Full wwPDB X-ray Structure Validation Report (i)

Jun 22, 2024 – 10:43 AM EDT

PDB ID	:	5LTC
Title	:	Crystal structure of doubly spin labelled VcSiaP R125
Authors	:	Peter, M.; Glaenzer, J.; Hagelueken, G.
Deposited on	:	2016-09-06
Resolution	:	2.10 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 (i) 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 (1)) were used in the production of this report:

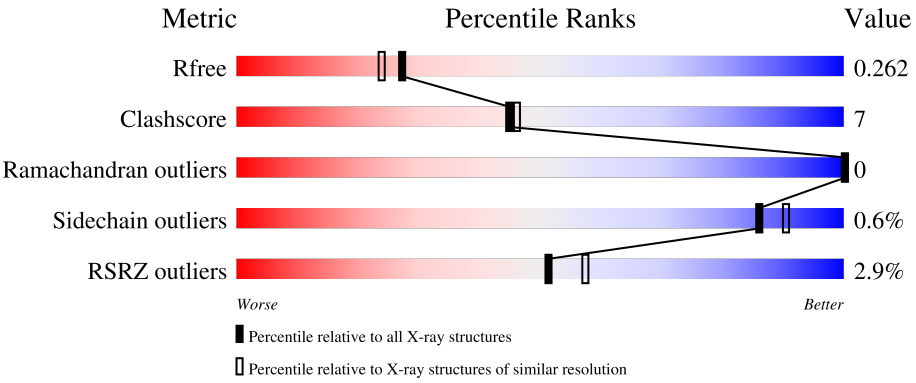
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 <=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	326	2% 82% 9% • 8%
1	B	326	3% 75% 15% • 8%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 4943 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 C4-dicarboxylate-binding periplasmic protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	299	Total	C	N	O	S	0	1	0
			2381	1507	395	460	19			
1	A	299	Total	C	N	O	S	0	2	0
			2381	1507	395	460	19			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-26	MET	-	initiating methionine	UNP A0A0H6HRA2
B	-25	SER	-	expression tag	UNP A0A0H6HRA2
B	-24	TYR	-	expression tag	UNP A0A0H6HRA2
B	-23	TYR	-	expression tag	UNP A0A0H6HRA2
B	-22	HIS	-	expression tag	UNP A0A0H6HRA2
B	-21	HIS	-	expression tag	UNP A0A0H6HRA2
B	-20	HIS	-	expression tag	UNP A0A0H6HRA2
B	-19	HIS	-	expression tag	UNP A0A0H6HRA2
B	-18	HIS	-	expression tag	UNP A0A0H6HRA2
B	-17	HIS	-	expression tag	UNP A0A0H6HRA2
B	-16	ASP	-	expression tag	UNP A0A0H6HRA2
B	-15	TYR	-	expression tag	UNP A0A0H6HRA2
B	-14	ASP	-	expression tag	UNP A0A0H6HRA2
B	-13	ILE	-	expression tag	UNP A0A0H6HRA2
B	-12	PRO	-	expression tag	UNP A0A0H6HRA2
B	-11	THR	-	expression tag	UNP A0A0H6HRA2
B	-10	THR	-	expression tag	UNP A0A0H6HRA2
B	-9	GLU	-	expression tag	UNP A0A0H6HRA2
B	-8	ASN	-	expression tag	UNP A0A0H6HRA2
B	-7	LEU	-	expression tag	UNP A0A0H6HRA2
B	-6	TYR	-	expression tag	UNP A0A0H6HRA2
B	-5	PHE	-	expression tag	UNP A0A0H6HRA2
B	-4	GLN	-	expression tag	UNP A0A0H6HRA2
B	-3	GLY	-	expression tag	UNP A0A0H6HRA2
B	-2	ALA	-	expression tag	UNP A0A0H6HRA2

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	MET	-	expression tag	UNP A0A0H6HRA2
B	0	GLY	ALA	conflict	UNP A0A0H6HRA2
B	54	R1A	GLN	conflict	UNP A0A0H6HRA2
B	125	ALA	ARG	conflict	UNP A0A0H6HRA2
B	173	R1A	LEU	conflict	UNP A0A0H6HRA2
A	-26	MET	-	initiating methionine	UNP A0A0H6HRA2
A	-25	SER	-	expression tag	UNP A0A0H6HRA2
A	-24	TYR	-	expression tag	UNP A0A0H6HRA2
A	-23	TYR	-	expression tag	UNP A0A0H6HRA2
A	-22	HIS	-	expression tag	UNP A0A0H6HRA2
A	-21	HIS	-	expression tag	UNP A0A0H6HRA2
A	-20	HIS	-	expression tag	UNP A0A0H6HRA2
A	-19	HIS	-	expression tag	UNP A0A0H6HRA2
A	-18	HIS	-	expression tag	UNP A0A0H6HRA2
A	-17	HIS	-	expression tag	UNP A0A0H6HRA2
A	-16	ASP	-	expression tag	UNP A0A0H6HRA2
A	-15	TYR	-	expression tag	UNP A0A0H6HRA2
A	-14	ASP	-	expression tag	UNP A0A0H6HRA2
A	-13	ILE	-	expression tag	UNP A0A0H6HRA2
A	-12	PRO	-	expression tag	UNP A0A0H6HRA2
A	-11	THR	-	expression tag	UNP A0A0H6HRA2
A	-10	THR	-	expression tag	UNP A0A0H6HRA2
A	-9	GLU	-	expression tag	UNP A0A0H6HRA2
A	-8	ASN	-	expression tag	UNP A0A0H6HRA2
A	-7	LEU	-	expression tag	UNP A0A0H6HRA2
A	-6	TYR	-	expression tag	UNP A0A0H6HRA2
A	-5	PHE	-	expression tag	UNP A0A0H6HRA2
A	-4	GLN	-	expression tag	UNP A0A0H6HRA2
A	-3	GLY	-	expression tag	UNP A0A0H6HRA2
A	-2	ALA	-	expression tag	UNP A0A0H6HRA2
A	-1	MET	-	expression tag	UNP A0A0H6HRA2
A	0	GLY	ALA	conflict	UNP A0A0H6HRA2
A	54	R1A	GLN	conflict	UNP A0A0H6HRA2
A	125	ALA	ARG	conflict	UNP A0A0H6HRA2
A	173	R1A	LEU	conflict	UNP A0A0H6HRA2

- Molecule 2 is water.

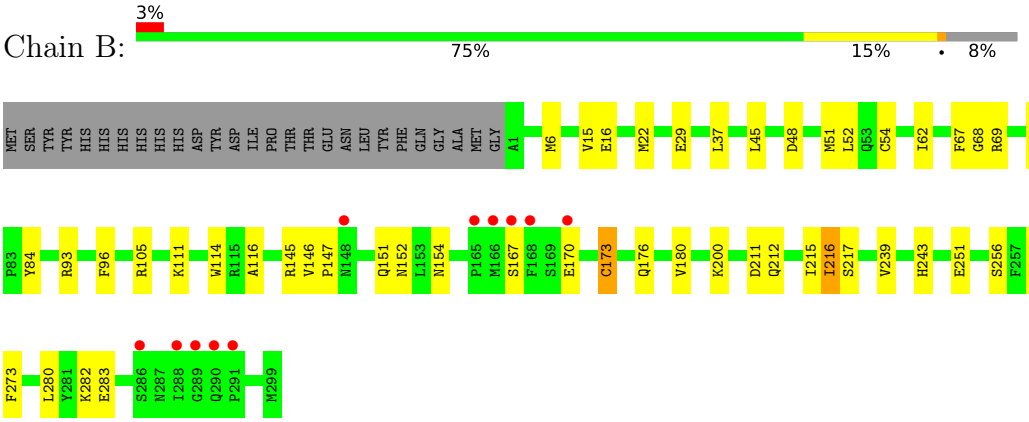
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	67	Total O 67 67	0	0
2	A	114	Total O 114 114	0	0

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.

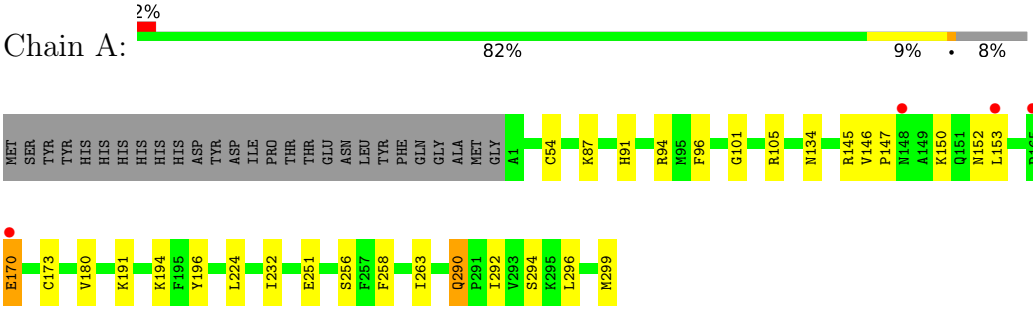
• Molecule 1: C4-dicarboxylate-binding periplasmic protein

Chain B:



• Molecule 1: C4-dicarboxylate-binding periplasmic protein

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 2 21	Depositor
Cell constants a, b, c, α, β, γ	72.27Å 78.10Å 116.24Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.29 – 2.10 64.83 – 2.10	Depositor EDS
% Data completeness (in resolution range)	97.1 (45.29-2.10) 90.9 (64.83-2.10)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.99 (at 2.10Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.219 , 0.263 0.219 , 0.262	Depositor DCC
R_{free} test set	2022 reflections (5.32%)	wwPDB-VP
Wilson B-factor (Å^2)	35.5	Xtriage
Anisotropy	0.116	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 46.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	4943	wwPDB-VP
Average B, all atoms (Å^2)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 63.49 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 9.5872e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: R1A

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	0.50	3/2389 (0.1%)	0.75	3/3228 (0.1%)
1	B	0.42	0/2389	0.73	2/3228 (0.1%)
All	All	0.46	3/4778 (0.1%)	0.74	5/6456 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	170	GLU	CD-OE1	-6.45	1.18	1.25
1	A	290	GLN	C-N	5.75	1.45	1.34
1	A	170	GLU	CD-OE2	-5.30	1.19	1.25

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	153	LEU	CB-CG-CD1	-12.05	90.51	111.00
1	B	263	ILE	CG1-CB-CG2	-10.64	88.00	111.40
1	B	93	ARG	CB-CG-CD	5.95	127.07	111.60
1	A	153	LEU	CB-CG-CD2	5.94	121.10	111.00
1	A	153	LEU	CB-CA-C	5.37	120.41	110.20

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	2381	0	2356	23	1
1	B	2381	0	2356	39	1
2	A	114	0	0	3	2
2	B	67	0	0	6	2
All	All	4943	0	4712	62	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 7.

All (62) 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:251:GLU:OE2	2:B:301:HOH:O	1.90	0.89
1:B:82:LEU:O	2:B:302:HOH:O	1.90	0.87
1:B:78:GLU:OE2	1:B:151:GLN:NE2	2.13	0.81
1:B:211:ASP:OD1	2:B:303:HOH:O	2.00	0.78
1:B:111:LYS:O	2:B:304:HOH:O	2.02	0.78
1:A:256:SER:OG	2:A:302:HOH:O	2.03	0.76
1:B:146:VAL:HG22	1:B:152:ASN:HB3	1.69	0.75
1:A:251:GLU:OE2	2:A:303:HOH:O	2.04	0.75
1:B:145:ARG:HB2	1:B:180:VAL:HG11	1.69	0.74
1:A:296:LEU:HA	1:A:299:MET:HE2	1.73	0.70
1:A:145:ARG:HB2	1:A:180:VAL:HG11	1.76	0.66
1:A:87:LYS:HD2	1:A:91:HIS:ND1	2.13	0.64
1:B:146:VAL:CG2	1:B:152:ASN:HB3	2.30	0.62
1:B:146:VAL:HG22	1:B:147:PRO:HD2	1.82	0.61
1:A:146:VAL:HG13	1:A:147:PRO:HD2	1.81	0.61
1:A:94:ARG:HD3	2:A:301:HOH:O	2.00	0.60
1:B:116:ALA:O	2:B:305:HOH:O	2.16	0.60
1:B:68:GLY:HA3	1:B:81:MET:HE3	1.84	0.58
1:A:101:GLY:O	1:A:105:ARG:HG3	2.04	0.58
1:B:62:ILE:CG1	1:B:216:ILE:HD12	2.35	0.57
1:A:196:TYR:HB2	1:A:263:ILE:HD11	1.87	0.57
1:B:29:GLU:OE1	2:B:306:HOH:O	2.18	0.56
1:A:150:LYS:N	1:A:150:LYS:HD3	2.22	0.55
1:B:146:VAL:HG22	1:B:152:ASN:CB	2.36	0.55
1:B:15:VAL:HG12	1:B:243:HIS:CE1	2.42	0.54
1:B:167:SER:HB3	1:B:170:GLU:OE1	2.07	0.54
1:A:290:GLN:NE2	1:A:292:ILE:HD11	2.24	0.53
1:B:22:MET:CE	1:B:239:VAL:HG13	2.38	0.52
1:A:258:PHE:HB3	1:A:263:ILE:HD12	1.92	0.51
1:B:256:SER:O	1:B:259:LYS:HG2	2.09	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:45:LEU:HB2	1:B:51:MET:HE3	1.94	0.50
1:B:200:LYS:C	1:B:263:ILE:HD12	2.32	0.50
1:B:96:PHE:CE1	1:B:105:ARG:HD3	2.48	0.49
1:A:96:PHE:CE1	1:A:105:ARG:HD2	2.48	0.49
1:A:191:LYS:O	1:A:194:LYS:HD3	2.13	0.48
1:B:48:ASP:OD2	1:B:69:ARG:NE	2.41	0.48
1:B:22:MET:HE2	1:B:239:VAL:HG13	1.94	0.48
1:A:96:PHE:CZ	1:A:105:ARG:HD2	2.48	0.48
1:B:173:R1A:HE3	1:B:176:GLN:OE1	2.13	0.48
1:A:173[A]:R1A:H73	1:A:173[A]:R1A:H82	1.96	0.47
1:A:145:ARG:HD3	1:A:145:ARG:C	2.35	0.47
1:B:258:PHE:HB3	1:B:263:ILE:HG21	1.97	0.46
1:B:22:MET:HE2	1:B:22:MET:HB3	1.86	0.46
1:B:62:ILE:HG12	1:B:216:ILE:HD12	1.96	0.46
1:B:16:GLU:OE1	1:B:212:GLN:NE2	2.49	0.46
1:B:216:ILE:HG13	1:B:217:SER:N	2.30	0.46
1:B:45:LEU:HB2	1:B:51:MET:CE	2.47	0.45
1:A:146:VAL:HG13	1:A:152:ASN:HB3	1.98	0.45
1:A:150:LYS:HD3	1:A:150:LYS:H	1.80	0.45
1:B:146:VAL:HG21	1:B:152:ASN:O	2.17	0.45
1:A:169:SER:OG	1:A:170:GLU:OE1	2.35	0.44
1:B:67:PHE:CE2	1:B:80:VAL:HG11	2.54	0.43
1:B:282:LYS:HD3	1:B:283:GLU:N	2.34	0.43
1:B:6:MET:HB2	1:B:37:LEU:HD11	2.01	0.42
1:B:259:LYS:HA	1:B:263:ILE:HG22	2.00	0.42
1:A:224:LEU:HD13	1:A:232:ILE:HD12	2.01	0.42
1:B:84:TYR:CE2	1:B:273:PHE:HB3	2.55	0.42
1:B:52:LEU:HB3	1:B:114:TRP:CZ2	2.55	0.41
1:A:296:LEU:HD23	1:A:299:MET:CE	2.51	0.41
1:B:62:ILE:HA	1:B:215:ILE:O	2.19	0.41
1:B:154:ASN:HB3	1:B:280:LEU:HD22	2.02	0.41
1:A:150:LYS:H	1:A:150:LYS:CD	2.34	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)
2:B:367:HOH:O	2:A:413:HOH:O[2_759]	2.01	0.19
2:B:315:HOH:O	2:A:302:HOH:O[4_654]	2.15	0.05
1:B:200:LYS:NZ	1:A:134:ASN:OD1[2_749]	2.18	0.02

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	295/326 (90%)	293 (99%)	2 (1%)	0	100	100
1	B	295/326 (90%)	293 (99%)	2 (1%)	0	100	100
All	All	590/652 (90%)	586 (99%)	4 (1%)	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	256/280 (91%)	255 (100%)	1 (0%)	91	94
1	B	256/280 (91%)	254 (99%)	2 (1%)	81	86
All	All	512/560 (91%)	509 (99%)	3 (1%)	86	90

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	81	MET
1	B	216	ILE
1	A	294	SER

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

Mol	Chain	Res	Type
1	B	287	ASN
1	A	290	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

4 non-standard protein/DNA/RNA residues 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	$\#\|Z\| > 2$
1	R1A	B	173	1	15,18,19	2.00	5 (33%)	15,27,29	1.41	1 (6%)
1	R1A	B	54	1	15,18,19	1.84	5 (33%)	15,27,29	1.34	1 (6%)
1	R1A	A	54	1	15,18,19	1.95	5 (33%)	15,27,29	1.41	1 (6%)

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
1	R1A	B	173	1	-	3/5/32/34	0/1/1/1
1	R1A	B	54	1	-	1/5/32/34	0/1/1/1
1	R1A	A	54	1	-	1/5/32/34	0/1/1/1

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	54	R1A	CE-SD	-4.24	1.76	1.81
1	B	173	R1A	CE-SD	-4.12	1.76	1.81
1	B	54	R1A	CE-SD	-3.57	1.77	1.81
1	B	173	R1A	C2-N1	3.40	1.56	1.47

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	54	R1A	C2-N1	3.35	1.56	1.47
1	A	54	R1A	C2-N1	3.33	1.56	1.47
1	B	173	R1A	C5-N1	3.32	1.56	1.47
1	A	54	R1A	C5-N1	3.18	1.55	1.47
1	B	54	R1A	C5-N1	3.11	1.55	1.47
1	B	173	R1A	C4-C3	2.53	1.35	1.32
1	A	54	R1A	C4-C3	2.36	1.35	1.32
1	B	173	R1A	O1-N1	-2.35	1.16	1.26
1	A	54	R1A	O1-N1	-2.35	1.16	1.26
1	B	54	R1A	O1-N1	-2.32	1.16	1.26
1	B	54	R1A	C4-C3	2.23	1.35	1.32

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	54	R1A	CE-SD-SG	4.50	108.68	103.67
1	B	173	R1A	CE-SD-SG	4.49	108.68	103.67
1	B	54	R1A	CE-SD-SG	4.28	108.44	103.67

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	173	R1A	N-CA-CB-SG
1	B	173	R1A	CE-SD-SG-CB
1	B	54	R1A	CA-CB-SG-SD
1	A	54	R1A	CA-CB-SG-SD
1	B	173	R1A	CA-CB-SG-SD

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	173	R1A	1	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

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^{th} 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	297/326 (91%)	-0.07	6 (2%) 65 69	31, 49, 71, 92	0
1	B	297/326 (91%)	0.11	11 (3%) 41 48	39, 57, 87, 108	0
All	All	594/652 (91%)	0.02	17 (2%) 51 57	31, 53, 80, 108	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	165	PRO	5.2
1	B	165	PRO	4.1
1	B	286	SER	4.1
1	B	148	ASN	4.0
1	A	166	MET	3.1
1	B	167	SER	3.1
1	A	167	SER	3.1
1	B	170	GLU	3.0
1	B	289	GLY	2.9
1	B	291	PRO	2.8
1	B	168	PHE	2.7
1	B	166	MET	2.6
1	A	153	LEU	2.6
1	A	170	GLU	2.4
1	A	148	ASN	2.3
1	B	290	GLN	2.2
1	B	288	ILE	2.1

6.2 Non-standard residues in protein, DNA, RNA chains

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, 95^{th} 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
1	R1A	B	173	18/19	0.82	0.23	80,114,126,127	0
1	R1A	A	173[A]	18/19	0.88	0.19	63,79,89,93	15
1	R1A	B	54	18/19	0.94	0.15	42,75,82,87	0
1	R1A	A	54	18/19	0.96	0.14	45,81,91,92	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.