



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 22, 2024 – 04:53 PM EDT

PDB ID : 6O8F
Title : Crystal structure of UvrB bound to duplex DNA
Authors : Lee, S.-J.; Verdine, G.L.
Deposited on : 2019-03-10
Resolution : 2.81 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

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>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 1.20.1
EDS : 2.37.1
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) : 2.37.1

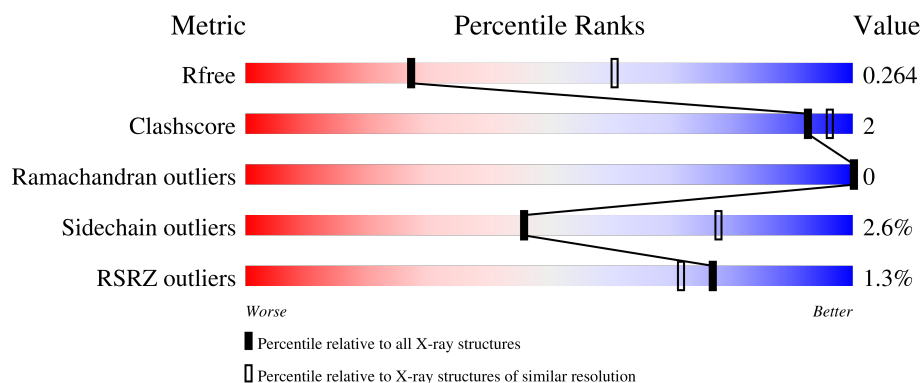
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.81 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	3617 (2.84-2.80)
Clashscore	141614	4060 (2.84-2.80)
Ramachandran outliers	138981	3978 (2.84-2.80)
Sidechain outliers	138945	3980 (2.84-2.80)
RSRZ outliers	127900	3552 (2.84-2.80)

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 of 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 $\leq 5\%$. 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	593	<div> <div></div> <div>94%</div> <div>6%</div> </div>
1	B	593	<div> <div>2%</div> <div>93%</div> <div>6%</div> </div>
2	C	20	<div> <div>75%</div> <div>25%</div> </div>
2	E	20	<div> <div>70%</div> <div>30%</div> </div>
3	D	20	<div> <div>95%</div> <div>5%</div> </div>

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Mol	Chain	Length	Quality of chain
3	F	20	 <div>90%10%</div>

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 11217 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 UvrABC system protein B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	591	Total	C	N	O	S	0	0	0
			4781	3013	854	904	10			
1	B	591	Total	C	N	O	S	0	0	0
			4775	3008	851	906	10			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	144	SER	CYS	conflict	UNP P56981
A	190	ARG	-	insertion	UNP P56981
A	211	SER	CYS	conflict	UNP P56981
A	233	GLU	LYS	conflict	UNP P56981
A	251	CYS	THR	conflict	UNP P56981
A	303	SER	CYS	conflict	UNP P56981
B	144	SER	CYS	conflict	UNP P56981
B	190	ARG	-	insertion	UNP P56981
B	211	SER	CYS	conflict	UNP P56981
B	233	GLU	LYS	conflict	UNP P56981
B	251	CYS	THR	conflict	UNP P56981
B	303	SER	CYS	conflict	UNP P56981

- Molecule 2 is a DNA chain called DNA (5'-D(*GP*CP*TP*CP*TP*AP*GP*AP*TP*TP*TP*TP*CP*AP*TP*AP*CP*GP*GP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	20	Total	C	N	O	P	0	0	0
			404	195	69	121	19			
2	E	20	Total	C	N	O	P	0	0	0
			404	195	69	121	19			

- Molecule 3 is a DNA chain called DNA (5'-D(*GP*CP*CP*GP*TP*AP*TP*GP*CP*CP*AP*AP*TP*CP*TP*AP*GP*AP*GP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	20	Total	C	N	O	P	0	0	0
			406	194	76	117	19			
3	F	20	Total	C	N	O	P	0	0	0
			406	194	76	117	19			

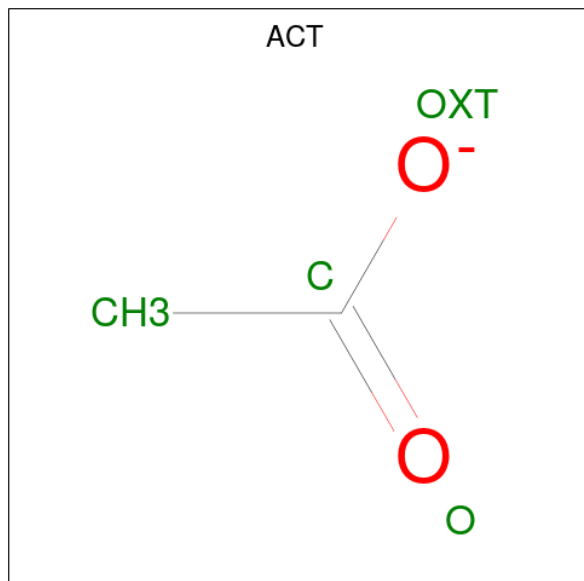
- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Cl	0	0
			1	1		

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 6 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



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

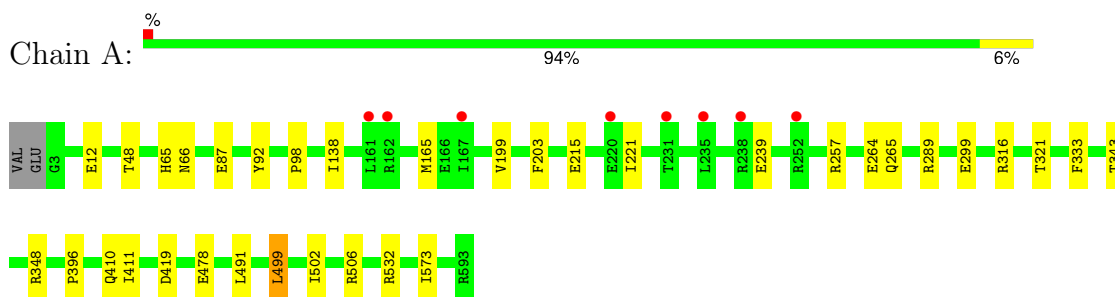
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	22	Total 22	O 22	0	0
7	B	9	Total 9	O 9	0	0
7	D	1	Total 1	O 1	0	0

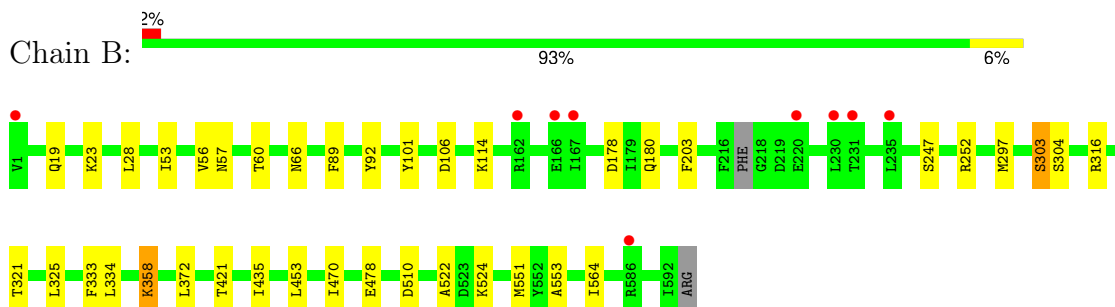
3 Residue-property plots

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.

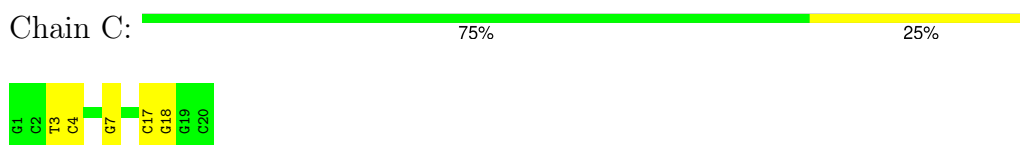
• Molecule 1: UvrABC system protein B



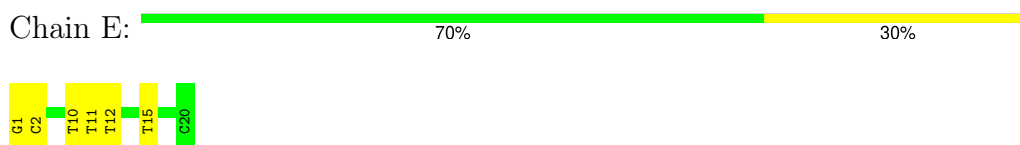
• Molecule 1: UvrABC system protein B



• Molecule 2: DNA (5'-D(*GP*CP*TP*CP*TP*AP*GP*AP*TP*TP*TP*TP*CP*AP*TP*AP*CP*GP*GP*C)-3')



• Molecule 2: DNA (5'-D(*GP*CP*TP*CP*TP*AP*GP*AP*TP*TP*TP*TP*CP*AP*TP*AP*CP*GP*GP*C)-3')



- Molecule 3: DNA (5'-D(*GP*CP*CP*GP*TP*AP*TP*GP*CP*CP*AP*AP*TP*CP*TP*AP*GP*AP*GP*C)-3')

Chain D:  95% 5%



- Molecule 3: DNA (5'-D(*GP*CP*CP*GP*TP*AP*TP*GP*CP*CP*AP*AP*TP*CP*TP*AP*GP*AP*GP*C)-3')

Chain F:  90% 10%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	58.16Å 265.25Å 68.31Å 90.00° 114.39° 90.00°	Depositor
Resolution (Å)	132.62 – 2.81 56.33 – 2.81	Depositor EDS
% Data completeness (in resolution range)	99.7 (132.62-2.81) 99.7 (56.33-2.81)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.63 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.8.0151, REFMAC	Depositor
R, R_{free}	0.220 , 0.264 0.222 , 0.264	Depositor DCC
R_{free} test set	2298 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	42.0	Xtriage
Anisotropy	0.084	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 31.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.035 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	11217	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.86% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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, ACT, CL

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	0.40	0/4863	0.69	1/6570 (0.0%)
1	B	0.39	0/4855	0.65	0/6559
2	C	0.37	0/451	0.77	0/694
2	E	0.35	0/451	0.77	0/694
3	D	0.34	0/455	0.83	0/700
3	F	0.37	0/455	0.80	0/700
All	All	0.39	0/11530	0.69	1/15917 (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	A	348	ARG	NE-CZ-NH1	5.34	122.97	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	4781	0	4814	11	0
1	B	4775	0	4809	17	0
2	C	404	0	229	3	0
2	E	404	0	229	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	D	406	0	226	1	0
3	F	406	0	226	1	0
4	A	1	0	0	0	0
5	A	3	0	0	0	0
5	B	1	0	0	0	0
6	C	4	0	3	0	0
7	A	22	0	0	0	0
7	B	9	0	0	0	0
7	D	1	0	0	0	0
All	All	11217	0	10536	33	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 2.

All (33) 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:B:19:GLN:OE1	1:B:23:LYS:NZ	2.30	0.64
1:B:53:ILE:HG12	1:B:60:THR:HG21	1.87	0.57
1:B:60:THR:HG22	1:B:334:LEU:HB3	1.86	0.55
1:B:551:MET:CE	1:B:564:ILE:HD11	2.36	0.55
1:B:358:LYS:HB3	1:B:372:LEU:HD23	1.87	0.55
1:A:98:PRO:HG3	3:D:11:DA:C2	2.43	0.54
1:A:502:ILE:HG21	2:C:7:DG:H4'	1.93	0.50
1:B:297:MET:HG3	1:B:303:SER:HB2	1.93	0.50
1:B:28:LEU:HD12	1:B:56:VAL:HG11	1.95	0.49
1:B:316:ARG:NH2	1:B:321:THR:O	2.46	0.48
1:A:165:MET:HB2	1:A:221:ILE:HD12	1.96	0.47
1:A:199:VAL:HG12	1:A:215:GLU:HG2	1.97	0.47
1:A:396:PRO:O	1:A:532:ARG:NH1	2.48	0.47
2:E:1:DG:H1'	2:E:2:DC:C6	2.49	0.46
2:C:3:DT:H2''	2:C:4:DC:H5''	1.98	0.46
1:A:411:ILE:HD11	1:A:573:ILE:HG21	1.98	0.46
1:A:491:LEU:HD22	1:A:499:LEU:HD22	1.97	0.46
1:B:89:PHE:CD1	1:B:325:LEU:HD22	2.51	0.45
1:A:87:GLU:HB2	1:A:138:ILE:HG12	1.99	0.45
3:F:17:DG:C2'	3:F:18:DA:H5'	2.47	0.44
1:B:101:TYR:OH	1:B:106:ASP:OD1	2.34	0.44
1:A:65:HIS:HB3	1:A:343:THR:OG1	2.18	0.44
1:A:316:ARG:NH2	1:A:321:THR:O	2.48	0.44
2:E:11:DT:H2'	2:E:12:DT:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:180:GLN:HG3	1:B:247:SER:HB3	2.01	0.42
1:B:28:LEU:CD1	1:B:56:VAL:HG11	2.50	0.42
1:B:66:ASN:HA	2:E:10:DT:H5'	2.00	0.42
1:B:522:ALA:HB3	1:B:553:ALA:HB2	2.02	0.42
1:B:453:LEU:HD13	1:B:524:LYS:HD3	2.01	0.41
1:A:48:THR:OG1	1:A:410:GLN:NE2	2.48	0.40
2:C:17:DC:H2''	2:C:18:DG:C8	2.55	0.40
1:B:304:SER:O	2:E:15:DT:OP1	2.40	0.40
1:B:435:ILE:HG23	1:B:470:ILE:HD11	2.03	0.40

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	589/593 (99%)	574 (98%)	15 (2%)	0	100	100
1	B	587/593 (99%)	565 (96%)	22 (4%)	0	100	100
All	All	1176/1186 (99%)	1139 (97%)	37 (3%)	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	518/520 (100%)	503 (97%)	15 (3%)	42	74
1	B	518/520 (100%)	506 (98%)	12 (2%)	50	80
All	All	1036/1040 (100%)	1009 (97%)	27 (3%)	46	78

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	GLU
1	A	66	ASN
1	A	92	TYR
1	A	203	PHE
1	A	239	GLU
1	A	257	ARG
1	A	264	GLU
1	A	265	GLN
1	A	289	ARG
1	A	299	GLU
1	A	333	PHE
1	A	419	ASP
1	A	478	GLU
1	A	499	LEU
1	A	506	ARG
1	B	57	ASN
1	B	92	TYR
1	B	114	LYS
1	B	178	ASP
1	B	203	PHE
1	B	252	ARG
1	B	303	SER
1	B	333	PHE
1	B	358	LYS
1	B	421	THR
1	B	478	GLU
1	B	510	ASP

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

Mol	Chain	Res	Type
1	A	265	GLN
1	B	261	GLN

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](#)

Of 6 ligands modelled in this entry, 5 are monoatomic - leaving 1 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	$\# Z > 2$
6	ACT	C	101	-	3,3,3	0.85	0	3,3,3	0.72	0

There are no bond length outliers.

There are no bond angle outliers.

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 [i](#)

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, 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	591/593 (99%)	-0.12	8 (1%) 75 69	17, 35, 76, 98	0
1	B	591/593 (99%)	0.11	9 (1%) 73 67	27, 53, 87, 118	0
2	C	20/20 (100%)	-0.33	0 100 100	21, 40, 61, 71	0
2	E	20/20 (100%)	-0.17	0 100 100	30, 49, 74, 75	0
3	D	20/20 (100%)	-0.15	0 100 100	29, 47, 74, 89	0
3	F	20/20 (100%)	-0.13	0 100 100	35, 49, 80, 81	0
All	All	1262/1266 (99%)	-0.02	17 (1%) 77 72	17, 43, 83, 118	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	230	LEU	5.5
1	B	231	THR	3.8
1	A	162	ARG	3.1
1	B	167	ILE	3.1
1	A	161	LEU	2.9
1	B	162	ARG	2.7
1	B	586	ARG	2.5
1	B	220	GLU	2.5
1	B	235	LEU	2.5
1	A	220	GLU	2.4
1	A	231	THR	2.4
1	B	166	GLU	2.4
1	A	167	ILE	2.3
1	A	238	ARG	2.2
1	B	1	VAL	2.2
1	A	235	LEU	2.1
1	A	252	ARG	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 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(\AA^2)	Q<0.9
6	ACT	C	101	4/4	0.58	0.26	65,68,69,70	0
5	MG	A	603	1/1	0.91	0.11	26,26,26,26	0
5	MG	B	601	1/1	0.93	0.18	50,50,50,50	0
5	MG	A	604	1/1	0.94	0.16	33,33,33,33	0
4	CL	A	601	1/1	0.95	0.14	50,50,50,50	0
5	MG	A	602	1/1	0.97	0.12	25,25,25,25	0

6.5 Other polymers [i](#)

There are no such residues in this entry.