



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:22 PM UTC

PDB ID : 7AAC / pdb_00007aac
Title : Crystal structure of the catalytic domain of human PARP1 in complex with veliparib
Authors : Schimpl, M.; Ogden, T.E.H.; Yang, J.-C.; Easton, L.E.; Underwood, E.; Rawlins, P.B.; Johannes, J.W.; Embrey, K.J.; Neuhaus, D.
Deposited on : 2020-09-04
Resolution : 1.59 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

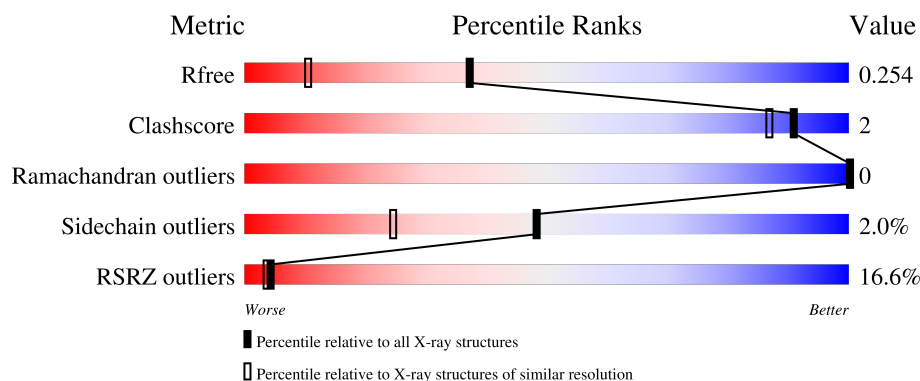
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.59 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	4673 (1.60-1.60)
Clashscore	190562	4931 (1.60-1.60)
Ramachandran outliers	187476	4831 (1.60-1.60)
Sidechain outliers	187428	4830 (1.60-1.60)
RSRZ outliers	180081	4672 (1.60-1.60)

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	10% 93% 6% ..
1	B	352	23% 93% 6% ..

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6013 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.

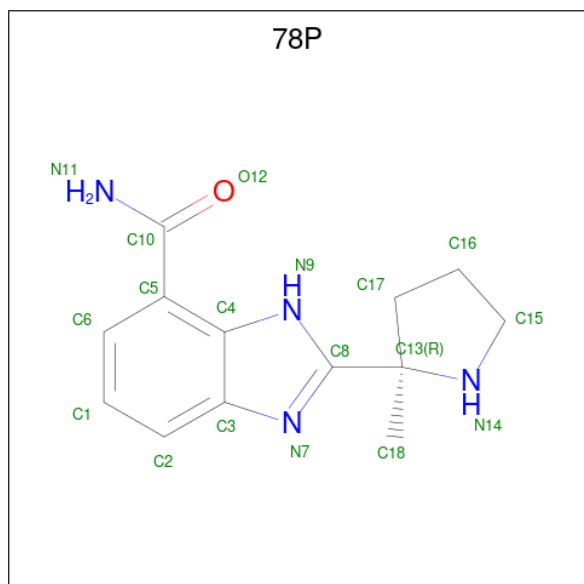
- Molecule 1 is a protein called Poly [ADP-ribose] polymerase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	350	Total	C	N	O	S	0	1	0
			2740	1744	462	522	12			
1	B	350	Total	C	N	O	S	0	1	0
			2745	1748	463	522	12			

There are 6 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
A	762	ALA	VAL	engineered mutation	UNP P09874
B	660	GLY	-	expression tag	UNP P09874
B	661	SER	-	expression tag	UNP P09874
B	762	ALA	VAL	engineered mutation	UNP P09874

- Molecule 2 is (2R)-2-(7-carbamoyl-1H-benzimidazol-2-yl)-2-methylpyrrolidinium (CCD ID: 78P) (formula: C₁₃H₁₆N₄O) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			18	13	4	1		
2	B	1	Total	C	N	O	0	0
			18	13	4	1		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

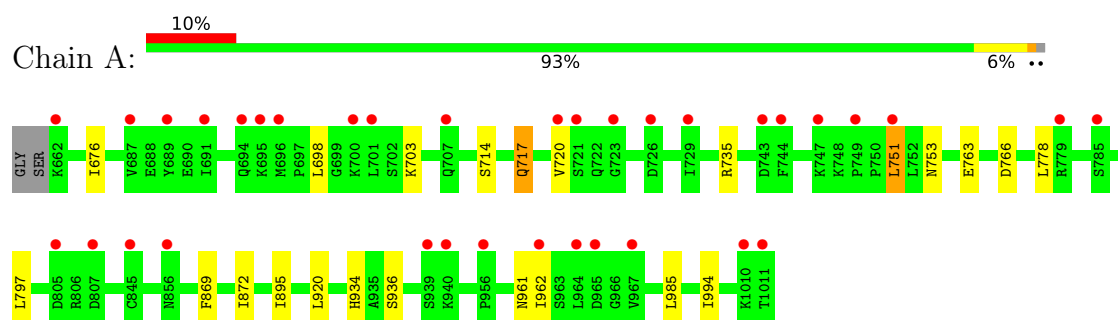
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	275	Total	O	0	0
			275	275		
4	B	207	Total	O	0	0
			207	207		

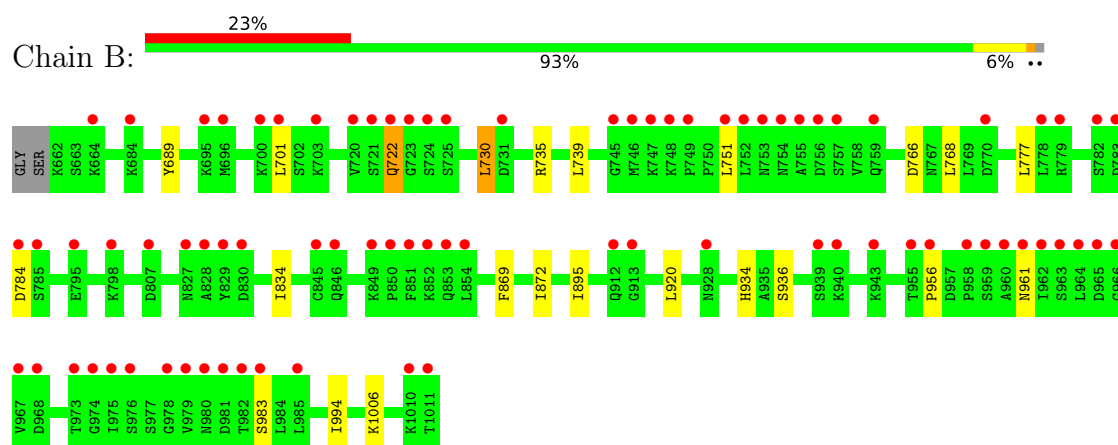
3 Residue-property plots [i](#)

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: Poly [ADP-ribose] polymerase 1



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	48.22Å 91.63Å 162.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	31.80 – 1.59 31.80 – 1.59	Depositor EDS
% Data completeness (in resolution range)	68.6 (31.80-1.59) 69.0 (31.80-1.59)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.12 (at 1.59Å)	Xtriage
Refinement program	BUSTER 2.11.6	Depositor
R, R_{free}	0.210 , 0.242 0.223 , 0.254	Depositor DCC
R_{free} test set	3298 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	16.2	Xtriage
Anisotropy	0.138	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 37.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6013	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.67% 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: SO4, 78P

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	0/2795	1.12	4/3775 (0.1%)
1	B	0.84	0/2800	1.16	7/3780 (0.2%)
All	All	0.84	0/5595	1.14	11/7555 (0.1%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	869	PHE	CA-CB-CG	-8.02	105.78	113.80
1	B	869	PHE	CA-CB-CG	-7.76	106.04	113.80
1	A	703	LYS	CA-C-N	6.41	129.19	120.54
1	A	703	LYS	C-N-CA	6.41	129.19	120.54
1	B	766	ASP	CA-CB-CG	6.13	118.73	112.60
1	B	689	TYR	CA-C-N	5.89	130.94	122.40
1	B	689	TYR	C-N-CA	5.89	130.94	122.40
1	B	777	LEU	CA-C-N	5.40	127.52	120.28
1	B	777	LEU	C-N-CA	5.40	127.52	120.28
1	A	766	ASP	CA-CB-CG	5.39	117.99	112.60
1	B	784	ASP	CA-CB-CG	5.06	117.66	112.60

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	2740	0	2768	10	0
1	B	2745	0	2781	9	0
2	A	18	0	16	1	0
2	B	18	0	16	1	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	275	0	0	1	0
4	B	207	0	0	2	0
All	All	6013	0	5581	19	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 2.

All (19) 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:763:GLU:HG2	4:A:1359:HOH:O	1.89	0.71
1:A:934:HIS:HD2	4:B:1274:HOH:O	1.79	0.64
1:B:956:PRO:HB3	4:B:1252:HOH:O	2.05	0.55
1:B:834:ILE:HD11	1:B:1006:LYS:HB2	1.88	0.55
1:A:872:ILE:HG21	1:A:920:LEU:HD11	1.91	0.53
2:B:1101:78P:H9	2:B:1101:78P:H111	1.57	0.53
2:A:1101:78P:H9	2:A:1101:78P:H111	1.58	0.52
1:A:895:ILE:HD11	1:A:994:ILE:HG22	1.93	0.51
1:B:895:ILE:HD11	1:B:994:ILE:HG22	1.93	0.50
1:B:934:HIS:CD2	1:B:983:SER:HB3	2.47	0.49
1:A:751:LEU:HD22	1:A:753:ASN:HB3	1.96	0.48
1:B:872:ILE:HG21	1:B:920:LEU:HD11	1.94	0.47
1:A:985:LEU:HD21	1:B:722:GLN:HG3	1.97	0.46
1:B:730:LEU:HD11	1:B:751:LEU:HD21	1.97	0.45
1:A:676:ILE:HD11	1:A:797:LEU:HD11	1.98	0.44
1:B:701:LEU:HD11	1:B:768:LEU:HD22	2.01	0.43
1:A:936:SER:HA	1:B:936:SER:HA	2.02	0.42
1:A:717:GLN:HA	1:A:720:VAL:HG22	2.02	0.41
1:A:714:SER:O	1:A:717:GLN:HG3	2.21	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	349/352 (99%)	348 (100%)	1 (0%)	0	100	100
1	B	349/352 (99%)	348 (100%)	1 (0%)	0	100	100
All	All	698/704 (99%)	696 (100%)	2 (0%)	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	304/308 (99%)	297 (98%)	7 (2%)	44	20
1	B	305/308 (99%)	300 (98%)	5 (2%)	55	33
All	All	609/616 (99%)	597 (98%)	12 (2%)	48	24

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	698	LEU
1	A	717	GLN
1	A	735	ARG
1	A	751	LEU
1	A	778	LEU
1	A	961	ASN
1	A	962	ILE
1	B	722	GLN

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Mol	Chain	Res	Type
1	B	730	LEU
1	B	735	ARG
1	B	739	LEU
1	B	961	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	767	ASN
1	A	868	ASN
1	A	906	ASN
1	A	934	HIS
1	B	707	GLN
1	B	728	GLN
1	B	767	ASN
1	B	868	ASN
1	B	875	GLN
1	B	906	ASN
1	B	1008	ASN

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](#)

4 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	$\# Z > 2$
3	SO4	A	1102	-	4,4,4	0.38	0	6,6,6	0.31	0
3	SO4	B	1102	-	4,4,4	0.38	0	6,6,6	0.28	0
2	78P	A	1101	-	19,20,20	0.49	0	20,30,30	1.09	1 (5%)
2	78P	B	1101	-	19,20,20	0.44	0	20,30,30	0.91	1 (5%)

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	78P	A	1101	-	-	0/4/19/19	0/3/3/3
2	78P	B	1101	-	-	0/4/19/19	0/3/3/3

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1101	78P	C4-C3-N7	-2.66	108.09	109.91
2	B	1101	78P	C4-C3-N7	-2.36	108.30	109.91

There are no chirality outliers.

There are no torsion outliers.

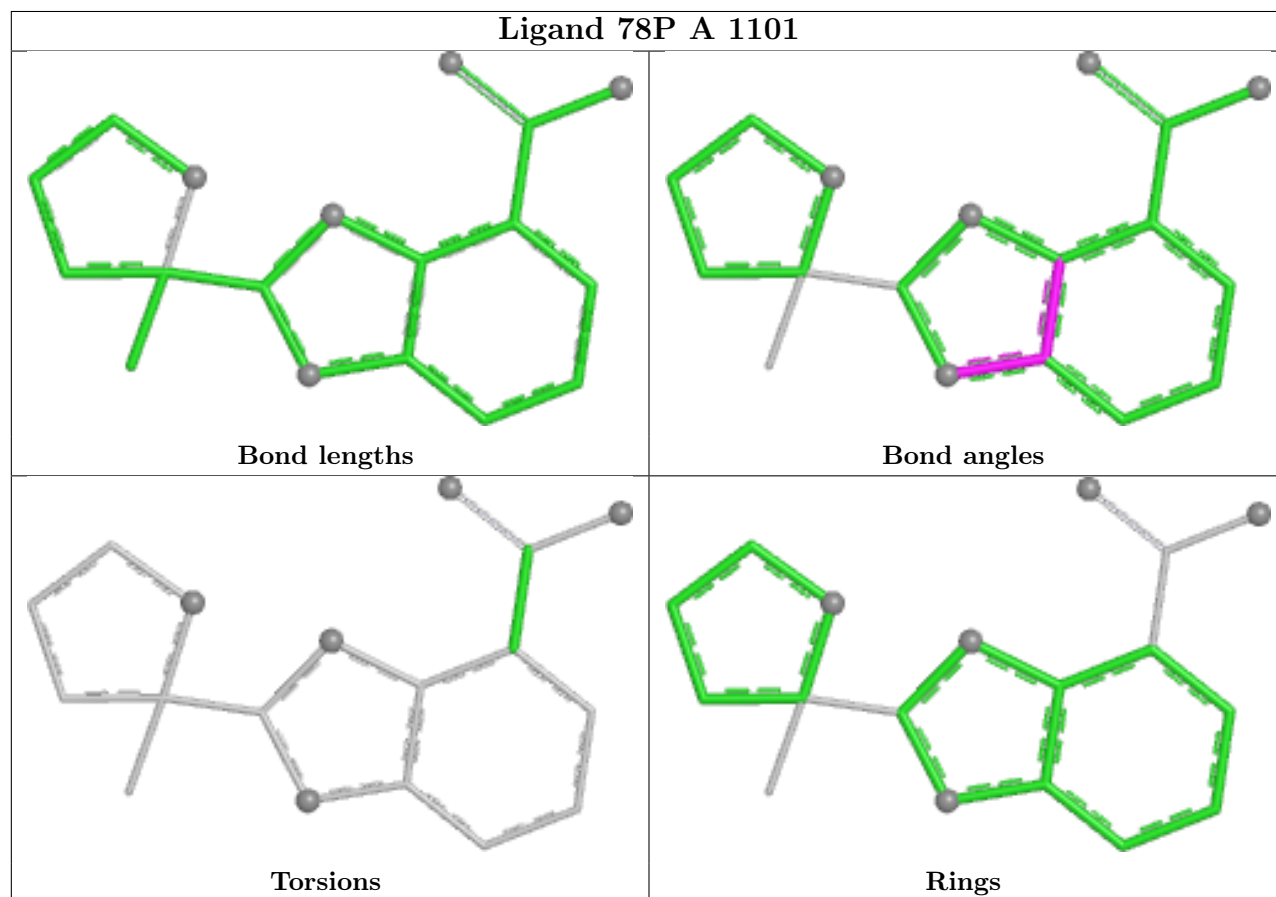
There are no ring outliers.

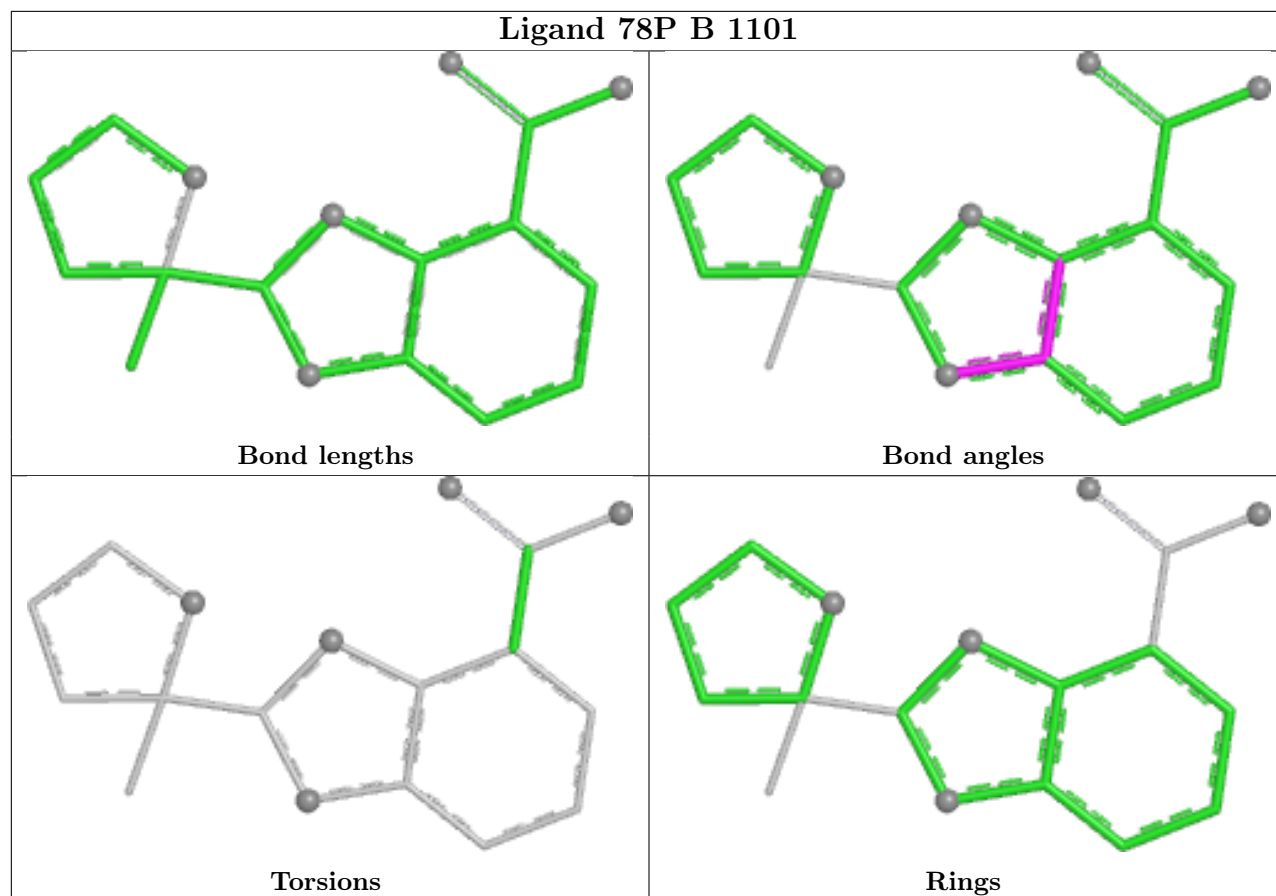
2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1101	78P	1	0
2	B	1101	78P	1	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	350/352 (99%)	0.61	35 (10%)	12 12	5, 18, 38, 67	1 (0%)
1	B	350/352 (99%)	1.11	81 (23%)	2 2	8, 24, 49, 84	1 (0%)
All	All	700/704 (99%)	0.86	116 (16%)	4 4	5, 21, 47, 84	2 (0%)

All (116) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1011	THR	8.1
1	A	1011	THR	6.8
1	B	854	LEU	6.1
1	B	827	ASN	5.5
1	B	975	ILE	5.1
1	B	723	GLY	5.0
1	B	828	ALA	4.8
1	B	724	SER	4.7
1	B	980	ASN	4.7
1	A	747	LYS	4.6
1	B	981	ASP	4.4
1	B	748	LYS	4.3
1	B	979	VAL	4.0
1	B	783	ASP	4.0
1	B	853	GLN	4.0
1	A	807	ASP	3.9
1	B	967	VAL	3.9
1	B	940	LYS	3.8
1	B	849	LYS	3.8
1	B	983	SER	3.8
1	A	689	TYR	3.7
1	B	959	SER	3.7
1	B	721	SER	3.6
1	B	966	GLY	3.5

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Mol	Chain	Res	Type	RSRZ
1	B	851	PHE	3.5
1	B	722	GLN	3.4
1	B	964	LEU	3.4
1	B	982	THR	3.4
1	B	913	GLY	3.4
1	B	725	SER	3.4
1	B	963	SER	3.4
1	A	720	VAL	3.3
1	A	751	LEU	3.3
1	B	978	GLY	3.3
1	B	751	LEU	3.2
1	B	720	VAL	3.1
1	B	955	THR	3.1
1	A	744	PHE	3.1
1	B	845	CYS	3.1
1	A	696	MET	3.0
1	A	964	LEU	3.0
1	B	961	ASN	3.0
1	B	1010	LYS	3.0
1	B	696	MET	3.0
1	B	747	LYS	3.0
1	B	965	ASP	3.0
1	B	779	ARG	2.9
1	B	755	ALA	2.9
1	B	958	PRO	2.9
1	A	965	ASP	2.9
1	B	695	LYS	2.9
1	B	939	SER	2.9
1	B	795	GLU	2.9
1	B	749	PRO	2.8
1	A	962	ILE	2.8
1	B	956	PRO	2.8
1	B	850	PRO	2.7
1	B	778	LEU	2.7
1	B	912	GLN	2.7
1	B	785	SER	2.7
1	B	746	MET	2.7
1	A	939	SER	2.6
1	A	726	ASP	2.6
1	B	731	ASP	2.6
1	A	729	ILE	2.6
1	A	743	ASP	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	745	GLY	2.6
1	B	700	LYS	2.5
1	B	754	ASN	2.5
1	B	684	LYS	2.5
1	B	782	SER	2.5
1	A	845	CYS	2.5
1	B	976	SER	2.5
1	A	940	LYS	2.5
1	A	700	LYS	2.4
1	A	701	LEU	2.4
1	B	973	THR	2.4
1	A	956	PRO	2.4
1	B	784	ASP	2.4
1	B	752	LEU	2.4
1	A	694	GLN	2.4
1	A	695	LYS	2.4
1	A	723	GLY	2.4
1	A	687	VAL	2.4
1	B	962	ILE	2.4
1	B	798	LYS	2.4
1	B	985	LEU	2.4
1	A	856	ASN	2.4
1	B	807	ASP	2.3
1	B	968	ASP	2.3
1	B	846	GLN	2.3
1	B	756	ASP	2.3
1	A	691	ILE	2.3
1	B	960	ALA	2.3
1	A	749	PRO	2.3
1	A	721	SER	2.3
1	B	829	TYR	2.3
1	A	967	VAL	2.2
1	A	1010	LYS	2.2
1	B	770	ASP	2.2
1	B	664	LYS	2.2
1	B	703	LYS	2.2
1	B	852	LYS	2.2
1	B	974	GLY	2.2
1	A	785	SER	2.2
1	A	779	ARG	2.2
1	A	805	ASP	2.2
1	B	830	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	943	LYS	2.1
1	A	707	GLN	2.1
1	B	757	SER	2.1
1	B	701	LEU	2.1
1	A	662	LYS	2.1
1	B	928	ASN	2.0
1	B	759	GLN	2.0
1	B	753	ASN	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](#)

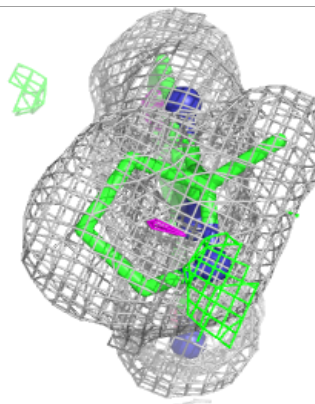
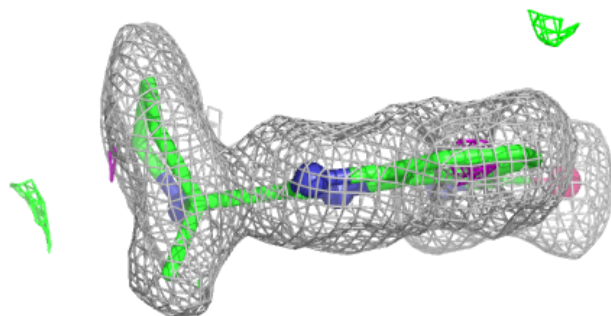
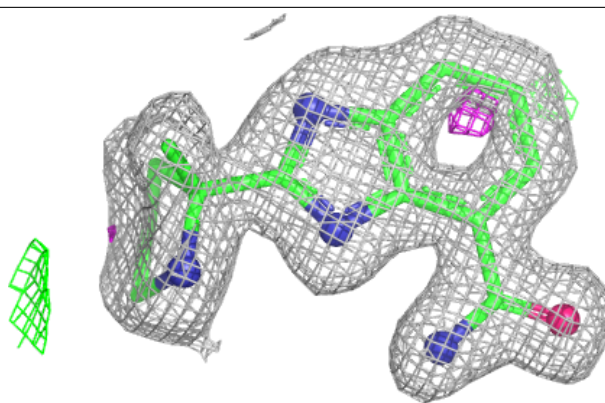
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	78P	B	1101	18/18	0.95	0.07	3,9,19,20	0
3	SO4	B	1102	5/5	0.95	0.09	21,27,28,31	0
2	78P	A	1101	18/18	0.96	0.06	7,8,17,19	0
3	SO4	A	1102	5/5	0.97	0.11	13,19,23,23	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.

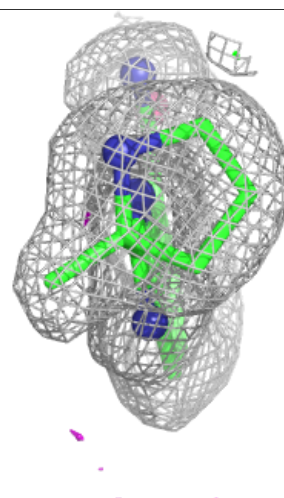
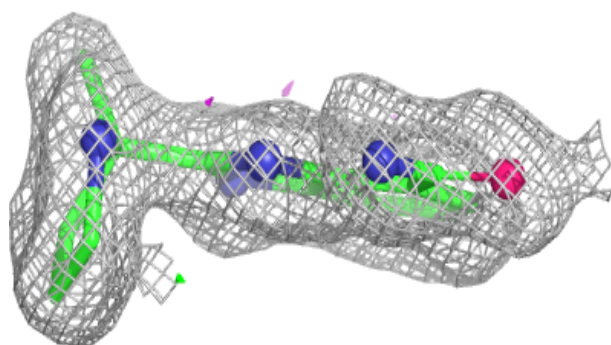
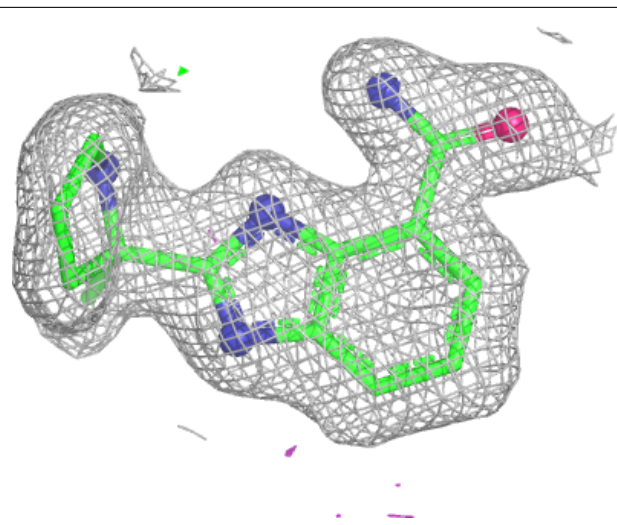
Electron density around 78P B 1101:

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



Electron density around 78P A 1101:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.