



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 08:20 PM GMT

PDB ID : 1JUP
Title : Crystal structure of the multidrug binding transcriptional repressor QacR bound to malachite green
Authors : Schumacher, M.A.; Miller, M.C.; Grkovic, S.; Brown, M.H.; Skurray, R.A.; Brennan, R.G.
Deposited on : 2001-08-24
Resolution : 2.95 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

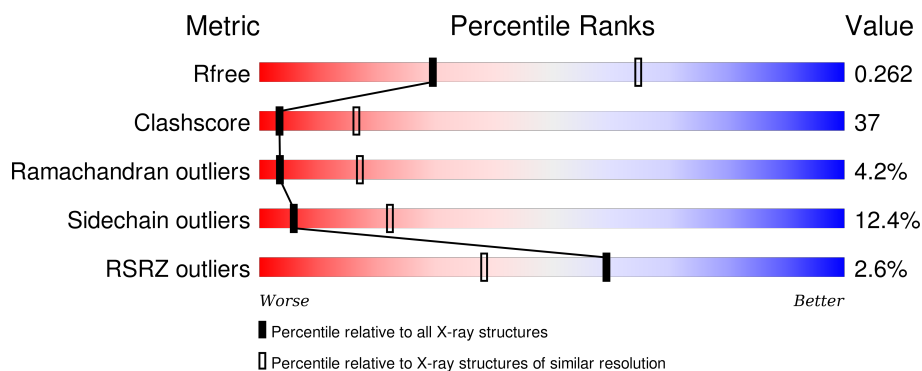
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.95 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	2184 (3.00-2.92)
Clashscore	102246	2552 (3.00-2.92)
Ramachandran outliers	100387	2468 (3.00-2.92)
Sidechain outliers	100360	2471 (3.00-2.92)
RSRZ outliers	91569	2201 (3.00-2.92)

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. 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	194	<div> <div></div> <div>41% 46% 8% . .</div> </div>
1	B	194	<div> <div>4%</div> <div>34% 48% 12% . .</div> </div>
1	D	194	<div> <div>5%</div> <div>42% 46% 7% . .</div> </div>
1	E	194	<div> <div>%</div> <div>42% 46% 7% . .</div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	A	799	-	-	-	X
2	SO4	A	802	-	-	-	X
2	SO4	B	199	-	-	-	X
2	SO4	B	499	-	-	-	X
2	SO4	B	700	-	-	X	-
2	SO4	D	399	-	-	-	X
2	SO4	E	639	-	-	-	X
2	SO4	E	699	-	-	-	X
2	SO4	E	901	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6330 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 HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN QACA 5'REGION.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	186	Total	C	N	O	S	0	0	0
			1547	998	252	295	2			
1	D	186	Total	C	N	O	S	0	0	0
			1547	998	252	295	2			
1	A	186	Total	C	N	O	S	0	0	0
			1547	998	252	295	2			
1	E	186	Total	C	N	O	S	0	0	0
			1547	998	252	295	2			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	72	ALA	CYS	ENGINEERED	UNP P0A0N4
B	141	SER	CYS	ENGINEERED	UNP P0A0N4
B	189	HIS	-	EXPRESSION TAG	UNP P0A0N4
B	190	HIS	-	EXPRESSION TAG	UNP P0A0N4
B	191	HIS	-	EXPRESSION TAG	UNP P0A0N4
B	192	HIS	-	EXPRESSION TAG	UNP P0A0N4
B	193	HIS	-	EXPRESSION TAG	UNP P0A0N4
B	194	HIS	-	EXPRESSION TAG	UNP P0A0N4
D	72	ALA	CYS	ENGINEERED	UNP P0A0N4
D	141	SER	CYS	ENGINEERED	UNP P0A0N4
D	189	HIS	-	EXPRESSION TAG	UNP P0A0N4
D	190	HIS	-	EXPRESSION TAG	UNP P0A0N4
D	191	HIS	-	EXPRESSION TAG	UNP P0A0N4
D	192	HIS	-	EXPRESSION TAG	UNP P0A0N4
D	193	HIS	-	EXPRESSION TAG	UNP P0A0N4
D	194	HIS	-	EXPRESSION TAG	UNP P0A0N4
A	72	ALA	CYS	ENGINEERED	UNP P0A0N4
A	141	SER	CYS	ENGINEERED	UNP P0A0N4
A	189	HIS	-	EXPRESSION TAG	UNP P0A0N4
A	190	HIS	-	EXPRESSION TAG	UNP P0A0N4

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Chain	Residue	Modelled	Actual	Comment	Reference
A	191	HIS	-	EXPRESSION TAG	UNP P0A0N4
A	192	HIS	-	EXPRESSION TAG	UNP P0A0N4
A	193	HIS	-	EXPRESSION TAG	UNP P0A0N4
A	194	HIS	-	EXPRESSION TAG	UNP P0A0N4
E	72	ALA	CYS	ENGINEERED	UNP P0A0N4
E	141	SER	CYS	ENGINEERED	UNP P0A0N4
E	189	HIS	-	EXPRESSION TAG	UNP P0A0N4
E	190	HIS	-	EXPRESSION TAG	UNP P0A0N4
E	191	HIS	-	EXPRESSION TAG	UNP P0A0N4
E	192	HIS	-	EXPRESSION TAG	UNP P0A0N4
E	193	HIS	-	EXPRESSION TAG	UNP P0A0N4
E	194	HIS	-	EXPRESSION TAG	UNP P0A0N4

- Molecule 2 is SULFATE ION (three-letter code: SO₄) (formula: O₄S).



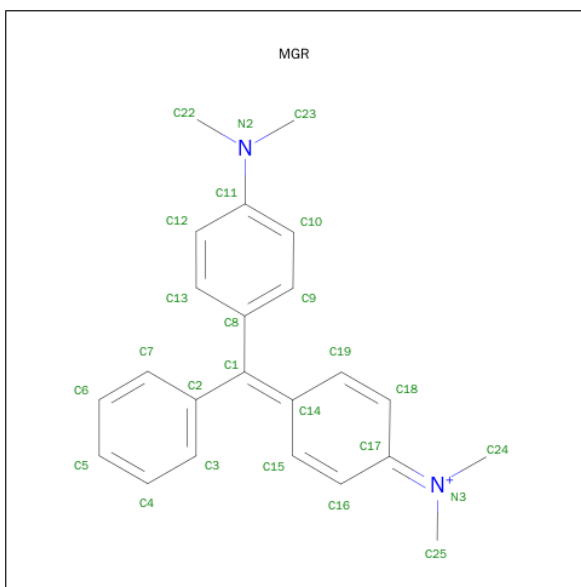
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0
2	E	1	Total O S 5 4 1	0	0
2	D	1	Total O S 5 4 1	0	0
2	E	1	Total O S 5 4 1	0	0

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

- Molecule 3 is MALACHITE GREEN (three-letter code: MGR) (formula: C₂₃H₂₅N₂).



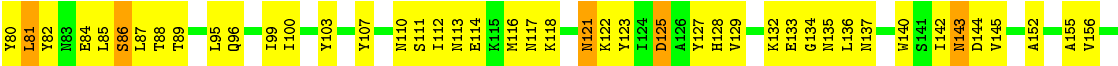
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	C N	0	0
			25	23 2		

- Molecule 4 is water.

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



● Molecule 1: HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN QACA 5'REGION



4 Data and refinement statistics

Property	Value	Source
Space group	P 4 ₂ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	174.20 Å 174.20 Å 96.30 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	64.60 – 2.95 64.60 – 2.87	Depositor EDS
% Data completeness (in resolution range)	81.9 (64.60-2.95) 78.1 (64.60-2.87)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.32 (at 2.86 Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.238 , 0.281 0.221 , 0.262	Depositor DCC
R_{free} test set	2580 reflections (9.91%)	DCC
Wilson B-factor (Å ²)	64.6	Xtriage
Anisotropy	0.050	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 55.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Outliers	0 of 26898 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6330	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.10% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: MGR, SO4

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	0.78	1/1578 (0.1%)	0.80	0/2126
1	B	0.74	0/1578	0.80	1/2126 (0.0%)
1	D	0.67	0/1578	0.78	0/2126
1	E	0.75	0/1578	0.80	0/2126
All	All	0.74	1/6312 (0.0%)	0.80	1/8504 (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	B	0	1
1	D	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	123	TYR	CD1-CE1	5.14	1.47	1.39

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	85	LEU	CA-CB-CG	5.39	127.69	115.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	123	TYR	Sidechain
1	D	20	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	1547	0	1536	114	0
1	B	1547	0	1536	152	0
1	D	1547	0	1536	114	0
1	E	1547	0	1536	99	0
2	A	25	0	0	2	0
2	B	25	0	0	2	0
2	D	20	0	0	0	0
2	E	40	0	0	1	0
3	A	25	0	25	4	0
4	A	2	0	0	0	0
4	B	1	0	0	0	0
4	D	2	0	0	0	0
4	E	2	0	0	0	0
All	All	6330	0	6169	457	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 37.

The worst 5 of 457 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:14:LEU:HD23	1:B:23:THR:HB	1.34	1.07
1:E:44:LYS:HG2	1:E:45:THR:HG23	1.42	0.98
1:D:2:ASN:HD22	1:D:3:LEU:H	0.98	0.97
1:A:120:GLU:HB3	3:A:200:MGR:H242	1.48	0.94
1:A:21:ASN:HD22	1:A:21:ASN:H	1.13	0.94

There are no symmetry-related clashes.

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	184/194 (95%)	163 (89%)	18 (10%)	3 (2%)	12	45
1	B	184/194 (95%)	142 (77%)	29 (16%)	13 (7%)	1	6
1	D	184/194 (95%)	158 (86%)	20 (11%)	6 (3%)	5	23
1	E	184/194 (95%)	144 (78%)	31 (17%)	9 (5%)	3	14
All	All	736/776 (95%)	607 (82%)	98 (13%)	31 (4%)	3	17

5 of 31 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	92	TYR
1	B	145	VAL
1	B	165	GLU
1	D	164	HIS
1	A	164	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	169/177 (96%)	143 (85%)	26 (15%)	3	14
1	B	169/177 (96%)	145 (86%)	24 (14%)	4	17
1	D	169/177 (96%)	152 (90%)	17 (10%)	9	32
1	E	169/177 (96%)	152 (90%)	17 (10%)	9	32
All	All	676/708 (96%)	592 (88%)	84 (12%)	6	22

5 of 84 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	121	ASN
1	A	49	LEU
1	E	136	LEU
1	D	167	ASN
1	A	3	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 46 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	167	ASN
1	A	110	ASN
1	E	117	ASN
1	D	176	ASN
1	A	21	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

23 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	MGR	A	200	-	27,27,27	3.61	17 (62%)	37,37,37	1.38	7 (18%)
2	SO4	A	299	-	4,4,4	0.29	0	6,6,6	0.12	0
2	SO4	A	799	-	4,4,4	0.33	0	6,6,6	0.08	0
2	SO4	A	800	-	4,4,4	0.31	0	6,6,6	0.11	0
2	SO4	A	801	-	4,4,4	0.23	0	6,6,6	0.15	0
2	SO4	A	802	-	4,4,4	0.10	0	6,6,6	0.15	0
2	SO4	B	1000	-	4,4,4	0.21	0	6,6,6	0.09	0
2	SO4	B	195	-	4,4,4	0.22	0	6,6,6	0.17	0
2	SO4	B	199	-	4,4,4	0.33	0	6,6,6	0.16	0
2	SO4	B	499	-	4,4,4	0.34	0	6,6,6	0.08	0
2	SO4	B	700	-	4,4,4	0.30	0	6,6,6	0.11	0
2	SO4	D	399	-	4,4,4	0.18	0	6,6,6	0.09	0
2	SO4	D	899	-	4,4,4	0.26	0	6,6,6	0.18	0
2	SO4	D	900	-	4,4,4	0.26	0	6,6,6	0.10	0
2	SO4	D	999	-	4,4,4	0.94	0	6,6,6	0.14	0
2	SO4	E	579	-	4,4,4	0.23	0	6,6,6	0.13	0
2	SO4	E	639	-	4,4,4	0.18	0	6,6,6	0.06	0
2	SO4	E	699	-	4,4,4	0.38	0	6,6,6	0.12	0
2	SO4	E	900	-	4,4,4	0.30	0	6,6,6	0.12	0
2	SO4	E	901	-	4,4,4	0.30	0	6,6,6	0.18	0
2	SO4	E	902	-	4,4,4	0.25	0	6,6,6	0.13	0
2	SO4	E	903	-	4,4,4	0.33	0	6,6,6	0.06	0
2	SO4	E	904	-	4,4,4	0.30	0	6,6,6	0.11	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	MGR	A	200	-	-	2/20/30/30	0/3/3/3
2	SO4	A	299	-	-	0/0/0/0	0/0/0/0
2	SO4	A	799	-	-	0/0/0/0	0/0/0/0
2	SO4	A	800	-	-	0/0/0/0	0/0/0/0
2	SO4	A	801	-	-	0/0/0/0	0/0/0/0
2	SO4	A	802	-	-	0/0/0/0	0/0/0/0
2	SO4	B	1000	-	-	0/0/0/0	0/0/0/0
2	SO4	B	195	-	-	0/0/0/0	0/0/0/0
2	SO4	B	199	-	-	0/0/0/0	0/0/0/0
2	SO4	B	499	-	-	0/0/0/0	0/0/0/0
2	SO4	B	700	-	-	0/0/0/0	0/0/0/0
2	SO4	D	399	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SO4	D	899	-	-	0/0/0/0	0/0/0/0
2	SO4	D	900	-	-	0/0/0/0	0/0/0/0
2	SO4	D	999	-	-	0/0/0/0	0/0/0/0
2	SO4	E	579	-	-	0/0/0/0	0/0/0/0
2	SO4	E	639	-	-	0/0/0/0	0/0/0/0
2	SO4	E	699	-	-	0/0/0/0	0/0/0/0
2	SO4	E	900	-	-	0/0/0/0	0/0/0/0
2	SO4	E	901	-	-	0/0/0/0	0/0/0/0
2	SO4	E	902	-	-	0/0/0/0	0/0/0/0
2	SO4	E	903	-	-	0/0/0/0	0/0/0/0
2	SO4	E	904	-	-	0/0/0/0	0/0/0/0

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	200	MGR	C15-C14	2.09	1.47	1.43
3	A	200	MGR	C4-C3	2.34	1.43	1.38
3	A	200	MGR	C23-N2	2.35	1.51	1.45
3	A	200	MGR	C6-C7	2.39	1.43	1.38
3	A	200	MGR	C16-C15	2.51	1.41	1.35

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	200	MGR	C18-C17-N3	-3.35	118.87	121.77
3	A	200	MGR	C7-C2-C3	-2.40	115.03	118.60
3	A	200	MGR	C2-C1-C14	-2.03	118.21	121.53
3	A	200	MGR	C13-C8-C9	-2.01	115.61	118.60
3	A	200	MGR	C13-C8-C1	2.33	124.31	120.92

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	200	MGR	C16-C17-N3-C24
3	A	200	MGR	C18-C17-N3-C24

There are no ring outliers.

5 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	200	MGR	4	0
2	A	800	SO4	1	0
2	A	801	SO4	1	0
2	B	700	SO4	2	0
2	E	902	SO4	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	186/194 (95%)	-0.04	0 100 100	29, 52, 86, 110	0
1	B	186/194 (95%)	0.09	7 (3%) 44 26	35, 64, 118, 137	0
1	D	186/194 (95%)	0.20	10 (5%) 29 17	39, 65, 98, 112	0
1	E	186/194 (95%)	0.07	2 (1%) 82 65	36, 54, 92, 104	0
All	All	744/776 (95%)	0.08	19 (2%) 59 38	29, 58, 104, 137	0

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	41	TYR	4.9
1	B	28	ILE	4.1
1	E	140	TRP	4.0
1	B	32	SER	3.6
1	D	140	TRP	3.4

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, 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	LLDF	B-factors(\AA^2)	Q<0.9
2	SO4	B	199	5/5	0.79	0.69	15.69	154,154,154,155	0
2	SO4	A	799	5/5	0.82	0.63	14.35	140,140,140,140	0
2	SO4	E	699	5/5	0.80	0.47	10.84	151,151,151,152	0
2	SO4	E	639	5/5	0.55	0.63	10.02	195,195,195,196	0
2	SO4	B	499	5/5	0.61	0.41	8.95	160,161,161,161	0
2	SO4	D	399	5/5	0.85	0.53	6.56	198,198,198,199	0
2	SO4	A	802	5/5	0.81	0.32	6.19	170,171,171,171	0
2	SO4	E	901	5/5	0.79	0.27	2.78	147,148,148,148	0
3	MGR	A	200	25/25	0.95	0.29	1.79	27,30,32,34	0
2	SO4	A	801	5/5	0.75	0.30	1.40	166,167,167,167	0
2	SO4	D	900	5/5	0.82	0.19	-0.29	148,148,148,148	0
2	SO4	A	299	5/5	0.82	0.18	-	152,152,152,152	0
2	SO4	E	900	5/5	0.79	0.21	-	143,143,143,143	0
2	SO4	B	1000	5/5	0.82	0.17	-	186,186,187,187	0
2	SO4	D	999	5/5	0.81	0.30	-	111,111,111,114	0
2	SO4	B	700	5/5	0.64	0.41	-	199,199,199,200	0
2	SO4	A	800	5/5	0.68	0.34	-	141,141,141,141	0
2	SO4	E	903	5/5	0.85	0.48	-	175,176,176,176	0
2	SO4	B	195	5/5	0.67	0.28	-	184,185,185,185	0
2	SO4	E	579	5/5	0.66	0.38	-	182,182,182,182	0
2	SO4	D	899	5/5	0.74	0.26	-	161,161,162,162	0
2	SO4	E	904	5/5	0.28	0.49	-	179,179,179,180	0
2	SO4	E	902	5/5	0.44	0.71	-	188,188,188,188	0

6.5 Other polymers ⓘ

There are no such residues in this entry.