



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 22, 2016 – 04:14 PM EDT

PDB ID : 5FWS
Title : Wnt modulator Kremen crystal form I at 1.90Å
Authors : Zebisch, M.; Jackson, V.A.; Jones, E.Y.
Deposited on : 2016-02-21
Resolution : 1.90 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

<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 : unknown
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027939
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-20027939

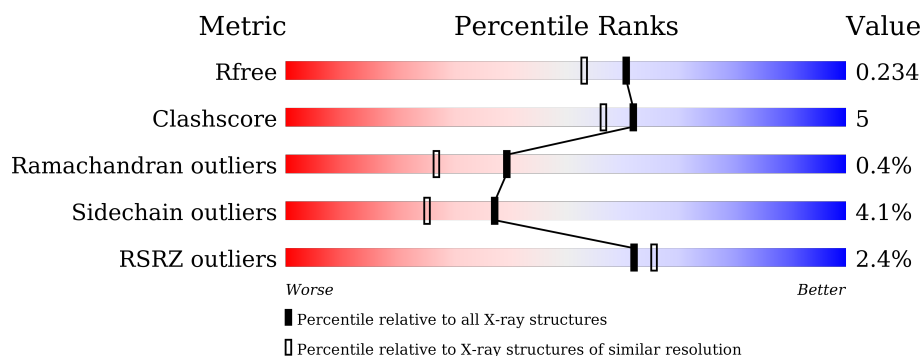
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (1.90-1.90)

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	406	

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	SO4	A	1323	-	-	-	X
3	NAG	A	1324	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NAG	A	1326	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 2387 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 KREMEN PROTEIN 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	288	Total	C	N	O	S	0	0	0
			2260	1438	384	418	20			

There are 61 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	MET	-	INITIATING METHIONINE	UNP Q96MU8
A	-9	GLY	-	EXPRESSION TAG	UNP Q96MU8
A	-8	ILE	-	EXPRESSION TAG	UNP Q96MU8
A	-7	LEU	-	EXPRESSION TAG	UNP Q96MU8
A	-6	PRO	-	EXPRESSION TAG	UNP Q96MU8
A	-5	SER	-	EXPRESSION TAG	UNP Q96MU8
A	-4	PRO	-	EXPRESSION TAG	UNP Q96MU8
A	-3	GLY	-	EXPRESSION TAG	UNP Q96MU8
A	-2	MET	-	EXPRESSION TAG	UNP Q96MU8
A	-1	PRO	-	EXPRESSION TAG	UNP Q96MU8
A	0	ALA	-	EXPRESSION TAG	UNP Q96MU8
A	1	LEU	-	EXPRESSION TAG	UNP Q96MU8
A	2	LEU	-	EXPRESSION TAG	UNP Q96MU8
A	3	SER	-	EXPRESSION TAG	UNP Q96MU8
A	4	LEU	-	EXPRESSION TAG	UNP Q96MU8
A	5	VAL	-	EXPRESSION TAG	UNP Q96MU8
A	6	SER	-	EXPRESSION TAG	UNP Q96MU8
A	7	LEU	-	EXPRESSION TAG	UNP Q96MU8
A	8	LEU	-	EXPRESSION TAG	UNP Q96MU8
A	9	SER	-	EXPRESSION TAG	UNP Q96MU8
A	10	VAL	-	EXPRESSION TAG	UNP Q96MU8
A	11	LEU	-	EXPRESSION TAG	UNP Q96MU8
A	12	LEU	-	EXPRESSION TAG	UNP Q96MU8
A	13	MET	-	EXPRESSION TAG	UNP Q96MU8
A	14	GLY	-	EXPRESSION TAG	UNP Q96MU8
A	15	CYS	-	EXPRESSION TAG	UNP Q96MU8
A	16	VAL	-	EXPRESSION TAG	UNP Q96MU8

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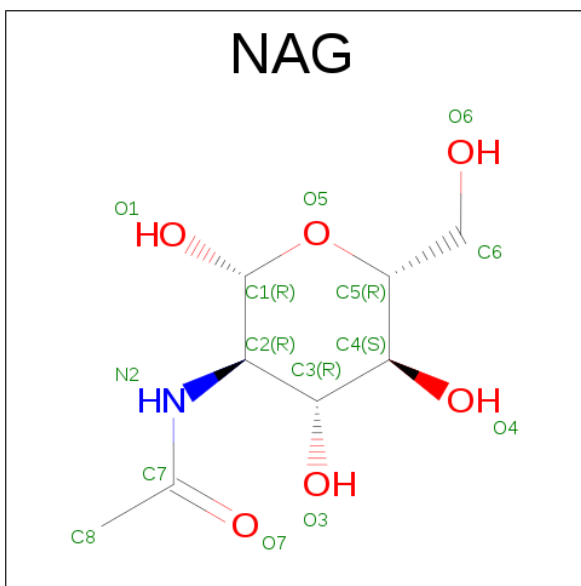
Chain	Residue	Modelled	Actual	Comment	Reference
A	17	ALA	-	EXPRESSION TAG	UNP Q96MU8
A	18	GLU	-	EXPRESSION TAG	UNP Q96MU8
A	19	THR	-	EXPRESSION TAG	UNP Q96MU8
A	20	GLY	-	EXPRESSION TAG	UNP Q96MU8
A	21	ALA	-	EXPRESSION TAG	UNP Q96MU8
A	22	PRO	-	EXPRESSION TAG	UNP Q96MU8
A	23	SER	-	EXPRESSION TAG	UNP Q96MU8
A	24	PRO	-	EXPRESSION TAG	UNP Q96MU8
A	25	GLY	-	EXPRESSION TAG	UNP Q96MU8
A	26	LEU	-	EXPRESSION TAG	UNP Q96MU8
A	27	GLY	-	EXPRESSION TAG	UNP Q96MU8
A	28	PRO	-	EXPRESSION TAG	UNP Q96MU8
A	325	GLY	-	INSERTION	UNP Q96MU8
A	326	SER	-	INSERTION	UNP Q96MU8
A	327	GLU	-	INSERTION	UNP Q96MU8
A	328	ASN	-	INSERTION	UNP Q96MU8
A	329	LEU	-	INSERTION	UNP Q96MU8
A	330	TYR	-	INSERTION	UNP Q96MU8
A	331	PHE	-	INSERTION	UNP Q96MU8
A	332	GLN	-	INSERTION	UNP Q96MU8
A	333	GLY	-	INSERTION	UNP Q96MU8
A	334	GLY	-	INSERTION	UNP Q96MU8
A	335	SER	-	INSERTION	UNP Q96MU8
A	385	THR	-	EXPRESSION TAG	UNP Q96MU8
A	386	HIS	-	EXPRESSION TAG	UNP Q96MU8
A	387	HIS	-	EXPRESSION TAG	UNP Q96MU8
A	388	HIS	-	EXPRESSION TAG	UNP Q96MU8
A	389	HIS	-	EXPRESSION TAG	UNP Q96MU8
A	390	HIS	-	EXPRESSION TAG	UNP Q96MU8
A	391	HIS	-	EXPRESSION TAG	UNP Q96MU8
A	392	HIS	-	EXPRESSION TAG	UNP Q96MU8
A	393	HIS	-	EXPRESSION TAG	UNP Q96MU8
A	394	HIS	-	EXPRESSION TAG	UNP Q96MU8
A	395	HIS	-	EXPRESSION TAG	UNP Q96MU8

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



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

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	79	Total	O	0	2
			79	79		

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 ($\text{RSRZ} > 2$). 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.

Chain A:

Amino Acid	Percentage
GLN	2%
ALA	57%
ASN	13%
LEU	2%
SER	29%
VAL	
SER	
LEU	
PRO	
GLY	
ILE	
LEU	
PRO	
SER	
GLY	
MET	
ALA	
LEU	
LEU	
SER	
LEU	
VAL	
SER	
LEU	
GLY	
ALA	
GLY	
THR	
GLY	
ALA	
ALA	
GLY	
THR	
GLY	
ALA	
PRO	
SER	
PRO	
GLY	
LEU	
GLY	
GLY	
GLY	
P30	
E31	
C32	
Y40	
Y46	
Q50	
F57	
E60	
T61	
F62	
Q63	
H64	
P65	
Y66	

4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	50.94Å 50.94Å 188.39Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	62.80 – 1.90 44.12 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.7 (62.80-1.90) 99.7 (44.12-1.90)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.91 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.8.0073	Depositor
R, R_{free}	0.179 , 0.227 0.187 , 0.234	Depositor DCC
R_{free} test set	1153 reflections (5.22%)	DCC
Wilson B-factor (Å ²)	25.4	Xtriage
Anisotropy	0.203	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 37.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.053 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	2387	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.00% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CA, NAG, 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	1.03	1/2334 (0.0%)	1.04	10/3174 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	305	SER	CB-OG	-12.84	1.25	1.42

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	208	ASP	CB-CG-OD1	9.09	126.48	118.30
1	A	152	ARG	NE-CZ-NH1	8.12	124.36	120.30
1	A	208	ASP	CB-CG-OD2	-7.59	111.47	118.30
1	A	152	ARG	NE-CZ-NH2	-7.00	116.80	120.30
1	A	174	ASP	CB-CG-OD1	6.97	124.57	118.30
1	A	206	LEU	CA-CB-CG	-6.92	99.39	115.30
1	A	32	CYS	CA-CB-SG	-5.50	104.09	114.00
1	A	85	ARG	NE-CZ-NH1	5.38	122.99	120.30
1	A	155	ARG	NE-CZ-NH1	5.07	122.83	120.30
1	A	153	SER	CB-CA-C	-5.05	100.50	110.10

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	2260	0	2079	24	0
2	A	5	0	0	0	0
3	A	42	0	39	1	0
4	A	1	0	0	0	0
5	A	79	0	0	0	0
All	All	2387	0	2118	24	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 5.

All (24) 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:256:PHE:CE2	1:A:316:VAL:HG22	2.35	0.62
1:A:62:PHE:CE1	1:A:69:LEU:HD12	2.35	0.61
1:A:269:GLU:OE2	1:A:281:ARG:NH1	2.39	0.55
1:A:289:PRO:O	1:A:290:LEU:C	2.45	0.55
1:A:283:HIS:HD2	1:A:285:ARG:H	1.55	0.54
1:A:125:ASP:OD2	1:A:162:GLU:OE2	2.27	0.53
1:A:238:ARG:H	1:A:305:SER:HB3	1.73	0.52
1:A:57:PHE:O	1:A:61:THR:HG23	2.14	0.47
1:A:32:CYS:SG	1:A:40:TYR:HB2	2.54	0.47
1:A:314:PHE:CD1	1:A:316:VAL:HG23	2.50	0.46
1:A:150:PHE:O	1:A:154:GLN:HG2	2.16	0.45
1:A:69:LEU:HD23	1:A:69:LEU:HA	1.87	0.45
1:A:175:TYR:CG	1:A:206:LEU:HD22	2.52	0.44
1:A:70:LYS:HD3	1:A:71:TYR:CE1	2.54	0.43
1:A:66:TYR:CZ	1:A:88:ASP:HB3	2.54	0.43
1:A:64:HIS:HB3	1:A:96:TYR:CZ	2.53	0.42
1:A:105:TYR:N	1:A:105:TYR:CD1	2.88	0.42
1:A:256:PHE:CD2	1:A:316:VAL:HG22	2.54	0.42
1:A:215:GLY:HA2	1:A:241:TYR:O	2.20	0.42
1:A:133:THR:OG1	1:A:172:ASN:ND2	2.45	0.42
1:A:265:ALA:HB3	1:A:306:ASP:OD2	2.19	0.42
1:A:129:PRO:HG2	1:A:177:LYS:NZ	2.35	0.41
1:A:236:THR:HB	1:A:307:ARG:HA	2.03	0.41
1:A:60:GLU:HB3	3:A:1325:NAG:H82	2.02	0.41

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	284/406 (70%)	275 (97%)	8 (3%)	1 (0%)	39	27

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	72	PRO

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	241/339 (71%)	231 (96%)	10 (4%)	37	25

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	63	GLN
1	A	80	GLU
1	A	92	SER
1	A	161	MET
1	A	172	ASN
1	A	206	LEU
1	A	264	SER
1	A	291	SER
1	A	302	TYR
1	A	312	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	73	ASN
1	A	140	ASN
1	A	283	HIS

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 5 ligands modelled in this entry, 1 is 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	SO4	A	1323	-	4,4,4	0.45	0	6,6,6	0.57	0
3	NAG	A	1324	1	14,14,15	0.77	0	15,19,21	1.98	4 (26%)
3	NAG	A	1325	1	14,14,15	0.66	0	15,19,21	1.68	5 (33%)
3	NAG	A	1326	1	14,14,15	0.68	0	15,19,21	2.10	6 (40%)

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	SO4	A	1323	-	-	0/0/0/0	0/0/0/0
3	NAG	A	1324	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1325	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1326	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1324	NAG	C2-N2-C7	-4.58	117.15	123.11
3	A	1326	NAG	C4-C3-C2	-3.07	106.58	111.34
3	A	1324	NAG	O3-C3-C4	-2.93	103.75	110.36
3	A	1325	NAG	C2-N2-C7	-2.91	119.33	123.11
3	A	1325	NAG	C4-C3-C2	-2.72	107.11	111.34
3	A	1326	NAG	C2-N2-C7	-2.53	119.81	123.11
3	A	1325	NAG	C3-C4-C5	-2.19	106.32	110.23
3	A	1325	NAG	O6-C6-C5	-2.04	104.49	111.30
3	A	1326	NAG	O5-C5-C6	2.03	111.68	107.34
3	A	1325	NAG	O3-C3-C2	2.09	113.84	109.37
3	A	1326	NAG	C8-C7-N2	2.18	120.28	116.10
3	A	1324	NAG	C8-C7-N2	2.29	120.48	116.10
3	A	1324	NAG	C1-O5-C5	2.69	116.10	112.14
3	A	1326	NAG	O5-C5-C4	2.72	114.63	110.13
3	A	1326	NAG	C1-O5-C5	5.12	119.66	112.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1325	NAG	1	0

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 [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	288/406 (70%)	-0.24	7 (2%) 62 66	19, 32, 64, 87	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	290	LEU	5.3
1	A	69	LEU	3.5
1	A	70	LYS	2.7
1	A	46	TRP	2.5
1	A	50	GLN	2.4
1	A	72	PRO	2.2
1	A	62	PHE	2.1

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	A	1323	5/5	0.90	0.24	7.15	56,61,77,78	0
3	NAG	A	1326	14/15	0.76	0.28	3.59	63,73,81,81	0
3	NAG	A	1324	14/15	0.86	0.23	2.38	48,57,61,66	0
3	NAG	A	1325	14/15	0.90	0.15	0.67	49,55,61,65	0
4	CA	A	1327	1/1	0.89	0.09	-0.76	58,58,58,58	0

6.5 Other polymers [i](#)

There are no such residues in this entry.