



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 09:04 am BST

PDB ID : 5Z6Q
Title : Crystal structure of AAA of Spastin
Authors : Lin, Z.; Wang, C.; Shen, Y.
Deposited on : 2018-01-25
Resolution : 3.00 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtrriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

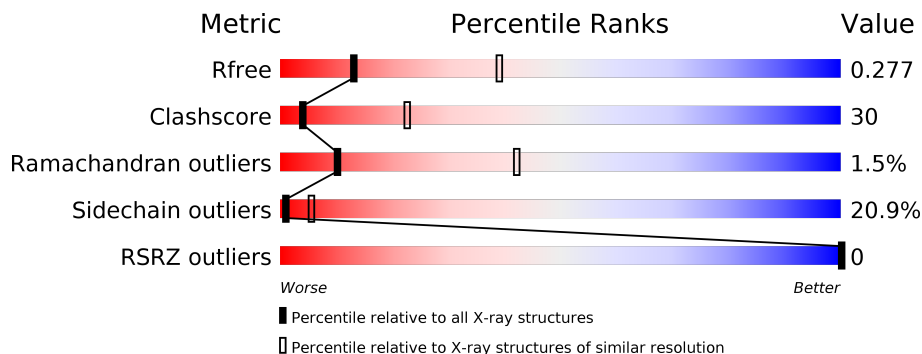
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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 $\leq 5\%$. 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	392	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1965 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 Spastin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	272	1964	1249	344	365	6	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	225	GLY	-	expression tag	UNP Q9UBP0
A	226	PRO	-	expression tag	UNP Q9UBP0
A	227	GLY	-	expression tag	UNP Q9UBP0
A	228	SER	-	expression tag	UNP Q9UBP0

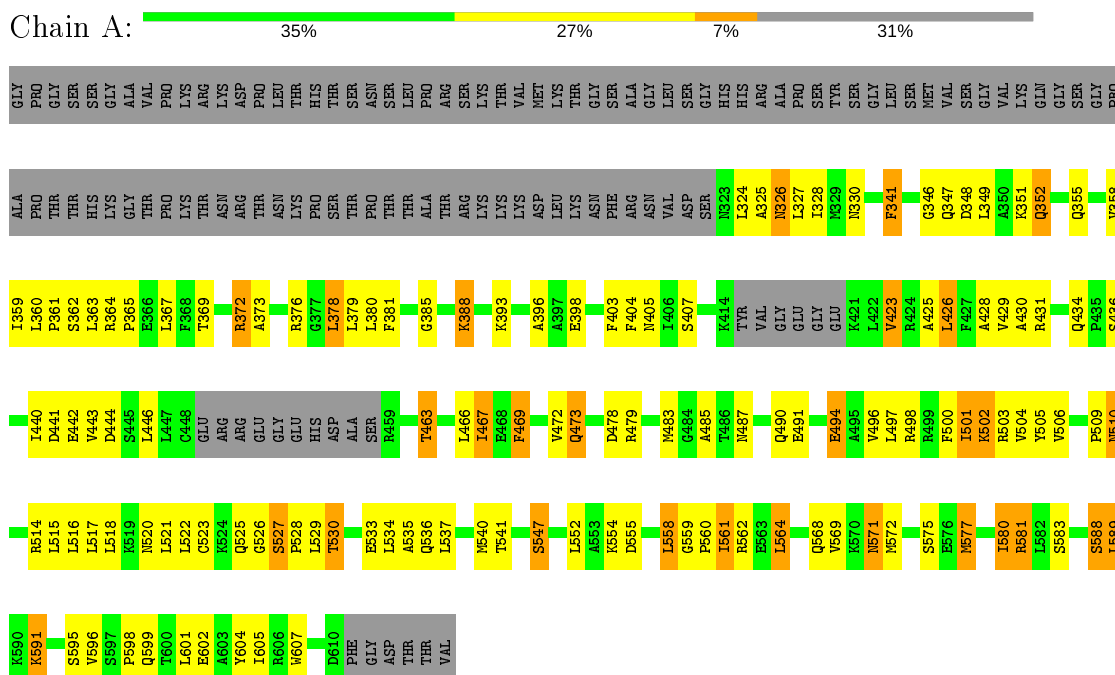
- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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: Spastin



4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	90.52Å 90.52Å 89.15Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	38.75 – 3.00 38.75 – 3.00	Depositor EDS
% Data completeness (in resolution range)	100.0 (38.75-3.00) 100.0 (38.75-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.25 (at 3.01Å)	Xtrriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.194 , 0.276 0.214 , 0.277	Depositor DCC
R_{free} test set	389 reflections (4.64%)	wwPDB-VP
Wilson B-factor (Å ²)	76.2	Xtrriage
Anisotropy	0.347	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 53.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.067 for h,-h-k,-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	1965	wwPDB-VP
Average B, all atoms (Å ²)	77.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.40% 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: 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	0.50	0/1989	0.67	0/2704

There are no bond length outliers.

There are no bond angle outliers.

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	1964	0	1923	117	1
2	A	1	0	0	0	0
All	All	1965	0	1923	117	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 30.

All (117) 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:555:ASP:OD1	1:A:588:SER:HB3	1.63	0.97
1:A:328:ILE:HD12	1:A:429:VAL:HG21	1.44	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:564:LEU:HD12	1:A:569:VAL:HG22	1.49	0.94
1:A:591:LYS:NZ	1:A:591:LYS:HB3	1.90	0.86
1:A:443:VAL:HG23	1:A:485:ALA:O	1.82	0.80
1:A:426:LEU:HD12	1:A:426:LEU:O	1.82	0.79
1:A:502:LYS:HZ2	1:A:502:LYS:HB3	1.50	0.76
1:A:364:ARG:HH11	1:A:364:ARG:HG2	1.51	0.76
1:A:388:LYS:NZ	1:A:487:ASN:HD21	1.84	0.75
1:A:428:ALA:HA	1:A:431:ARG:NH1	2.01	0.74
1:A:591:LYS:HZ3	1:A:591:LYS:HB3	1.53	0.74
1:A:328:ILE:HD13	1:A:426:LEU:HA	1.72	0.71
1:A:473:GLN:HA	1:A:473:GLN:HE21	1.57	0.70
1:A:388:LYS:HZ1	1:A:487:ASN:ND2	1.91	0.68
1:A:521:LEU:HD23	1:A:521:LEU:N	2.08	0.68
1:A:502:LYS:NZ	1:A:502:LYS:HB3	2.09	0.67
1:A:517:LEU:N	1:A:517:LEU:HD23	2.09	0.67
1:A:510:ASN:ND2	1:A:510:ASN:H	1.93	0.67
1:A:328:ILE:HD12	1:A:429:VAL:CG2	2.22	0.66
1:A:510:ASN:HD22	1:A:510:ASN:H	1.45	0.65
1:A:431:ARG:O	1:A:434:GLN:HG3	1.97	0.65
1:A:388:LYS:NZ	1:A:487:ASN:ND2	2.45	0.64
1:A:388:LYS:HD2	1:A:506:VAL:HB	1.78	0.64
1:A:341:PHE:HB2	1:A:398:GLU:CD	2.17	0.64
1:A:440:ILE:HD12	1:A:483:MET:O	1.99	0.63
1:A:388:LYS:HZ1	1:A:487:ASN:HD21	1.46	0.63
1:A:530:THR:HG23	1:A:533:GLU:OE1	2.00	0.60
1:A:426:LEU:HD12	1:A:426:LEU:C	2.22	0.59
1:A:558:LEU:O	1:A:562:ARG:HG3	2.02	0.59
1:A:404:PHE:CZ	1:A:430:ALA:HA	2.37	0.59
1:A:324:LEU:HA	1:A:326:ASN:ND2	2.19	0.57
1:A:378:LEU:HD12	1:A:379:LEU:N	2.18	0.57
1:A:554:LYS:O	1:A:558:LEU:HD12	2.04	0.57
1:A:515:LEU:HD12	1:A:535:ALA:HA	1.88	0.56
1:A:403:PHE:CE2	1:A:405:ASN:HB2	2.42	0.55
1:A:423:VAL:C	1:A:425:ALA:H	2.11	0.55
1:A:355:GLN:HA	1:A:359:ILE:HB	1.88	0.54
1:A:601:LEU:O	1:A:604:TYR:HB2	2.08	0.54
1:A:404:PHE:CE2	1:A:436:SER:HB3	2.43	0.53
1:A:522:LEU:HB3	1:A:528:PRO:HD2	1.90	0.53
1:A:497:LEU:HD23	1:A:497:LEU:O	2.09	0.53
1:A:326:ASN:O	1:A:330:ASN:OD1	2.27	0.53
1:A:441:ASP:O	1:A:442:GLU:C	2.45	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:351:LYS:O	1:A:355:GLN:HB2	2.08	0.53
1:A:355:GLN:OE1	1:A:359:ILE:HG21	2.10	0.52
1:A:494:GLU:O	1:A:498:ARG:HG3	2.09	0.52
1:A:496:VAL:HG12	1:A:497:LEU:N	2.23	0.52
1:A:502:LYS:C	1:A:503:ARG:HD2	2.30	0.52
1:A:364:ARG:NH2	1:A:367:LEU:HD11	2.25	0.51
1:A:388:LYS:HZ2	1:A:487:ASN:HD21	1.56	0.51
1:A:518:LEU:O	1:A:522:LEU:HG	2.11	0.51
1:A:469:PHE:HD1	1:A:469:PHE:O	1.93	0.51
1:A:536:GLN:O	1:A:540:MET:HG3	2.10	0.51
1:A:591:LYS:HZ2	1:A:591:LYS:HB3	1.72	0.51
1:A:404:PHE:HE2	1:A:436:SER:HB3	1.76	0.50
1:A:537:LEU:O	1:A:541:THR:HG23	2.11	0.50
1:A:358:VAL:O	1:A:362:SER:HB2	2.11	0.49
1:A:490:GLN:HA	1:A:607:TRP:HE1	1.76	0.49
1:A:423:VAL:C	1:A:425:ALA:N	2.65	0.49
1:A:515:LEU:CD1	1:A:535:ALA:HA	2.42	0.49
1:A:328:ILE:CD1	1:A:426:LEU:HA	2.41	0.48
1:A:500:PHE:O	1:A:501:ILE:C	2.52	0.48
1:A:522:LEU:CD1	1:A:534:LEU:HD21	2.44	0.48
1:A:561:ILE:HG22	1:A:562:ARG:N	2.28	0.48
1:A:602:GLU:HA	1:A:605:ILE:HD12	1.96	0.48
1:A:425:ALA:O	1:A:429:VAL:HG23	2.13	0.48
1:A:326:ASN:ND2	1:A:326:ASN:H	2.12	0.47
1:A:364:ARG:NH1	1:A:364:ARG:HG2	2.26	0.47
1:A:497:LEU:HD23	1:A:503:ARG:NH2	2.29	0.47
1:A:347:GLN:NE2	1:A:506:VAL:HG13	2.30	0.47
1:A:364:ARG:CG	1:A:364:ARG:HH11	2.24	0.47
1:A:498:ARG:CB	1:A:498:ARG:HH11	2.27	0.47
1:A:346:GLY:O	1:A:351:LYS:HE2	2.14	0.47
1:A:564:LEU:HD12	1:A:569:VAL:CG2	2.34	0.46
1:A:463:THR:O	1:A:467:ILE:HD13	2.16	0.46
1:A:434:GLN:NE2	1:A:478:ASP:CB	2.79	0.46
1:A:509:PRO:HG2	1:A:514:ARG:HG2	1.98	0.46
1:A:385:GLY:HA3	1:A:547:SER:OG	2.17	0.45
1:A:522:LEU:HD12	1:A:534:LEU:HD21	1.98	0.45
1:A:469:PHE:CD1	1:A:469:PHE:C	2.89	0.45
1:A:469:PHE:HD1	1:A:469:PHE:C	2.19	0.45
1:A:502:LYS:NZ	1:A:502:LYS:CB	2.79	0.45
1:A:526:GLY:O	1:A:527:SER:C	2.55	0.45
1:A:560:PRO:HD3	1:A:580:ILE:HG22	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:571:ASN:N	1:A:571:ASN:OD1	2.50	0.44
1:A:347:GLN:HE21	1:A:506:VAL:HG13	1.82	0.43
1:A:403:PHE:HE2	1:A:405:ASN:HB2	1.81	0.43
1:A:497:LEU:HD23	1:A:497:LEU:C	2.39	0.43
1:A:381:PHE:CZ	1:A:505:TYR:HB2	2.53	0.43
1:A:380:LEU:HD23	1:A:504:VAL:HB	2.01	0.43
1:A:564:LEU:H	1:A:564:LEU:HG	1.48	0.43
1:A:560:PRO:CD	1:A:580:ILE:HG22	2.49	0.43
1:A:498:ARG:NH1	1:A:498:ARG:HB2	2.34	0.42
1:A:591:LYS:CB	1:A:591:LYS:HZ3	2.27	0.42
1:A:364:ARG:CG	1:A:364:ARG:NH1	2.83	0.42
1:A:434:GLN:NE2	1:A:478:ASP:HB3	2.34	0.42
1:A:324:LEU:HA	1:A:326:ASN:HD22	1.83	0.42
1:A:325:ALA:C	1:A:327:LEU:N	2.73	0.42
1:A:575:SER:C	1:A:577:MET:H	2.22	0.42
1:A:581:ARG:HB2	1:A:581:ARG:HE	1.34	0.42
1:A:589:LEU:HA	1:A:589:LEU:HD13	1.79	0.42
1:A:360:LEU:N	1:A:361:PRO:CD	2.84	0.41
1:A:466:LEU:HD23	1:A:466:LEU:HA	1.92	0.41
1:A:380:LEU:O	1:A:485:ALA:HA	2.21	0.41
1:A:446:LEU:HG	1:A:446:LEU:O	2.21	0.41
1:A:520:ASN:O	1:A:523:CYS:HB2	2.21	0.41
1:A:522:LEU:CD1	1:A:529:LEU:HB2	2.51	0.41
1:A:598:PRO:HD2	1:A:599:GLN:NE2	2.36	0.41
1:A:469:PHE:O	1:A:473:GLN:HG2	2.21	0.41
1:A:352:GLN:HA	1:A:352:GLN:NE2	2.36	0.41
1:A:376:ARG:H	1:A:501:ILE:HD12	1.85	0.41
1:A:363:LEU:O	1:A:365:PRO:HD3	2.21	0.40
1:A:372:ARG:O	1:A:373:ALA:C	2.59	0.40
1:A:552:LEU:CD1	1:A:589:LEU:HD13	2.52	0.40
1:A:396:ALA:HB2	1:A:403:PHE:HD1	1.87	0.40
1:A:443:VAL:CG2	1:A:485:ALA:N	2.84	0.40
1:A:559:GLY:N	1:A:560:PRO:CD	2.84	0.40

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:A:364:ARG:NH2	1:A:572:MET:O[6_554]	2.09	0.11

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	266/392 (68%)	239 (90%)	23 (9%)	4 (2%)	10 42

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	494	GLU
1	A	501	ILE
1	A	527	SER
1	A	423	VAL

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	191/329 (58%)	151 (79%)	40 (21%)	1 5

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	326	ASN
1	A	341	PHE
1	A	348	ASP
1	A	349	LEU
1	A	352	GLN
1	A	369	THR
1	A	372	ARG

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Mol	Chain	Res	Type
1	A	378	LEU
1	A	388	LYS
1	A	393	LYS
1	A	407	SER
1	A	426	LEU
1	A	444	ASP
1	A	463	THR
1	A	467	ILE
1	A	469	PHE
1	A	472	VAL
1	A	473	GLN
1	A	479	ARG
1	A	491	GLU
1	A	502	LYS
1	A	510	ASN
1	A	516	LEU
1	A	525	GLN
1	A	530	THR
1	A	547	SER
1	A	558	LEU
1	A	561	ILE
1	A	564	LEU
1	A	568	GLN
1	A	571	ASN
1	A	577	MET
1	A	580	ILE
1	A	581	ARG
1	A	583	SER
1	A	588	SER
1	A	589	LEU
1	A	591	LYS
1	A	595	SER
1	A	596	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	326	ASN
1	A	473	GLN
1	A	487	ASN
1	A	510	ASN
1	A	525	GLN

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Mol	Chain	Res	Type
1	A	568	GLN
1	A	599	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

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 [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	272/392 (69%)	-0.66	0 100 100	48, 75, 118, 144	0

There are no RSRZ outliers to report.

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. 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	CL	A	701	1/1	0.93	0.11	61,61,61,61	0

6.5 Other polymers [i](#)

There are no such residues in this entry.