Total	C	O		0	0
			13	6	7			
2	D	1	Total	C	O		0	0
			13	6	7			
2	E	1	Total	C	O		0	0
			13	6	7			
2	F	1	Total	C	O		0	0
			13	6	7			

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	A	1	6	3	3	0	0
3	C	1	6	3	3	0	0
3	D	1	6	3	3	0	0
3	F	1	6	3	3	0	0

- Molecule 4 is water.

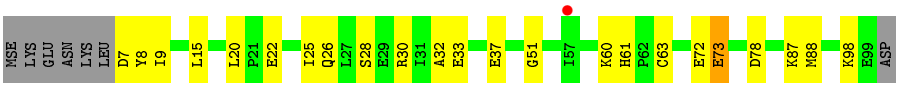
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	5	5	5	0	0
4	B	5	5	5	0	0
4	C	2	2	2	0	0
4	D	1	1	1	0	0
4	E	3	3	3	0	0
4	F	1	1	1	0	0

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.

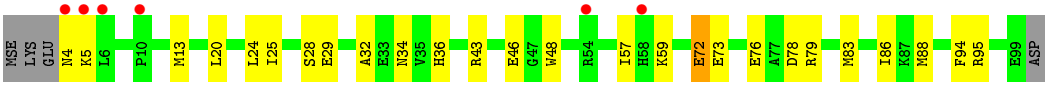
- Molecule 1: Putative ryanodine receptor

Chain A:



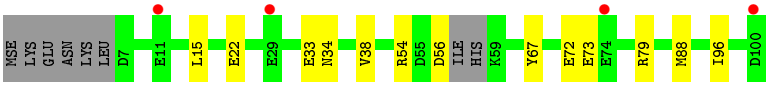
- Molecule 1: Putative ryanodine receptor

Chain B:



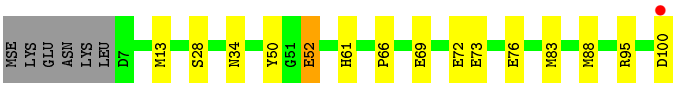
- Molecule 1: Putative ryanodine receptor

Chain C:



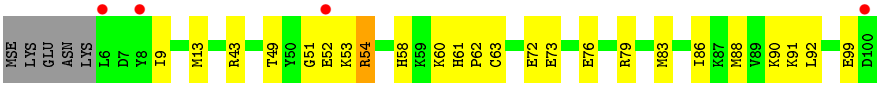
- Molecule 1: Putative ryanodine receptor

Chain D:



- Molecule 1: Putative ryanodine receptor

Chain E:



- Molecule 1: Putative ryanodine receptor

Chain F:

78%
16%
6%

MSE
LYS
GLU
ASN
LYS
LEU
D7
L20
L27
R30
I31
A32
E33
N34
E37
A40
I44
Y50
H61
L64
D78
N84
K87
R95
D100

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	74.62Å 89.99Å 74.48Å 90.00° 110.89° 90.00°	Depositor
Resolution (Å)	37.81 – 2.80 45.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	97.7 (37.81-2.80) 97.6 (45.00-2.80)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.35 (at 2.81Å)	Xtriage
Refinement program	PHENIX 1.14_3260	Depositor
R, R_{free}	0.189 , 0.253 0.189 , 0.253	Depositor DCC
R_{free} test set	1133 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å^2)	44.5	Xtriage
Anisotropy	0.875	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 27.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.439 for l,-k,h	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	4768	wwPDB-VP
Average B, all atoms (Å^2)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.16% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: GOL, CIT

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	0.47	0/780	0.56	0/1048
1	B	0.44	0/805	0.61	0/1081
1	C	0.49	0/768	0.65	0/1030
1	D	0.57	1/788 (0.1%)	0.61	0/1059
1	E	0.45	0/796	0.59	0/1070
1	F	0.43	0/788	0.55	0/1059
All	All	0.48	1/4725 (0.0%)	0.60	0/6347

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	B	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	52	GLU	CG-CD	-5.22	1.44	1.51

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	5	LYS	Peptide

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	767	0	754	15	0
1	B	792	0	784	22	1
1	C	757	0	739	13	0
1	D	775	0	758	11	1
1	E	783	0	769	22	0
1	F	775	0	758	11	0
2	A	13	0	5	0	0
2	B	26	0	10	2	0
2	D	13	0	5	1	0
2	E	13	0	5	0	0
2	F	13	0	5	0	0
3	A	6	0	8	0	0
3	C	6	0	8	1	0
3	D	6	0	8	0	0
3	F	6	0	8	0	0
4	A	5	0	0	0	0
4	B	5	0	0	0	0
4	C	2	0	0	0	0
4	D	1	0	0	0	0
4	E	3	0	0	0	0
4	F	1	0	0	0	0
All	All	4768	0	4624	84	1

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 84 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:88:MSE:HE2	1:B:34:ASN:HB2	1.59	0.83
1:E:9:ILE:HD12	1:E:9:ILE:O	1.79	0.82
1:E:53:LYS:HA	1:E:62:PRO:HG3	1.63	0.79
1:A:51:GLY:HA3	1:A:60:LYS:HB3	1.66	0.76
1:C:88:MSE:HE2	1:D:34:ASN:HB2	1.68	0.74

All (1) 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)
1:B:4:ASN:ND2	1:D:52:GLU:OE1[2_556]	2.11	0.09

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	91/100 (91%)	89 (98%)	2 (2%)	0	100	100
1	B	94/100 (94%)	91 (97%)	3 (3%)	0	100	100
1	C	88/100 (88%)	87 (99%)	1 (1%)	0	100	100
1	D	92/100 (92%)	92 (100%)	0	0	100	100
1	E	93/100 (93%)	86 (92%)	7 (8%)	0	100	100
1	F	92/100 (92%)	91 (99%)	1 (1%)	0	100	100
All	All	550/600 (92%)	536 (98%)	14 (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	85/88 (97%)	82 (96%)	3 (4%)	36	70
1	B	88/88 (100%)	86 (98%)	2 (2%)	50	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	84/88 (96%)	84 (100%)	0	100	100
1	D	86/88 (98%)	85 (99%)	1 (1%)	71	92
1	E	87/88 (99%)	85 (98%)	2 (2%)	50	82
1	F	86/88 (98%)	86 (100%)	0	100	100
All	All	516/528 (98%)	508 (98%)	8 (2%)	62	88

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	72	GLU
1	E	90	LYS
1	D	100	ASP
1	A	73	GLU
1	B	95	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	58	HIS
1	F	84	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)

10 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	GOL	A	302	-	5,5,5	1.27	1 (20%)	5,5,5	0.93	0
2	CIT	B	302	-	3,12,12	1.08	0	3,17,17	1.82	1 (33%)
2	CIT	E	201	-	3,12,12	1.28	0	3,17,17	2.00	1 (33%)
2	CIT	B	301	-	3,12,12	1.24	1 (33%)	3,17,17	1.67	1 (33%)
2	CIT	A	301	-	3,12,12	1.40	0	3,17,17	1.98	1 (33%)
3	GOL	D	201	-	5,5,5	0.98	0	5,5,5	1.10	0
2	CIT	D	202	-	3,12,12	1.18	0	3,17,17	1.86	1 (33%)
3	GOL	F	201	-	5,5,5	0.80	0	5,5,5	1.14	0
2	CIT	F	202	-	3,12,12	1.49	0	3,17,17	1.84	2 (66%)
3	GOL	C	201	-	5,5,5	1.20	1 (20%)	5,5,5	0.95	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	GOL	A	302	-	-	2/4/4/4	-
2	CIT	B	302	-	-	6/6/16/16	-
2	CIT	E	201	-	-	3/6/16/16	-
2	CIT	B	301	-	-	3/6/16/16	-
2	CIT	A	301	-	-	4/6/16/16	-
3	GOL	D	201	-	-	1/4/4/4	-
2	CIT	D	202	-	-	6/6/16/16	-
3	GOL	F	201	-	-	0/4/4/4	-
2	CIT	F	202	-	-	3/6/16/16	-
3	GOL	C	201	-	-	0/4/4/4	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	302	GOL	C3-C2	2.21	1.60	1.51
3	C	201	GOL	C3-C2	2.11	1.60	1.51
2	B	301	CIT	O7-C3	2.01	1.46	1.43

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	201	CIT	C3-C2-C1	-3.46	109.45	114.98
2	D	202	CIT	C3-C4-C5	-2.99	110.20	114.98
2	A	301	CIT	C3-C2-C1	-2.90	110.34	114.98
2	B	302	CIT	C3-C2-C1	2.84	119.53	114.98
2	B	301	CIT	C3-C4-C5	-2.80	110.50	114.98

There are no chirality outliers.

5 of 28 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	302	CIT	C1-C2-C3-O7
2	B	302	CIT	C1-C2-C3-C4
2	B	302	CIT	C1-C2-C3-C6
2	B	302	CIT	C2-C3-C4-C5
2	B	302	CIT	O7-C3-C4-C5

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	301	CIT	2	0
2	D	202	CIT	1	0
3	C	201	GOL	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, 95th 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^2)	Q<0.9
1	A	90/100 (90%)	0.42	1 (1%)	80	75	23, 50, 85, 112	1 (1%)
1	B	93/100 (93%)	0.59	6 (6%)	18	11	26, 48, 92, 152	1 (1%)
1	C	89/100 (89%)	0.42	4 (4%)	33	23	24, 41, 68, 98	0
1	D	91/100 (91%)	0.41	1 (1%)	80	75	26, 41, 68, 104	1 (1%)
1	E	92/100 (92%)	0.62	4 (4%)	35	25	27, 51, 90, 115	0
1	F	91/100 (91%)	0.43	0	100	100	25, 49, 92, 105	0
All	All	546/600 (91%)	0.48	16 (2%)	51	41	23, 46, 90, 152	3 (0%)

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	100	ASP	8.0
1	B	4	ASN	7.4
1	E	6	LEU	5.8
1	B	6	LEU	5.2
1	D	100	ASP	4.3

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, 95th 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^2)	Q<0.9
2	CIT	B	302	13/13	0.73	0.39	68,89,96,96	0
2	CIT	A	301	13/13	0.73	0.68	88,93,115,115	0
3	GOL	C	201	6/6	0.73	0.28	68,71,74,74	0
2	CIT	B	301	13/13	0.74	0.45	62,96,109,111	13
2	CIT	E	201	13/13	0.81	0.45	77,88,93,94	0
2	CIT	D	202	13/13	0.82	0.31	93,94,99,100	0
2	CIT	F	202	13/13	0.85	0.48	75,77,90,91	13
3	GOL	F	201	6/6	0.86	0.20	60,61,63,63	0
3	GOL	D	201	6/6	0.87	0.17	60,68,69,69	0
3	GOL	A	302	6/6	0.93	0.14	28,48,50,52	0

6.5 Other polymers (i)

There are no such residues in this entry.