



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 01:17 AM UTC

PDB ID : 4WEL / pdb_00004wel
Title : Crystal structure of Pseudomonas aeruginosa PBP3 with SMC-3176
Authors : Ferguson, A.D.
Deposited on : 2014-09-10
Resolution : 1.99 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

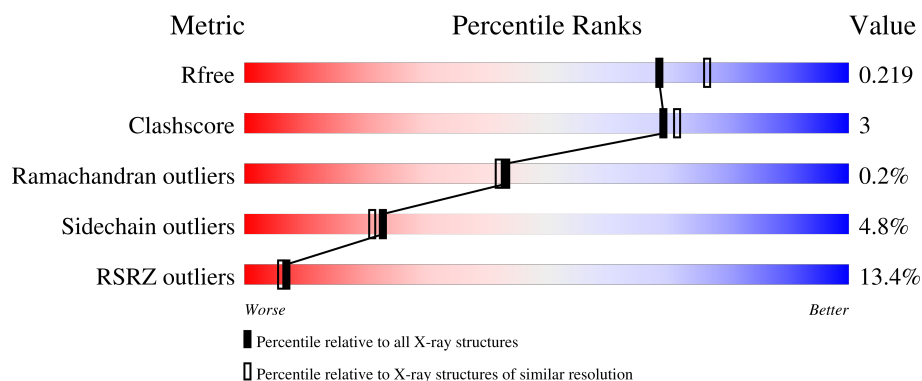
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.99 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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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 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	538	12% 82% 10% 7%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4087 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.

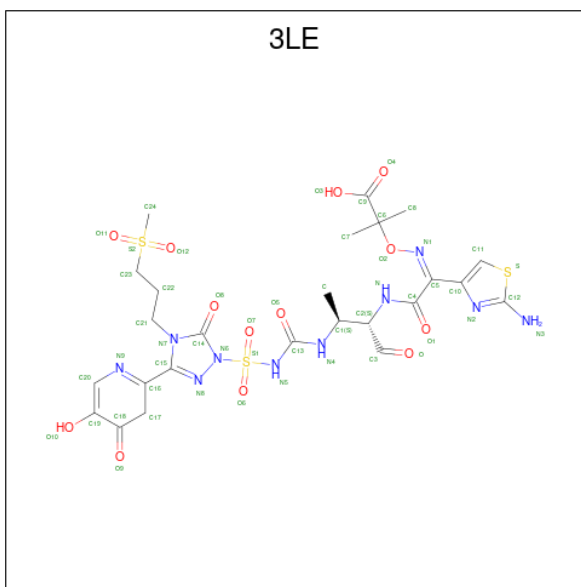
- Molecule 1 is a protein called Penicillin-binding protein 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	500	Total	C	N	O	S	0	0	0
			3820	2411	694	703	12			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	42	MET	-	initiating methionine	UNP S0J4R2
A	43	GLY	-	expression tag	UNP S0J4R2
A	44	HIS	-	expression tag	UNP S0J4R2
A	45	HIS	-	expression tag	UNP S0J4R2
A	46	HIS	-	expression tag	UNP S0J4R2
A	47	HIS	-	expression tag	UNP S0J4R2
A	48	HIS	-	expression tag	UNP S0J4R2
A	49	HIS	-	expression tag	UNP S0J4R2

- Molecule 2 is (3S,4S,7Z)-7-(2-amino-1,3-thiazol-4-yl)-4-formyl-1-[(3-(5-hydroxy-4-oxo-3,4-dihydropyridin-2-yl)-4-[3-(methylsulfonyl)propyl]-5-oxo-4,5-dihydro-1H-1,2,4-triazol-1-yl)sulfonyl]amino]-3,10,10-trimethyl-1,6-dioxo-9-oxa-2,5,8-triazaundec-7-en-11-oic acid (CCD ID: 3LE) (formula: C₂₅H₃₂N₁₀O₁₃S₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			51	25	10	13	3		

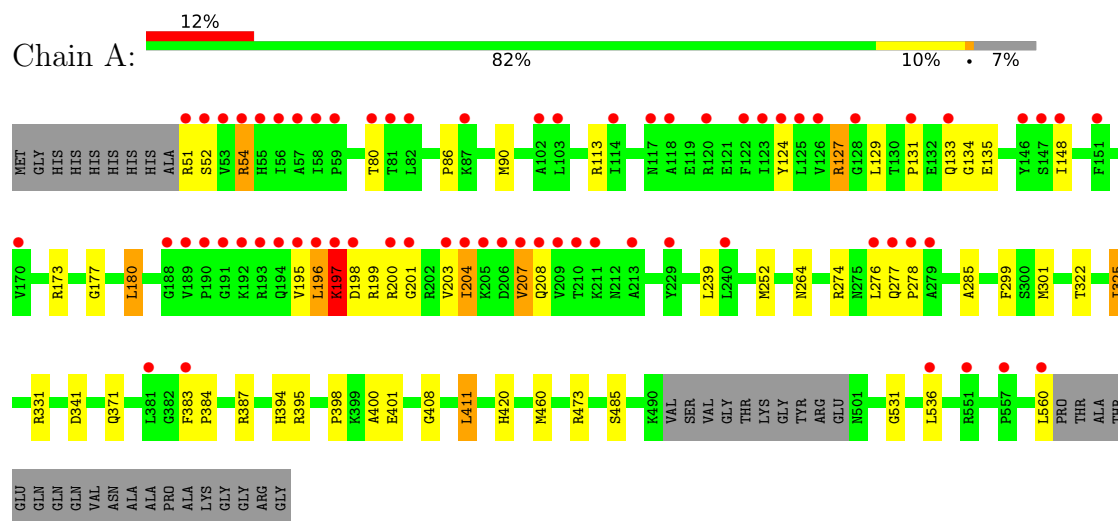
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	216	Total O 216 216	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: Penicillin-binding protein 3



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	68.44Å 83.34Å 89.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	60.96 – 1.99 60.96 – 1.99	Depositor EDS
% Data completeness (in resolution range)	100.0 (60.96-1.99) 99.9 (60.96-1.99)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.14 (at 1.98Å)	Xtriage
Refinement program	BUSTER 2.11.5	Depositor
R, R_{free}	0.190 , 0.220 (Not available) , 0.219	Depositor DCC
R_{free} test set	1788 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	33.5	Xtriage
Anisotropy	0.320	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 40.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4087	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.16% 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: 3LE

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	0.84	2/3894 (0.1%)	1.09	9/5281 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	460	MET	SD-CE	-6.29	1.63	1.79
1	A	301	MET	SD-CE	-5.81	1.65	1.79

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	387	ARG	CB-CG-CD	6.65	126.61	111.30
1	A	395	ARG	N-CA-C	-5.88	104.22	111.40
1	A	198	ASP	CA-CB-CG	5.35	117.95	112.60
1	A	325	ILE	CB-CA-C	5.33	116.62	111.23
1	A	299	PHE	CA-CB-CG	-5.33	108.47	113.80
1	A	341	ASP	CA-CB-CG	5.20	117.80	112.60
1	A	197	LYS	CG-CD-CE	5.17	123.19	111.30
1	A	131	PRO	CA-C-N	5.01	126.95	120.44
1	A	131	PRO	C-N-CA	5.01	126.95	120.44

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	3820	0	3879	26	0
2	A	51	0	29	2	0
3	A	216	0	0	2	0
All	All	4087	0	3908	27	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 3.

All (27) 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:473:ARG:HH22	2:A:601:3LE:H18	1.56	0.69
2:A:601:3LE:H12	2:A:601:3LE:H22	1.78	0.65
1:A:264:ASN:HD21	1:A:285:ALA:H	1.53	0.56
1:A:325:ILE:CD1	1:A:400:ALA:HA	2.37	0.54
1:A:196:LEU:HD23	1:A:204:ILE:HD12	1.92	0.51
1:A:180:LEU:HD13	1:A:384:PRO:HB3	1.94	0.49
1:A:207:VAL:HG22	1:A:208:GLN:HG2	1.95	0.49
1:A:408:GLY:HA2	1:A:411:LEU:HD21	1.95	0.49
1:A:51:ARG:HG2	3:A:749:HOH:O	2.13	0.48
1:A:195:VAL:CG2	1:A:203:VAL:HG13	2.44	0.47
1:A:394:HIS:HE1	3:A:834:HOH:O	1.98	0.47
1:A:124:TYR:CD1	1:A:127:ARG:HD3	2.50	0.47
1:A:80:THR:HG21	1:A:134:GLY:HA3	1.98	0.45
1:A:325:ILE:HD11	1:A:400:ALA:HA	1.98	0.44
1:A:325:ILE:HD12	1:A:400:ALA:HA	1.98	0.44
1:A:124:TYR:CE1	1:A:127:ARG:HD3	2.53	0.43
1:A:398:PRO:HD2	1:A:401:GLU:HB2	1.99	0.43
1:A:277:GLN:HA	1:A:278:PRO:HD3	1.91	0.43
1:A:252:MET:HE1	1:A:420:HIS:HD2	1.83	0.42
1:A:129:LEU:HD13	1:A:133:GLN:HB3	2.01	0.42
1:A:177:GLY:HA2	1:A:383:PHE:CE2	2.54	0.42
1:A:264:ASN:ND2	1:A:285:ALA:H	2.15	0.42
1:A:322:THR:HG22	1:A:331:ARG:HG2	2.02	0.41
1:A:197:LYS:HE2	1:A:201:GLY:HA2	2.03	0.40
1:A:86:PRO:O	1:A:90:MET:HG2	2.21	0.40
1:A:531:GLY:HA3	1:A:536:LEU:HD23	2.03	0.40
1:A:52:SER:HB3	1:A:54:ARG:CZ	2.51	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	475/538 (88%)	463 (98%)	11 (2%)	1 (0%)	43	42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	276	LEU

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	399/426 (94%)	380 (95%)	19 (5%)	23	21

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	54	ARG
1	A	113	ARG
1	A	127	ARG
1	A	135	GLU
1	A	148	ILE
1	A	173	ARG
1	A	180	LEU
1	A	196	LEU
1	A	197	LYS
1	A	199	ARG

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Mol	Chain	Res	Type
1	A	200	ARG
1	A	204	ILE
1	A	207	VAL
1	A	239	LEU
1	A	274	ARG
1	A	371	GLN
1	A	411	LEU
1	A	485	SER
1	A	560	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	264	ASN
1	A	336	ASN
1	A	394	HIS
1	A	427	ASN
1	A	458	GLN
1	A	463	GLN
1	A	468	GLN
1	A	475	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	$\# Z > 2$
2	3LE	A	601	1	47,53,53	1.65	2 (4%)	55,79,79	0.84	2 (3%)

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	3LE	A	601	1	-	10/45/69/69	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	3LE	C17-C16	-10.07	1.37	1.50
2	A	601	3LE	C6-C9	2.19	1.55	1.53

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	3LE	C17-C16-C15	2.30	122.77	118.35
2	A	601	3LE	C22-C23-S2	2.04	117.53	112.25

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	3LE	N4-C1-C2-N
2	A	601	3LE	C-C1-C2-C3
2	A	601	3LE	C-C1-C2-N
2	A	601	3LE	N8-N6-S1-O6
2	A	601	3LE	N8-N6-S1-O7
2	A	601	3LE	N-C4-C5-N1
2	A	601	3LE	C8-C6-C9-O4

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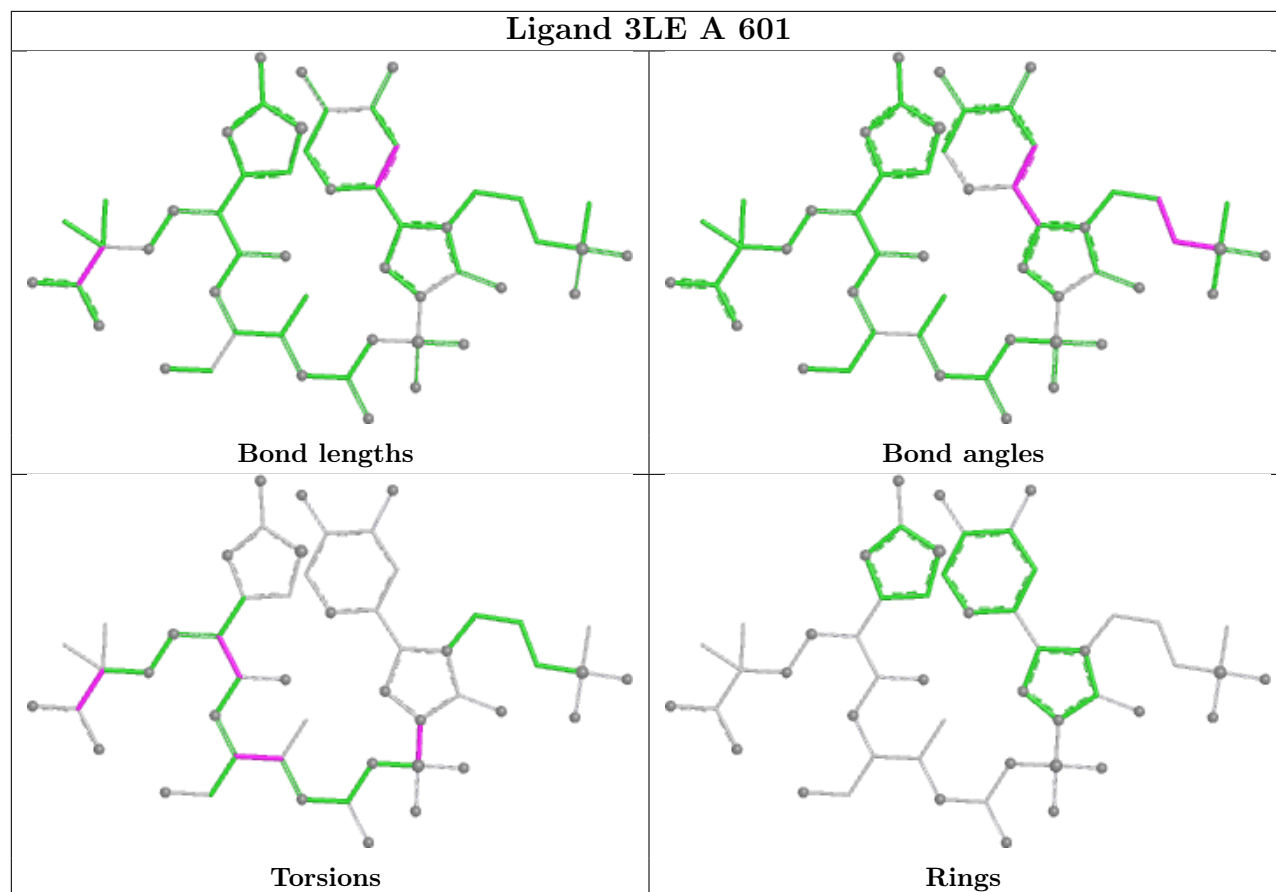
Mol	Chain	Res	Type	Atoms
2	A	601	3LE	C8-C6-C9-O3
2	A	601	3LE	O1-C4-C5-C10
2	A	601	3LE	O1-C4-C5-N1

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	3LE	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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

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	500/538 (92%)	0.51	67 (13%) 7 6	22, 38, 109, 145	1 (0%)

All (67) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	56	ILE	6.1
1	A	53	VAL	5.8
1	A	57	ALA	5.7
1	A	276	LEU	4.8
1	A	203	VAL	4.8
1	A	204	ILE	4.8
1	A	560	LEU	4.8
1	A	196	LEU	4.6
1	A	58	ILE	4.5
1	A	210	THR	4.5
1	A	383	PHE	4.2
1	A	147	SER	4.1
1	A	206	ASP	4.0
1	A	195	VAL	3.9
1	A	118	ALA	3.7
1	A	201	GLY	3.6
1	A	277	GLN	3.6
1	A	148	ILE	3.6
1	A	209	VAL	3.5
1	A	191	GLY	3.5
1	A	207	VAL	3.5
1	A	59	PRO	3.4
1	A	125	LEU	3.3
1	A	55	HIS	3.2
1	A	54	ARG	3.0
1	A	128	GLY	2.9
1	A	279	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	123	ILE	2.8
1	A	124	TYR	2.8
1	A	200	ARG	2.8
1	A	122	PHE	2.6
1	A	192	LYS	2.6
1	A	51	ARG	2.6
1	A	194	GLN	2.6
1	A	211	LYS	2.6
1	A	131	PRO	2.6
1	A	240	LEU	2.6
1	A	190	PRO	2.5
1	A	197	LYS	2.5
1	A	229	TYR	2.5
1	A	170	VAL	2.5
1	A	278	PRO	2.5
1	A	126	VAL	2.4
1	A	114	ILE	2.4
1	A	205	LYS	2.4
1	A	198	ASP	2.4
1	A	120	ARG	2.3
1	A	80	THR	2.3
1	A	52	SER	2.3
1	A	146	TYR	2.3
1	A	381	LEU	2.3
1	A	213	ALA	2.2
1	A	189	VAL	2.2
1	A	82	LEU	2.2
1	A	193	ARG	2.2
1	A	551	ARG	2.2
1	A	117	ASN	2.1
1	A	188	GLY	2.1
1	A	536	LEU	2.1
1	A	87	LYS	2.1
1	A	151	PHE	2.1
1	A	557	PRO	2.1
1	A	102	ALA	2.1
1	A	133	GLN	2.1
1	A	208	GLN	2.0
1	A	103	LEU	2.0
1	A	81	THR	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

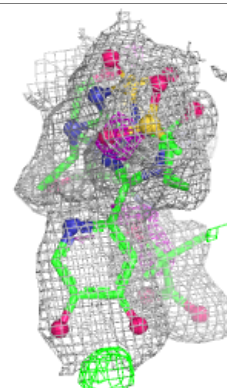
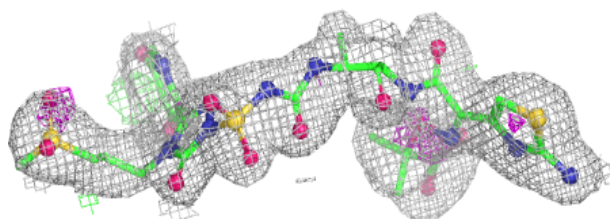
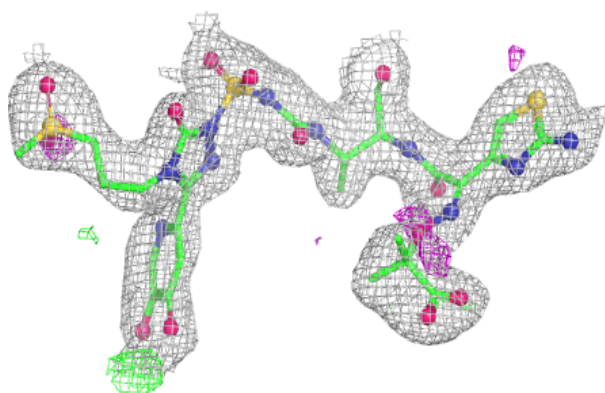
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	3LE	A	601	51/51	0.94	0.09	28,46,63,69	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around 3LE A 601:

2mF_o-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.