Full wwPDB X-ray Structure Validation Report (i)

Sep 12, 2023 – 07:44 AM EDT

PDB ID	:	4OQA
Title	:	Structure of Human PARP-1 bound to a DNA double strand break in complex with (2Z)-2-(2,4-dihydroxybenzylidene)-3-oxo-2,3-dihydro-1-benzofuran-7-carboxamide
Authors	:	Pascal, J.M.; Steffen, J.D.
Deposited on	:	2014-02-07
Resolution	:	3.65 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 (i)) were used in the production of this report:

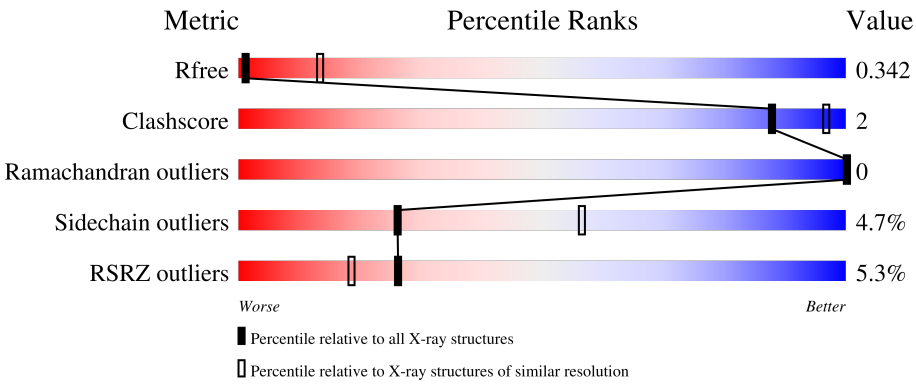
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 3.65 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	1557 (3.82-3.50)
Clashscore	141614	1037 (3.80-3.52)
Ramachandran outliers	138981	1004 (3.80-3.52)
Sidechain outliers	138945	1002 (3.80-3.52)
RSRZ outliers	127900	1441 (3.82-3.50)

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	267	2%, 77%, 5% •, 17%
1	D	267	5%, 77%, 5% •, 17%
2	C	505	5%, 82%, 9%, 10%
2	F	505	7%, 82%, 8%, 10%

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Mol	Chain	Length	Quality of chain
3	M	26	88% 12%
3	N	26	96%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 11768 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
			Total	C	N	O	S			
1	A	222	1755	1110	305	327	13	0	1	0
1	D	222	1755	1110	305	327	13	0	1	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	205	ASP	-	linker	UNP P09874
A	206	ILE	-	linker	UNP P09874
A	367	LEU	-	expression tag	UNP P09874
A	368	GLU	-	expression tag	UNP P09874
A	369	HIS	-	expression tag	UNP P09874
A	370	HIS	-	expression tag	UNP P09874
A	371	HIS	-	expression tag	UNP P09874
A	372	HIS	-	expression tag	UNP P09874
A	373	HIS	-	expression tag	UNP P09874
A	374	HIS	-	expression tag	UNP P09874
D	205	ASP	-	linker	UNP P09874
D	206	ILE	-	linker	UNP P09874
D	367	LEU	-	expression tag	UNP P09874
D	368	GLU	-	expression tag	UNP P09874
D	369	HIS	-	expression tag	UNP P09874
D	370	HIS	-	expression tag	UNP P09874
D	371	HIS	-	expression tag	UNP P09874
D	372	HIS	-	expression tag	UNP P09874
D	373	HIS	-	expression tag	UNP P09874
D	374	HIS	-	expression tag	UNP P09874

- Molecule 2 is a protein called Poly [ADP-ribose] polymerase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	456	3586	2296	605	672	13	0	0	0
2	F	456	3586	2296	605	672	13	0	0	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	1015	LEU	-	expression tag	UNP P09874
C	1016	GLU	-	expression tag	UNP P09874
C	1017	HIS	-	expression tag	UNP P09874
C	1018	HIS	-	expression tag	UNP P09874
C	1019	HIS	-	expression tag	UNP P09874
C	1020	HIS	-	expression tag	UNP P09874
C	1021	HIS	-	expression tag	UNP P09874
C	1022	HIS	-	expression tag	UNP P09874
F	1015	LEU	-	expression tag	UNP P09874
F	1016	GLU	-	expression tag	UNP P09874
F	1017	HIS	-	expression tag	UNP P09874
F	1018	HIS	-	expression tag	UNP P09874
F	1019	HIS	-	expression tag	UNP P09874
F	1020	HIS	-	expression tag	UNP P09874
F	1021	HIS	-	expression tag	UNP P09874
F	1022	HIS	-	expression tag	UNP P09874

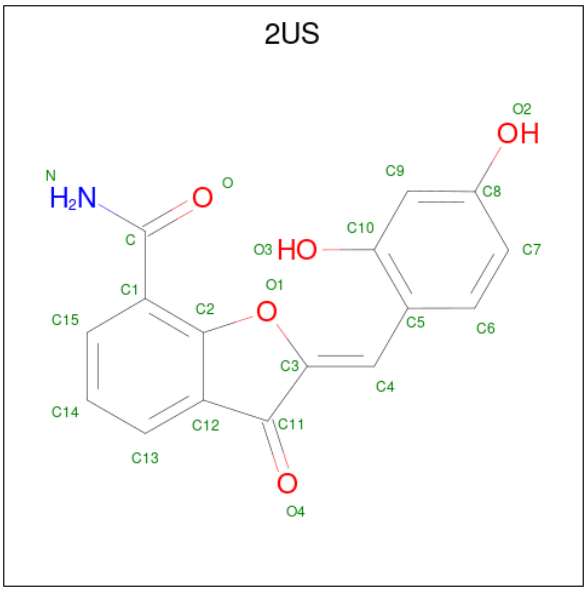
- Molecule 3 is a DNA chain called DNA (26-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	M	26	530	251	100	154	25	0	0	0
3	N	26	530	251	100	154	25	0	0	0

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
4	A	2	2	2	0	0
4	D	2	2	2	0	0

- Molecule 5 is (2Z)-2-(2,4-dihydroxybenzylidene)-3-oxo-2,3-dihydro-1-benzofuran-7-carboxamide (three-letter code: 2US) (formula: $C_{16}H_{11}NO_5$).



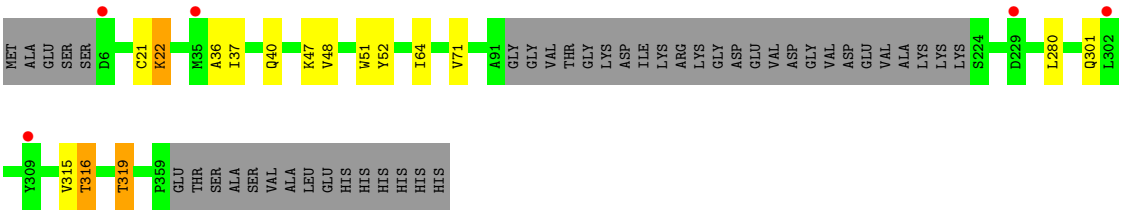
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
5	C	1	22	16	1	5	0	0

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.

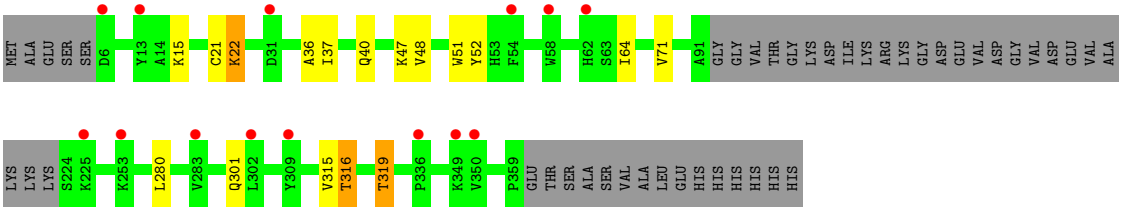
• Molecule 1: Poly [ADP-ribose] polymerase 1

Chain A:



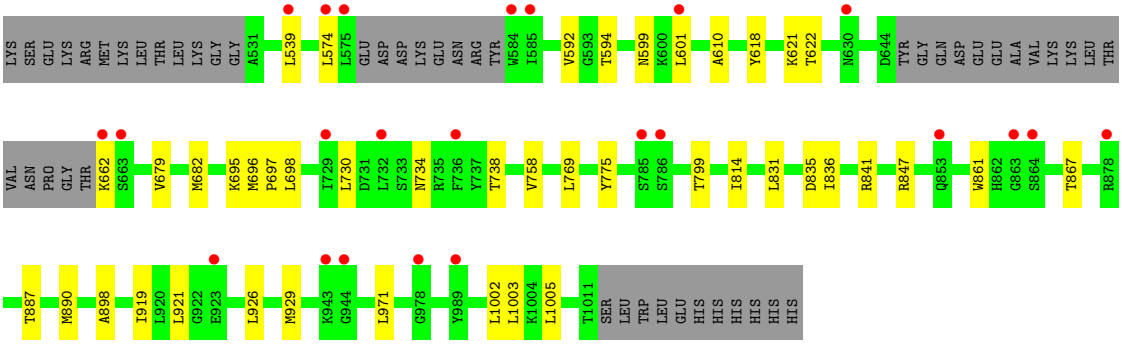
• Molecule 1: Poly [ADP-ribose] polymerase 1

Chain D:



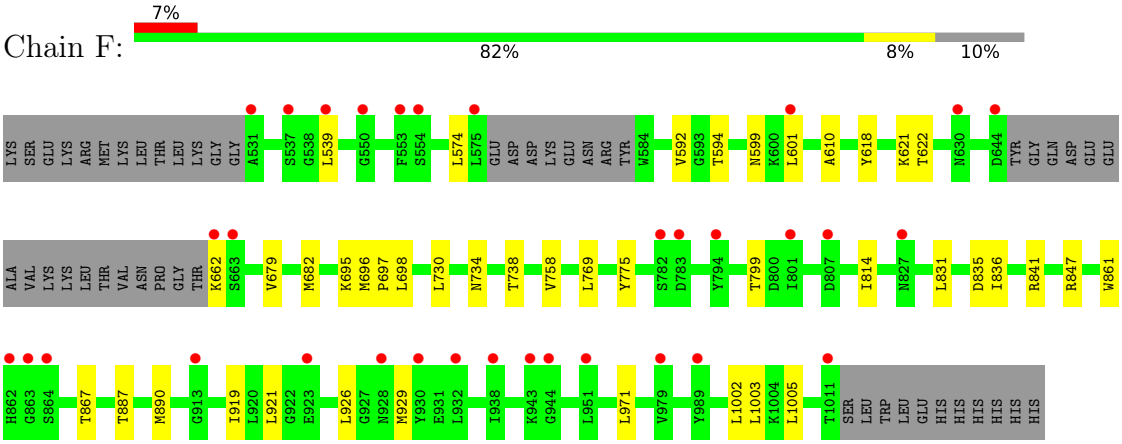
• Molecule 2: Poly [ADP-ribose] polymerase 1

Chain C:



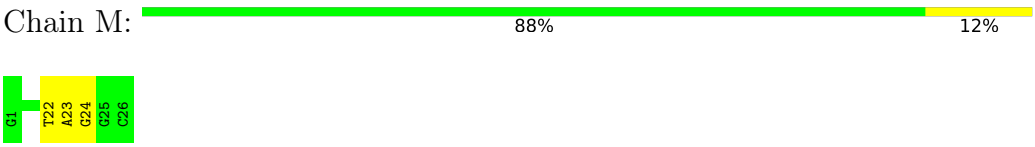
• Molecule 2: Poly [ADP-ribose] polymerase 1

Chain F:



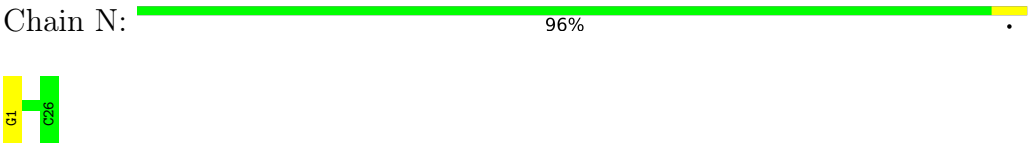
- Molecule 3: DNA (26-MER)

Chain M:



- Molecule 3: DNA (26-MER)

Chain N:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	65.16Å 114.23Å 294.24Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.65 35.32 – 3.65	Depositor EDS
% Data completeness (in resolution range)	98.1 (20.00-3.65) 98.4 (35.32-3.65)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.34 (at 3.66Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.298 , 0.334 0.298 , 0.342	Depositor DCC
R_{free} test set	1250 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	185.2	Xtriage
Anisotropy	0.391	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.25 , 160.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.44$, $< L^2 > = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	11768	wwPDB-VP
Average B, all atoms (Å^2)	257.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.32% of the height of the origin peak. No significant pseudotranslation is detected.*

[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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 2US, ZN

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	0.26	0/1795	0.40	0/2416
1	D	0.26	0/1795	0.40	0/2416
2	C	0.26	0/3660	0.42	0/4940
2	F	0.26	0/3660	0.43	0/4940
3	M	0.27	0/594	0.81	0/915
3	N	0.24	0/594	0.78	2/915 (0.2%)
All	All	0.26	0/12098	0.47	2/16542 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	N	1	DG	C5'-C4'-O4'	5.58	119.90	109.30
3	N	1	DG	C5'-C4'-C3'	5.09	123.27	114.10

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	1755	0	1712	6	0
1	D	1755	0	1712	7	0
2	C	3586	0	3604	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	F	3586	0	3604	16	0
3	M	530	0	292	2	0
3	N	530	0	292	0	0
4	A	2	0	0	0	0
4	D	2	0	0	0	0
5	C	22	0	10	1	0
All	All	11768	0	11226	45	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 (45) 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)
2:F:574:LEU:HD11	2:F:610:ALA:HB1	1.69	0.74
2:C:574:LEU:HD11	2:C:610:ALA:HB1	1.69	0.73
2:C:898:ALA:HB2	5:C:1101:2US:H2	1.74	0.68
1:D:36:ALA:HB2	1:D:51:TRP:CE3	2.40	0.56
1:A:36:ALA:HB2	1:A:51:TRP:CE3	2.40	0.56
2:C:831:LEU:HD12	2:C:1005:LEU:HD23	1.89	0.53
2:F:679:VAL:HG11	2:F:775:TYR:CZ	2.43	0.53
2:F:831:LEU:HD12	2:F:1005:LEU:HD23	1.89	0.53
2:C:679:VAL:HG11	2:C:775:TYR:CZ	2.44	0.53
1:D:319:THR:HG22	2:F:734:ASN:HD22	1.75	0.52
2:F:814:ILE:HG21	2:F:836:ILE:HD12	1.93	0.51
2:C:919:ILE:HG22	2:C:1005:LEU:HD11	1.94	0.49
2:C:814:ILE:HG21	2:C:836:ILE:HD12	1.93	0.49
2:F:919:ILE:HG22	2:F:1005:LEU:HD11	1.94	0.49
2:C:696:MET:N	2:C:697:PRO:HD2	2.27	0.49
2:F:696:MET:N	2:F:697:PRO:HD2	2.27	0.49
1:D:315:VAL:HG13	1:D:316:THR:HG22	1.95	0.49
1:A:315:VAL:HG13	1:A:316:THR:HG22	1.95	0.48
2:C:861:TRP:CD2	2:C:921:LEU:HD21	2.50	0.47
2:F:861:TRP:CD2	2:F:921:LEU:HD21	2.50	0.46
3:M:22:DT:H2"	3:M:23:DA:C8	2.51	0.45
2:C:926:LEU:HD13	2:C:929:MET:HE3	1.99	0.45
2:C:618:TYR:CE2	2:C:622:THR:HG21	2.52	0.45
2:F:926:LEU:HD13	2:F:929:MET:HE3	1.98	0.44
1:A:319:THR:HG22	2:C:734:ASN:HD22	1.82	0.44
2:C:539:LEU:HD11	2:C:601:LEU:HD21	2.00	0.44
2:F:618:TYR:CE2	2:F:622:THR:HG21	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:539:LEU:HD11	2:F:601:LEU:HD21	2.00	0.43
2:F:682:MET:HG2	2:F:867:THR:HG22	2.02	0.42
2:C:682:MET:HG2	2:C:867:THR:HG22	2.02	0.42
2:F:799:THR:HG22	2:F:841:ARG:HA	2.02	0.42
2:C:814:ILE:CG2	2:C:1003:LEU:HD21	2.50	0.42
1:D:36:ALA:HB2	1:D:51:TRP:CZ3	2.55	0.41
2:F:696:MET:N	2:F:697:PRO:CD	2.82	0.41
1:A:64:ILE:HD13	1:A:71:VAL:CG2	2.51	0.41
1:D:64:ILE:HD13	1:D:71:VAL:CG2	2.51	0.41
2:C:696:MET:N	2:C:697:PRO:CD	2.83	0.41
2:F:814:ILE:CG2	2:F:1003:LEU:HD21	2.50	0.41
1:D:22:LYS:HB3	1:D:52:TYR:CE1	2.56	0.41
1:A:22:LYS:HB3	1:A:52:TYR:CE1	2.56	0.41
1:A:36:ALA:HB2	1:A:51:TRP:CZ3	2.55	0.41
2:F:618:TYR:O	2:F:622:THR:HG22	2.21	0.41
2:C:618:TYR:O	2:C:622:THR:HG22	2.21	0.40
2:C:799:THR:HG22	2:C:841:ARG:HA	2.02	0.40
1:D:15:LYS:HB3	3:M:24:DG:H5'	2.04	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	219/267 (82%)	212 (97%)	7 (3%)	0	100	100
1	D	219/267 (82%)	212 (97%)	7 (3%)	0	100	100
2	C	450/505 (89%)	424 (94%)	26 (6%)	0	100	100
2	F	450/505 (89%)	423 (94%)	27 (6%)	0	100	100
All	All	1338/1544 (87%)	1271 (95%)	67 (5%)	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	189/237 (80%)	179 (95%)	10 (5%)	22	54
1	D	189/237 (80%)	179 (95%)	10 (5%)	22	54
2	C	391/443 (88%)	374 (96%)	17 (4%)	29	58
2	F	391/443 (88%)	374 (96%)	17 (4%)	29	58
All	All	1160/1360 (85%)	1106 (95%)	54 (5%)	26	56

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	CYS
1	A	22	LYS
1	A	37	ILE
1	A	40	GLN
1	A	47	LYS
1	A	48	VAL
1	A	280	LEU
1	A	301	GLN
1	A	316	THR
1	A	319	THR
2	C	592	VAL
2	C	594	THR
2	C	599	ASN
2	C	621	LYS
2	C	662	LYS
2	C	695	LYS
2	C	698	LEU
2	C	730	LEU
2	C	738	THR
2	C	758	VAL
2	C	769	LEU
2	C	835	ASP
2	C	847	ARG
2	C	887	THR

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Mol	Chain	Res	Type
2	C	890	MET
2	C	971	LEU
2	C	1002	LEU
1	D	21	CYS
1	D	22	LYS
1	D	37	ILE
1	D	40	GLN
1	D	47	LYS
1	D	48	VAL
1	D	280	LEU
1	D	301	GLN
1	D	316	THR
1	D	319	THR
2	F	592	VAL
2	F	594	THR
2	F	599	ASN
2	F	621	LYS
2	F	662	LYS
2	F	695	LYS
2	F	698	LEU
2	F	730	LEU
2	F	738	THR
2	F	758	VAL
2	F	769	LEU
2	F	835	ASP
2	F	847	ARG
2	F	887	THR
2	F	890	MET
2	F	971	LEU
2	F	1002	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
2	C	567	ASN
2	C	573	GLN
2	C	599	ASN
2	C	613	HIS
2	C	820	ASN
2	C	856	ASN
2	C	906	ASN
2	C	961	ASN

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Mol	Chain	Res	Type
1	D	301	GLN
2	F	573	GLN
2	F	599	ASN
2	F	613	HIS
2	F	820	ASN
2	F	856	ASN
2	F	906	ASN
2	F	961	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 for Mogul analysis.

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	$\#\|Z\| > 2$
5	2US	C	1101	-	24,24,24	0.24	0	34,35,35	2.78	6 (17%)

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
5	2US	C	1101	-	-	4/8/20/20	0/3/3/3

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	C	1101	2US	C2-C12-C11	8.24	109.99	107.01
5	C	1101	2US	C4-C3-C11	-7.62	119.72	126.24
5	C	1101	2US	C12-C11-C3	-6.80	100.85	104.06
5	C	1101	2US	O4-C11-C3	6.65	132.30	126.16
5	C	1101	2US	O1-C3-C11	4.05	112.19	109.45
5	C	1101	2US	O1-C3-C4	4.04	128.06	124.43

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	1101	2US	C3-C4-C5-C6
5	C	1101	2US	C3-C4-C5-C10
5	C	1101	2US	O-C-C1-C2
5	C	1101	2US	N-C-C1-C2

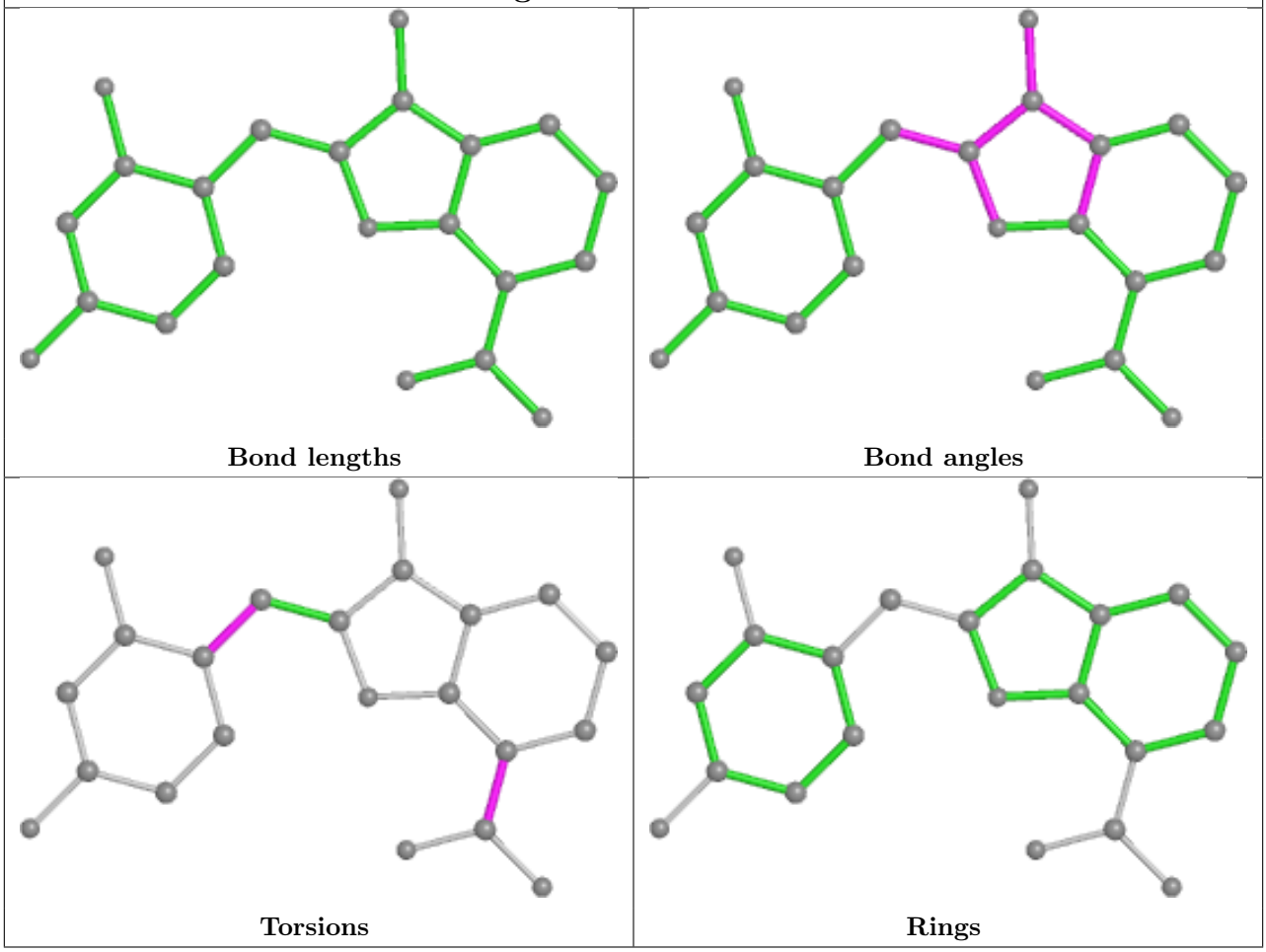
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	1101	2US	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 then 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.

Ligand 2US C 1101



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	222/267 (83%)	-0.14	5 (2%)	60	46	176, 213, 289, 314	0
1	D	222/267 (83%)	0.14	14 (6%)	20	12	211, 278, 351, 378	0
2	C	456/505 (90%)	0.27	23 (5%)	28	20	177, 237, 302, 335	0
2	F	456/505 (90%)	0.34	33 (7%)	15	10	210, 286, 335, 355	0
3	M	26/26 (100%)	-0.39	0	100	100	191, 239, 279, 281	0
3	N	26/26 (100%)	-0.45	0	100	100	219, 269, 290, 294	0
All	All	1408/1596 (88%)	0.18	75 (5%)	26	18	176, 260, 328, 378	0

All (75) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	575	LEU	5.2
2	F	1011	THR	5.1
2	F	575	LEU	4.9
1	D	58	TRP	4.6
2	F	951	LEU	4.6
2	F	863	GLY	4.2
1	D	283	VAL	4.1
2	F	644	ASP	4.0
2	C	785	SER	4.0
1	A	6	ASP	4.0
1	D	349	LYS	4.0
2	F	864	SER	3.7
1	D	54	PHE	3.7
2	F	662	LYS	3.6
2	C	943	LYS	3.6
2	F	663	SER	3.5
2	F	923	GLU	3.5
2	C	584	TRP	3.5
2	F	783	ASP	3.5

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Mol	Chain	Res	Type	RSRZ
2	C	539	LEU	3.4
2	F	943	LYS	3.4
1	D	6	ASP	3.3
2	F	630	ASN	3.3
1	D	309	TYR	3.1
2	F	550	GLY	3.1
2	F	807	ASP	2.9
2	C	978	GLY	2.8
1	D	31	ASP	2.7
1	A	35	MET	2.7
2	F	537	SER	2.6
1	D	302	LEU	2.6
1	A	229	ASP	2.6
2	F	930	TYR	2.6
2	C	786	SER	2.6
2	C	863	GLY	2.6
2	F	938	ILE	2.5
2	C	878	ARG	2.5
2	F	989	TYR	2.5
2	C	989	TYR	2.5
2	F	531	ALA	2.5
2	C	729	ILE	2.5
2	F	862	HIS	2.5
2	F	944	GLY	2.5
2	C	601	LEU	2.5
2	F	794	TYR	2.5
1	D	225	LYS	2.4
2	C	585	ILE	2.4
2	C	923	GLU	2.4
2	C	630	ASN	2.4
2	C	944	GLY	2.4
2	C	574	LEU	2.4
2	C	662	LYS	2.4
2	F	827	ASN	2.4
1	A	309	TYR	2.4
2	C	864	SER	2.4
2	F	932	LEU	2.4
1	A	302	LEU	2.4
2	F	928	ASN	2.3
2	F	801	ILE	2.3
2	F	979	VAL	2.3
1	D	350	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	253	LYS	2.3
1	D	336	PRO	2.2
2	C	663	SER	2.2
2	F	782	SER	2.2
2	F	601	LEU	2.2
2	F	913	GLY	2.2
2	C	736	PHE	2.1
2	F	553	PHE	2.1
1	D	13	TYR	2.1
2	C	732	LEU	2.1
2	C	853	GLN	2.1
2	F	539	LEU	2.0
2	F	554	SER	2.0
1	D	62	HIS	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 monosaccharides in this entry.

6.4 Ligands (i)

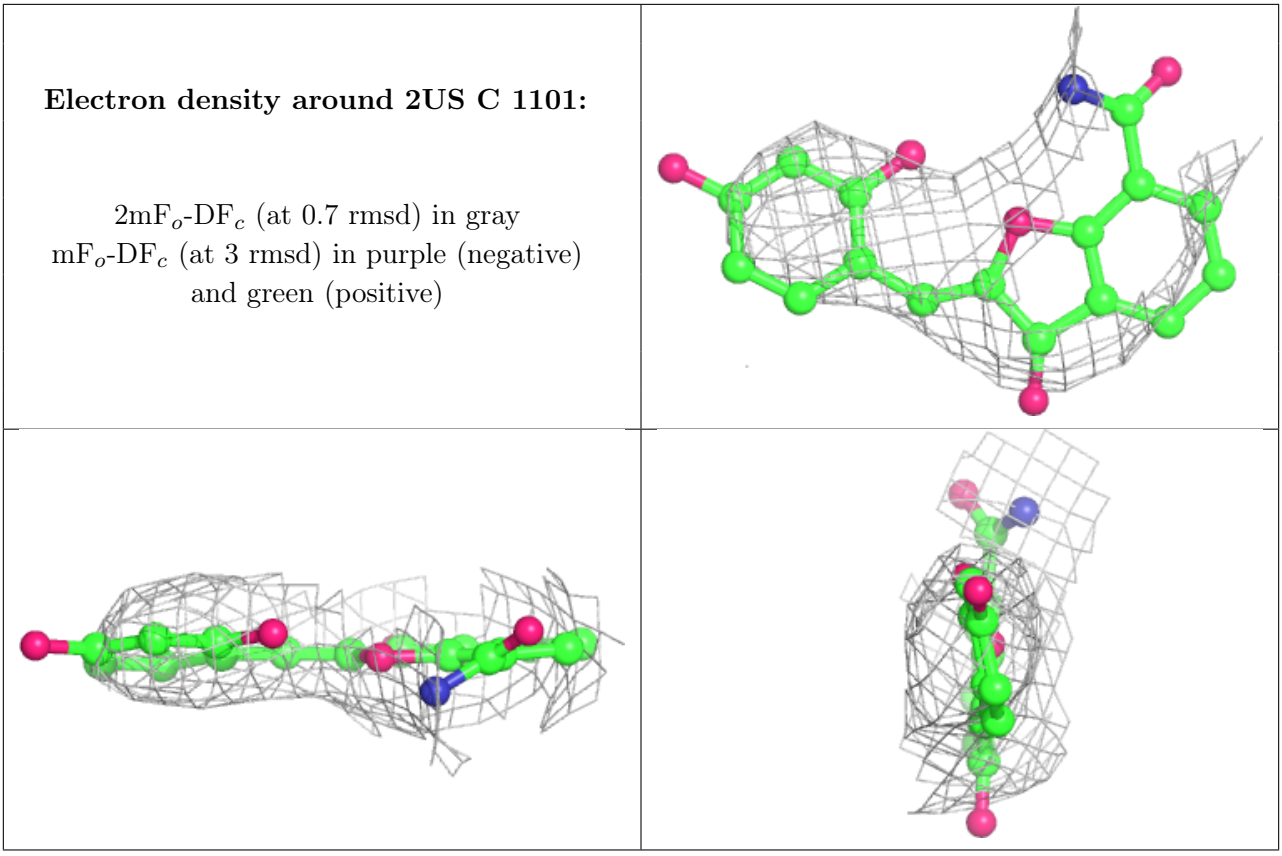
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	2US	C	1101	22/22	0.84	0.37	181,188,193,196	0
4	ZN	D	402	1/1	0.89	0.16	200,200,200,200	0
4	ZN	A	402	1/1	0.91	0.05	110,110,110,110	0
4	ZN	D	401	1/1	0.93	0.05	175,175,175,175	0
4	ZN	A	401	1/1	0.98	0.04	138,138,138,138	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 2US C 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 (i)

There are no such residues in this entry.