



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 09:26 PM UTC

PDB ID : 7KK4 / pdb_00007kk4
Title : Structure of the catalytic domain of PARP1 in complex with olaparib
Authors : Gajiwala, K.S.; Ryan, K.
Deposited on : 2020-10-27
Resolution : 1.96 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

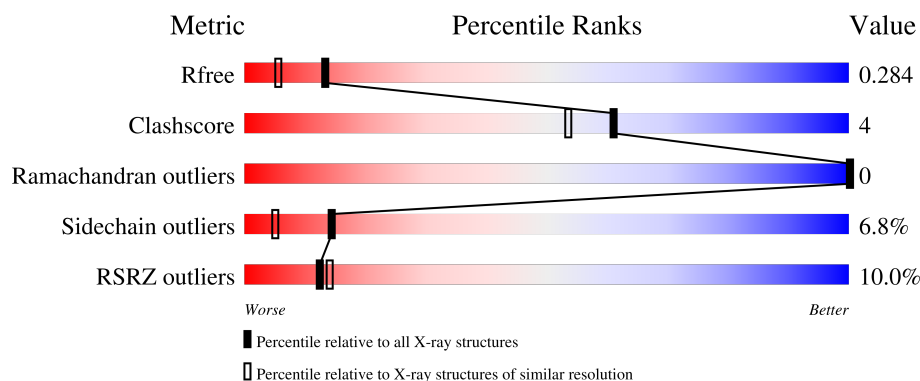
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.96 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	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	352	13% 81% 13% • •
1	B	352	7% 77% 18% • •

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 5601 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.

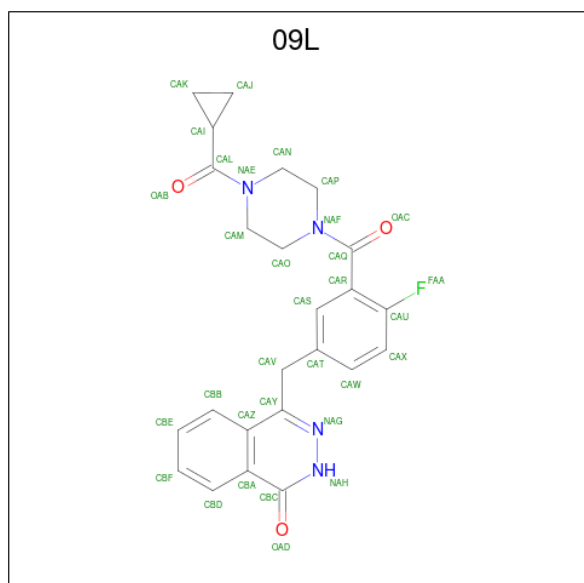
- Molecule 1 is a protein called Poly [ADP-ribose] polymerase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	340	Total	C	N	O	S	0	0	0
			2684	1713	453	508	10			
1	B	341	Total	C	N	O	S	0	0	0
			2693	1719	455	509	10			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	660	GLY	-	expression tag	UNP P09874
A	661	SER	-	expression tag	UNP P09874
B	660	GLY	-	expression tag	UNP P09874
B	661	SER	-	expression tag	UNP P09874

- Molecule 2 is 4-(3-{[4-(cyclopropylcarbonyl)piperazin-1-yl]carbonyl}-4-fluorobenzyl)phthalazin-1(2H)-one (CCD ID: 09L) (formula: C₂₄H₂₃FN₄O₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	0	0
			32	24	1	4	3		
2	B	1	Total	C	F	N	O	0	0
			32	24	1	4	3		

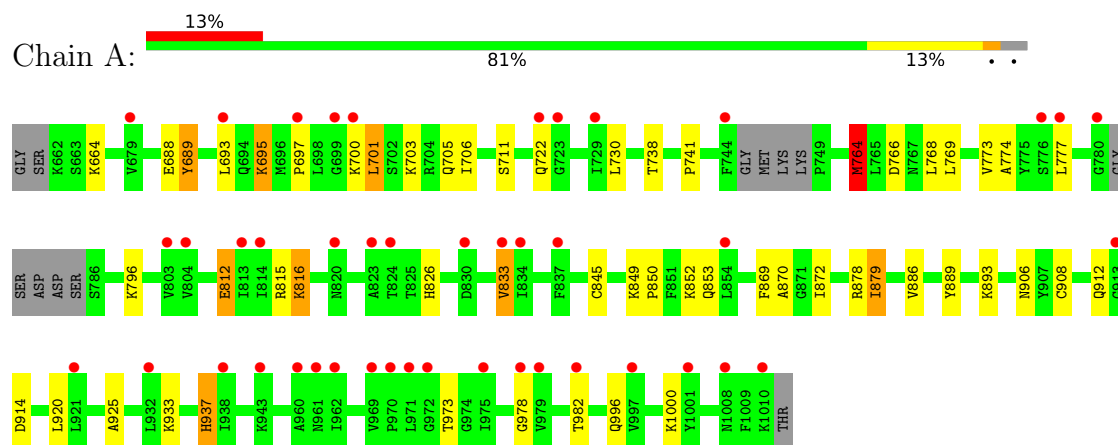
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	83	Total	O	0	0
			83	83		
3	B	77	Total	O	0	0
			77	77		

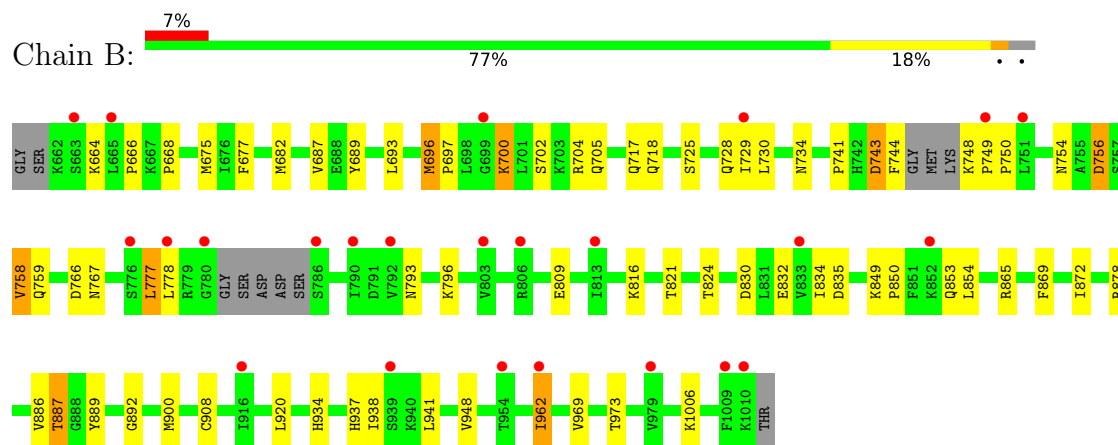
3 Residue-property plots

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: Poly [ADP-ribose] polymerase 1



- Molecule 1: Poly [ADP-ribose] polymerase 1



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	172.76Å 44.53Å 111.93Å 90.00° 127.42° 90.00°	Depositor
Resolution (Å)	55.89 – 1.96 55.89 – 1.96	Depositor EDS
% Data completeness (in resolution range)	68.0 (55.89-1.96) 68.0 (55.89-1.96)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.50 (at 1.97Å)	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
R, R_{free}	0.217 , 0.266 0.226 , 0.284	Depositor DCC
R_{free} test set	1499 reflections (3.06%)	wwPDB-VP
Wilson B-factor (Å ²)	45.7	Xtriage
Anisotropy	0.060	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 50.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.013 for -h-2*1,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5601	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.72% 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: 09L

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	0.89	1/2734 (0.0%)	1.42	17/3689 (0.5%)
1	B	0.86	0/2743	1.39	27/3701 (0.7%)
All	All	0.88	1/5477 (0.0%)	1.41	44/7390 (0.6%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	764	MET	SD-CE	-10.23	1.53	1.79

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	869	PHE	CA-CB-CG	-7.57	106.23	113.80
1	A	766	ASP	CA-CB-CG	7.38	119.98	112.60
1	A	812	GLU	CA-C-N	6.88	129.36	120.56
1	A	812	GLU	C-N-CA	6.88	129.36	120.56
1	B	743	ASP	CA-C-N	6.41	133.24	121.70
1	B	743	ASP	C-N-CA	6.41	133.24	121.70
1	A	937	HIS	CA-C-N	6.36	130.58	122.37
1	A	937	HIS	C-N-CA	6.36	130.58	122.37
1	B	689	TYR	CA-C-N	6.18	131.14	122.36
1	B	689	TYR	C-N-CA	6.18	131.14	122.36
1	B	705	GLN	CA-C-N	5.97	128.64	120.46
1	B	705	GLN	C-N-CA	5.97	128.64	120.46
1	A	705	GLN	CA-C-N	5.95	128.06	120.56
1	A	705	GLN	C-N-CA	5.95	128.06	120.56
1	B	869	PHE	CA-CB-CG	-5.93	107.87	113.80
1	B	729	ILE	CA-C-N	5.89	128.10	120.44
1	B	729	ILE	C-N-CA	5.89	128.10	120.44
1	A	816	LYS	CA-C-N	5.86	128.41	120.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	816	LYS	C-N-CA	5.86	128.41	120.38
1	B	766	ASP	CA-CB-CG	5.64	118.24	112.60
1	B	675	MET	CA-C-N	5.55	128.07	120.46
1	B	675	MET	C-N-CA	5.55	128.07	120.46
1	B	682	MET	CA-C-N	5.50	127.65	120.28
1	B	682	MET	C-N-CA	5.50	127.65	120.28
1	B	777	LEU	CA-C-N	5.46	128.14	120.28
1	B	777	LEU	C-N-CA	5.46	128.14	120.28
1	A	879	ILE	N-CA-C	-5.43	100.62	108.71
1	B	835	ASP	CA-CB-CG	5.39	117.99	112.60
1	A	738	THR	N-CA-C	-5.31	104.39	111.24
1	A	908	CYS	N-CA-C	-5.28	106.34	112.89
1	B	702	SER	CA-C-N	5.25	127.27	120.44
1	B	702	SER	C-N-CA	5.25	127.27	120.44
1	A	978	GLY	CA-C-N	5.25	127.61	120.63
1	A	978	GLY	C-N-CA	5.25	127.61	120.63
1	B	809	GLU	CA-C-N	5.21	127.57	120.54
1	B	809	GLU	C-N-CA	5.21	127.57	120.54
1	B	758	VAL	N-CA-CB	5.19	118.36	110.58
1	B	816	LYS	CA-C-N	5.17	127.21	120.28
1	B	816	LYS	C-N-CA	5.17	127.21	120.28
1	B	734	ASN	CA-CB-CG	5.09	117.69	112.60
1	B	908	CYS	CA-C-N	5.09	129.36	122.19
1	B	908	CYS	C-N-CA	5.09	129.36	122.19
1	A	689	TYR	CA-C-N	5.06	129.74	122.40
1	A	689	TYR	C-N-CA	5.06	129.74	122.40

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	2684	0	2728	21	0
1	B	2693	0	2740	24	0
2	A	32	0	23	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	32	0	23	2	0
3	A	83	0	0	0	0
3	B	77	0	0	0	0
All	All	5601	0	5514	46	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 4.

All (46) 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:717:GLN:HG2	1:B:887:THR:HG21	1.23	1.15
1:B:717:GLN:HG2	1:B:887:THR:CG2	2.05	0.86
1:B:696:MET:HE3	1:B:741:PRO:HD2	1.62	0.79
1:B:717:GLN:CG	1:B:887:THR:HG21	2.11	0.75
1:B:725:SER:H	1:B:728:GLN:HE21	1.41	0.68
1:A:689:TYR:HB3	1:A:764:MET:HG3	1.80	0.64
1:B:777:LEU:HD22	1:B:796:LYS:HB3	1.81	0.62
1:A:697:PRO:HD2	1:A:700:LYS:HB2	1.83	0.61
1:A:872:ILE:HG21	1:A:920:LEU:HD11	1.82	0.61
1:B:743:ASP:HA	1:B:744:PHE:C	2.27	0.60
1:B:834:ILE:HD11	1:B:1006:LYS:HB2	1.85	0.59
1:B:872:ILE:HG21	1:B:920:LEU:HD11	1.85	0.58
1:A:815:ARG:HG2	1:A:833:VAL:HG21	1.88	0.56
1:A:695:LYS:HE2	1:A:741:PRO:HB3	1.90	0.54
1:B:821:THR:HB	1:B:900:MET:HA	1.88	0.54
1:A:886:VAL:CG2	1:B:934:HIS:CD2	2.92	0.53
1:A:764:MET:HE3	1:A:768:LEU:HG	1.91	0.52
1:B:754:ASN:HD21	1:B:756:ASP:HB2	1.76	0.50
1:A:925:ALA:HB3	1:A:996:GLN:HG2	1.92	0.50
1:A:774:ALA:HB2	1:A:870:ALA:HB3	1.95	0.48
1:B:941:LEU:HD21	1:B:948:VAL:HG23	1.95	0.48
1:A:701:LEU:HD11	1:A:768:LEU:HD22	1.96	0.47
1:B:793:ASN:HA	1:B:796:LYS:HD2	1.97	0.47
1:B:889:TYR:O	1:B:937:HIS:HD2	1.97	0.47
1:B:767:ASN:ND2	1:B:865:ARG:HD2	2.30	0.46
2:A:9001:09L:H10	2:A:9001:09L:H5	1.70	0.46
1:B:878:ARG:O	2:B:9001:09L:H7	2.15	0.46
1:A:701:LEU:HD21	1:A:768:LEU:HD13	1.98	0.46
1:B:697:PRO:HD2	1:B:700:LYS:HG3	1.97	0.45
1:A:933:LYS:HG2	1:A:982:THR:HB	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:849:LYS:HB3	1:B:850:PRO:HD3	1.99	0.45
2:B:9001:09L:H5	2:B:9001:09L:H10	1.69	0.44
1:A:889:TYR:O	1:A:937:HIS:HD2	2.00	0.44
1:A:777:LEU:HD22	1:A:796:LYS:HB3	1.99	0.44
1:A:849:LYS:HB3	1:A:850:PRO:HD3	2.00	0.44
1:B:962:ILE:HG22	1:B:969:VAL:HB	2.00	0.44
1:A:878:ARG:O	2:A:9001:09L:H7	2.18	0.43
1:B:666:PRO:HB2	1:B:668:PRO:HD2	2.00	0.43
1:A:701:LEU:HD22	1:A:706:ILE:HD11	2.01	0.42
1:A:849:LYS:O	1:A:852:LYS:HB2	2.19	0.42
1:A:826:HIS:CD2	1:A:906:ASN:HD21	2.38	0.42
1:B:892:GLY:HA3	1:B:938:ILE:O	2.19	0.41
1:A:769:LEU:O	1:A:773:VAL:HG23	2.20	0.41
1:B:749:PRO:HA	1:B:750:PRO:HD2	2.02	0.41
1:B:677:PHE:CD1	1:B:778:LEU:HD13	2.57	0.40
1:A:886:VAL:HG12	1:A:893:LYS:HE2	2.03	0.40

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	334/352 (95%)	320 (96%)	14 (4%)	0	100	100
1	B	335/352 (95%)	327 (98%)	8 (2%)	0	100	100
All	All	669/704 (95%)	647 (97%)	22 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	300/309 (97%)	280 (93%)	20 (7%)	15	5
1	B	301/309 (97%)	280 (93%)	21 (7%)	14	4
All	All	601/618 (97%)	560 (93%)	41 (7%)	14	5

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	664	LYS
1	A	688	GLU
1	A	693	LEU
1	A	695	LYS
1	A	701	LEU
1	A	703	LYS
1	A	711	SER
1	A	722	GLN
1	A	730	LEU
1	A	764	MET
1	A	812	GLU
1	A	816	LYS
1	A	833	VAL
1	A	845	CYS
1	A	853	GLN
1	A	879	ILE
1	A	912	GLN
1	A	914	ASP
1	A	973	THR
1	A	1000	LYS
1	B	664	LYS
1	B	687	VAL
1	B	693	LEU
1	B	696	MET
1	B	700	LYS
1	B	704	ARG
1	B	718	GLN

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Mol	Chain	Res	Type
1	B	730	LEU
1	B	748	LYS
1	B	756	ASP
1	B	758	VAL
1	B	759	GLN
1	B	824	THR
1	B	830	ASP
1	B	832	GLU
1	B	853	GLN
1	B	854	LEU
1	B	886	VAL
1	B	887	THR
1	B	962	ILE
1	B	973	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	670	GLN
1	A	734	ASN
1	A	759	GLN
1	A	793	ASN
1	A	906	ASN
1	A	937	HIS
1	A	980	ASN
1	A	987	ASN
1	B	707	GLN
1	B	717	GLN
1	B	718	GLN
1	B	722	GLN
1	B	728	GLN
1	B	734	ASN
1	B	754	ASN
1	B	759	GLN
1	B	767	ASN
1	B	937	HIS
1	B	998	ASN

5.3.3 RNA ⓘ

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](#)

2 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	$\# Z > 2$
2	09L	B	9001	-	36,36,36	0.35	0	49,52,52	0.57	0
2	09L	A	9001	-	36,36,36	0.30	0	49,52,52	0.64	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
2	09L	B	9001	-	-	0/20/32/32	0/5/5/5
2	09L	A	9001	-	-	0/20/32/32	0/5/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

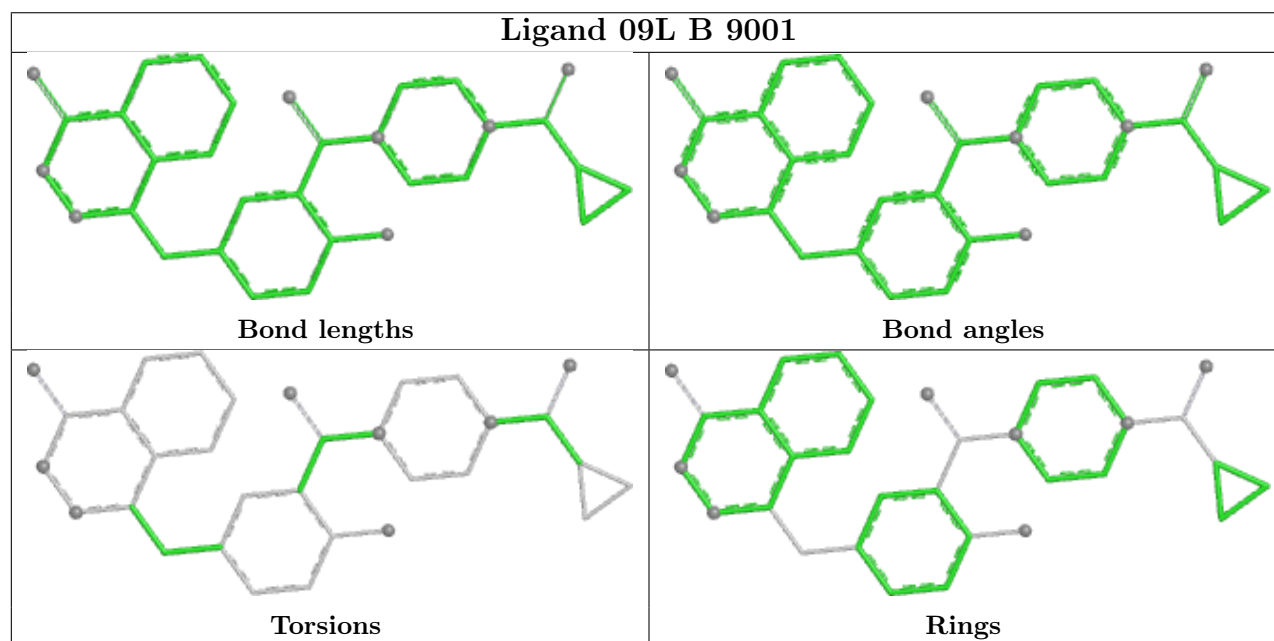
There are no torsion outliers.

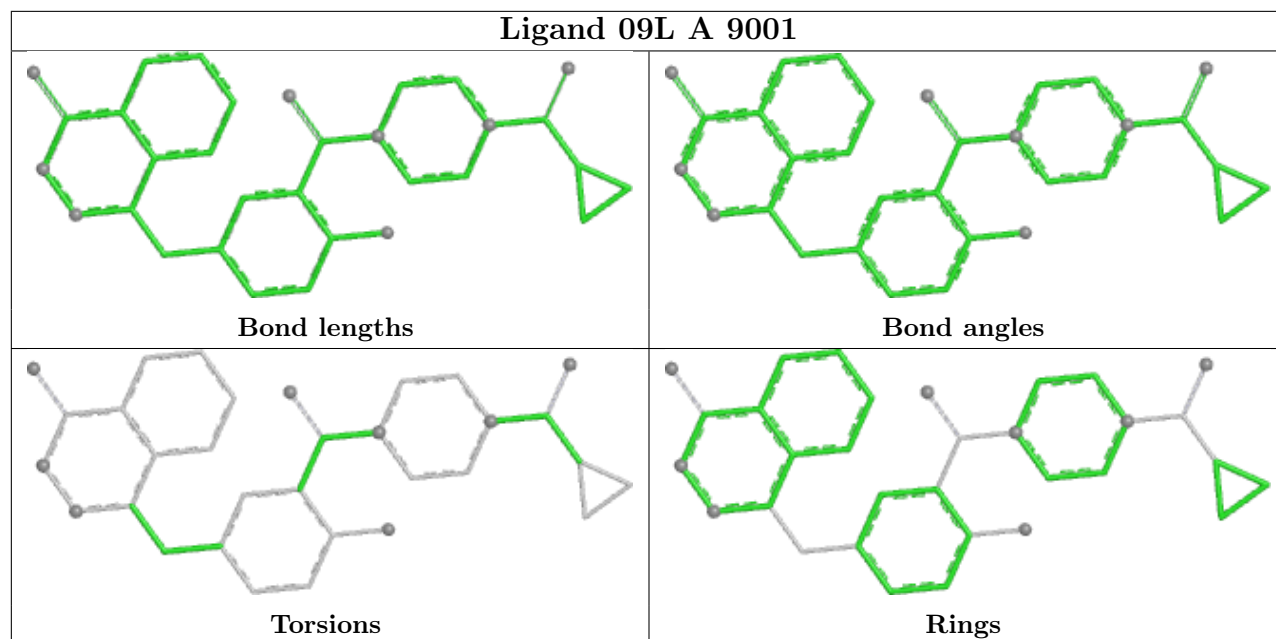
There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	9001	09L	2	0
2	A	9001	09L	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	340/352 (96%)	0.99	44 (12%) 7 9	29, 52, 78, 98	0
1	B	341/352 (96%)	0.78	24 (7%) 22 26	30, 50, 75, 97	0
All	All	681/704 (96%)	0.89	68 (9%) 12 14	29, 51, 76, 98	0

All (68) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	975	ILE	4.3
1	A	979	VAL	4.2
1	A	813	ILE	3.9
1	B	939	SER	3.8
1	B	813	ILE	3.7
1	A	744	PHE	3.5
1	B	780	GLY	3.5
1	B	729	ILE	3.4
1	A	823	ALA	3.2
1	A	834	ILE	3.2
1	A	729	ILE	3.1
1	A	803	VAL	3.1
1	A	969	VAL	3.0
1	A	1001	TYR	3.0
1	B	1010	LYS	3.0
1	A	780	GLY	3.0
1	B	749	PRO	3.0
1	A	854	LEU	2.9
1	A	971	LEU	2.9
1	A	693	LEU	2.9
1	B	962	ILE	2.9
1	A	938	ILE	2.8
1	B	778	LEU	2.7
1	B	1009	PHE	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	997	VAL	2.7
1	B	916	ILE	2.7
1	A	1010	LYS	2.6
1	A	913	GLY	2.6
1	A	777	LEU	2.6
1	B	665	LEU	2.6
1	A	700	LYS	2.6
1	A	824	THR	2.5
1	B	786	SER	2.5
1	A	697	PRO	2.5
1	A	943	LYS	2.4
1	A	960	ALA	2.4
1	A	982	THR	2.4
1	A	978	GLY	2.4
1	A	970	PRO	2.4
1	B	833	VAL	2.4
1	A	962	ILE	2.3
1	A	833	VAL	2.3
1	B	792	VAL	2.3
1	B	803	VAL	2.3
1	A	837	PHE	2.3
1	A	723	GLY	2.3
1	A	804	VAL	2.3
1	A	699	GLY	2.2
1	B	979	VAL	2.2
1	A	820	ASN	2.2
1	A	722	GLN	2.2
1	A	830	ASP	2.1
1	B	663	SER	2.1
1	B	806	ARG	2.1
1	A	1008	ASN	2.1
1	B	790	ILE	2.1
1	A	776	SER	2.1
1	A	679	VAL	2.1
1	A	921	LEU	2.1
1	B	954	THR	2.1
1	A	961	ASN	2.1
1	B	751	LEU	2.1
1	A	814	ILE	2.0
1	A	972	GLY	2.0
1	A	932	LEU	2.0
1	B	852	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	776	SER	2.0
1	B	699	GLY	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](#)

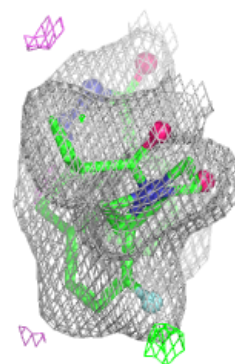
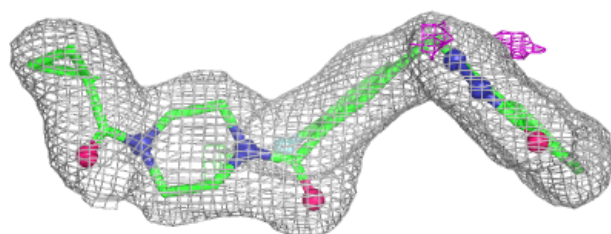
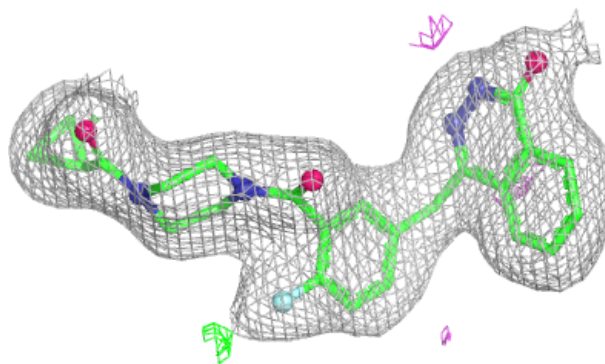
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists 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	09L	A	9001	32/32	0.94	0.07	28,32,36,36	0
2	09L	B	9001	32/32	0.95	0.07	28,34,38,39	0

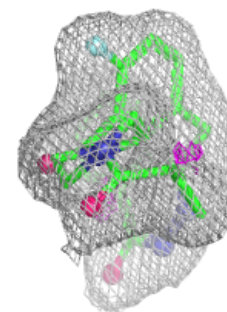
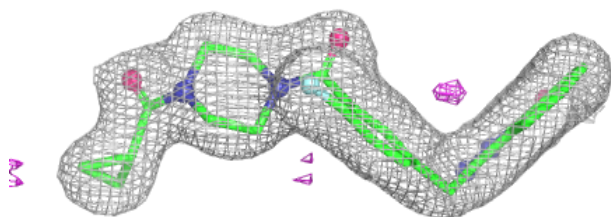
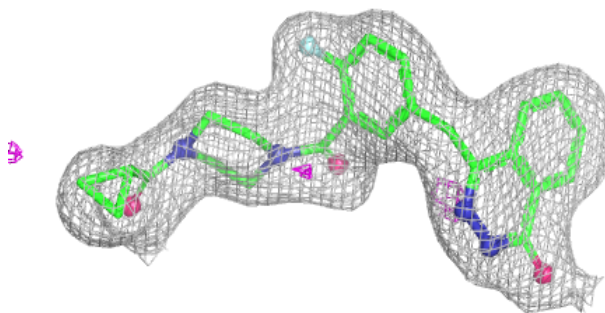
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 09L A 9001:

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

**Electron density around 09L B 9001:**

$2mF_o-DF_c$ (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.