



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 12, 2020 – 09:42 PM EST

PDB ID : 4O24  
Title : DNA Double-Strand Break Repair Pathway Choice Is Directed by Distinct MRE11 Nuclease Activities  
Authors : Shibata, A.; Moiani, D.; Arvai, A.S.; Perry, J.; Harding, S.M.; Genois, M.; Maity, R.; Rossum-Fikkert, S.; Kertokallio, A.; Romoli, F.; Ismail, A.; Ismalaj, E.; Petricci, E.; Neale, M.J.; Bristow, R.G.; Masson, J.; Wyman, C.; Jeggo, P.A.; Tainer, J.A.  
Deposited on : 2013-12-16  
Resolution : 2.30 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](mailto: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.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.0 (224370), CSD as540be (2019)  
Xtriage (Phenix) : 1.13  
EDS : 2.4  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)  
Refmac : 5.8.0158  
CCP4 : 7.0 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.4

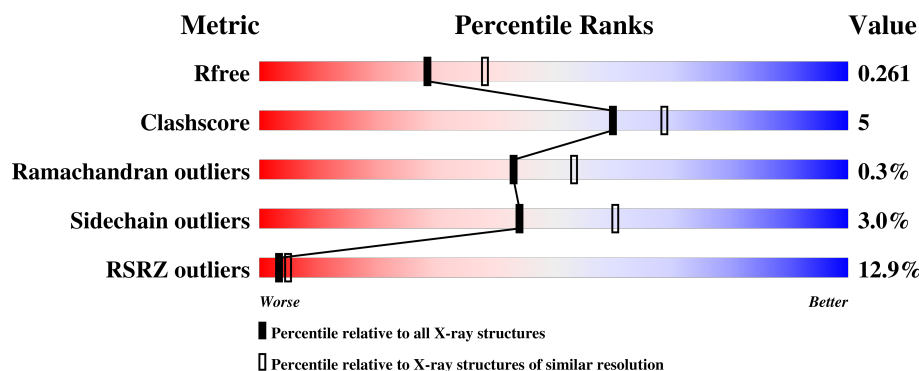
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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))
$R_{free}$	111664	4477 (2.30-2.30)
Clashscore	122126	5072 (2.30-2.30)
Ramachandran outliers	120053	5022 (2.30-2.30)
Sidechain outliers	120020	5021 (2.30-2.30)
RSRZ outliers	108989	4374 (2.30-2.30)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	335	<div> <div>12%</div> <div>87%</div> <div>10%</div> <div>..</div> </div>
1	B	335	<div> <div>13%</div> <div>82%</div> <div>13%</div> <div>..</div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5288 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.

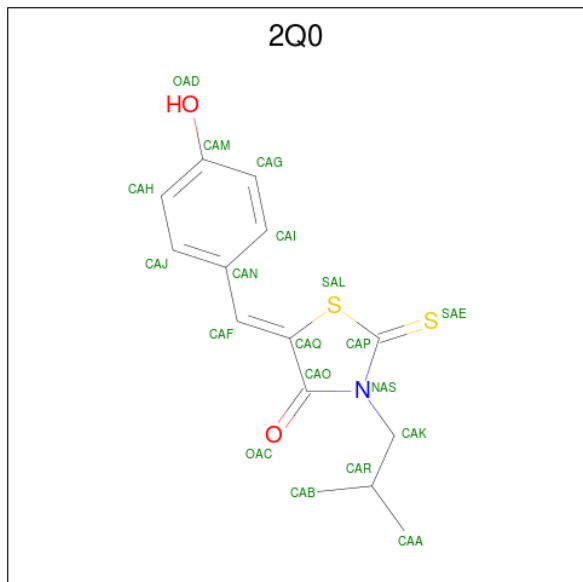
- Molecule 1 is a protein called Exonuclease, putative.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	331	Total	C	N	O	S	0	1	0
			2630	1691	449	484	6			
1	B	321	Total	C	N	O	S	0	0	0
			2513	1621	420	466	6			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	GLY	-	expression tag	UNP Q9X1X0
A	-9	SER	-	expression tag	UNP Q9X1X0
A	-8	ASP	-	expression tag	UNP Q9X1X0
A	-7	LYS	-	expression tag	UNP Q9X1X0
A	-6	ILE	-	expression tag	UNP Q9X1X0
A	-5	HIS	-	expression tag	UNP Q9X1X0
A	-4	HIS	-	expression tag	UNP Q9X1X0
A	-3	HIS	-	expression tag	UNP Q9X1X0
A	-2	HIS	-	expression tag	UNP Q9X1X0
A	-1	HIS	-	expression tag	UNP Q9X1X0
A	0	HIS	-	expression tag	UNP Q9X1X0
A	1	VAL	-	expression tag	UNP Q9X1X0
B	-10	GLY	-	expression tag	UNP Q9X1X0
B	-9	SER	-	expression tag	UNP Q9X1X0
B	-8	ASP	-	expression tag	UNP Q9X1X0
B	-7	LYS	-	expression tag	UNP Q9X1X0
B	-6	ILE	-	expression tag	UNP Q9X1X0
B	-5	HIS	-	expression tag	UNP Q9X1X0
B	-4	HIS	-	expression tag	UNP Q9X1X0
B	-3	HIS	-	expression tag	UNP Q9X1X0
B	-2	HIS	-	expression tag	UNP Q9X1X0
B	-1	HIS	-	expression tag	UNP Q9X1X0
B	0	HIS	-	expression tag	UNP Q9X1X0
B	1	VAL	-	expression tag	UNP Q9X1X0

- Molecule 2 is (5 {Z})-5-[(4-hydroxyphenyl)methylidene]-3-(2-methylpropyl)-2-sulfanylidene-1,3-thiazolidin-4-one (three-letter code: 2Q0) (formula: C<sub>14</sub>H<sub>15</sub>NO<sub>2</sub>S<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			19	14	1	2	2		
2	B	1	Total	C	N	O	S	0	0
			19	14	1	2	2		

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Mn	0	0
			2	2		
3	A	2	Total	Mn	0	0
			2	2		

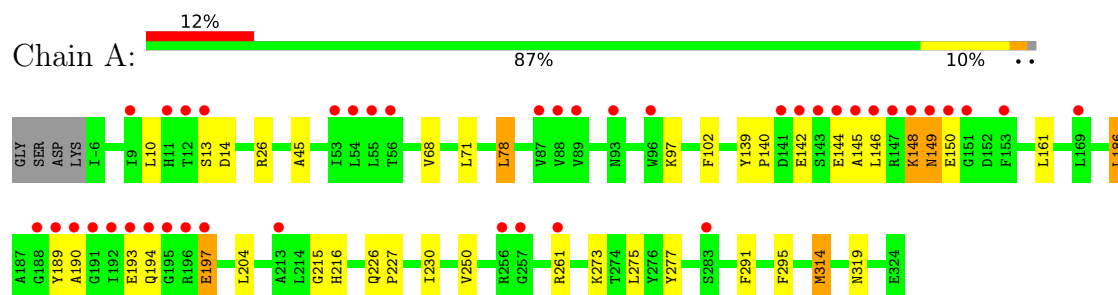
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	60	Total	O	0	0
			60	60		
4	B	43	Total	O	0	0
			43	43		

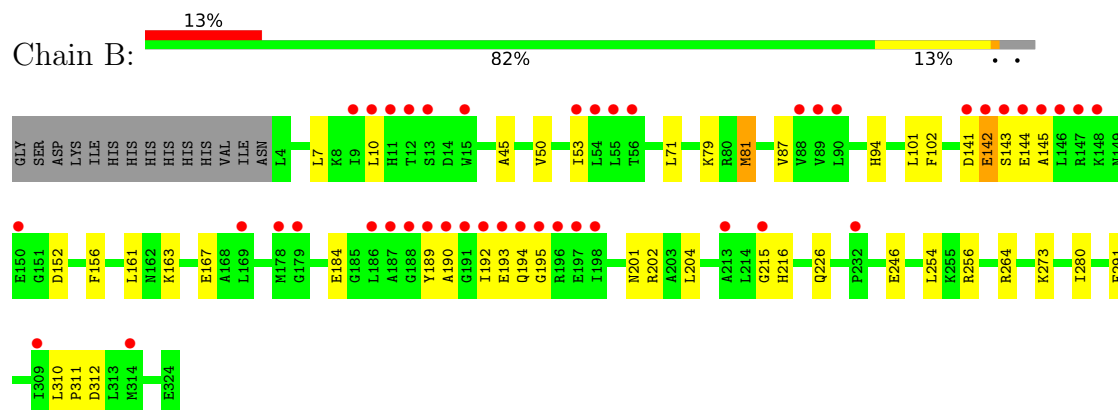
### 3 Residue-property plots [i](#)

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: Exonuclease, putative



- Molecule 1: Exonuclease, putative



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	48.18Å 113.53Å 81.56Å 90.00° 100.64° 90.00°	Depositor
Resolution (Å)	31.48 – 2.30 31.48 – 2.30	Depositor EDS
% Data completeness (in resolution range)	88.9 (31.48-2.30) 88.7 (31.48-2.30)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.82 (at 2.29Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, $R_{free}$	0.201 , 0.259 0.202 , 0.261	Depositor DCC
$R_{free}$ test set	1820 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	40.0	Xtriage
Anisotropy	0.694	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 50.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	5288	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.91% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: MN, 2Q0

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	0.22	0/2695	0.43	0/3651
1	B	0.22	0/2569	0.40	0/3483
All	All	0.22	0/5264	0.42	0/7134

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

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	2630	0	2588	23	0
1	B	2513	0	2459	25	0
2	A	19	0	16	3	0
2	B	19	0	16	3	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
4	A	60	0	0	0	0
4	B	43	0	0	1	0
All	All	5288	0	5079	51	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 5.

All (51) 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:197:GLU:OE2	1:A:216:HIS:NE2	2.20	0.73
1:A:149:ASN:HD22	1:A:150:GLU:HG2	1.56	0.71
1:B:10:LEU:HB2	1:B:50:VAL:HG11	1.76	0.68
1:B:201:ASN:HB3	1:B:204:LEU:HD13	1.77	0.66
2:A:401:2Q0:H16	2:A:401:2Q0:SAL	2.36	0.66
1:B:184:GLU:O	1:B:202:ARG:NH1	2.32	0.62
2:B:401:2Q0:SAL	2:B:401:2Q0:H16	2.39	0.62
1:B:194:GLN:N	1:B:195:GLY:HA3	2.15	0.62
1:B:246:GLU:O	1:B:264:ARG:NH2	2.34	0.59
1:B:280:ILE:HG21	1:B:310:LEU:HD11	1.85	0.58
1:A:161:LEU:HD13	1:A:204:LEU:HB3	1.85	0.57
1:A:102:PHE:HE1	2:B:401:2Q0:H7	1.71	0.56
1:B:161:LEU:HD13	1:B:204:LEU:HB3	1.87	0.55
1:B:53:ILE:HD13	1:B:81:MET:HG3	1.91	0.51
1:B:193:GLU:CB	1:B:194:GLN:HA	2.40	0.51
1:B:189:TYR:N	1:B:190:ALA:HB3	2.26	0.50
1:A:10:LEU:HD13	1:A:45:ALA:HB2	1.94	0.48
1:B:142:GLU:HA	1:B:144:GLU:N	2.28	0.48
1:A:186:LEU:H	1:A:186:LEU:HD23	1.79	0.48
1:B:163:LYS:NZ	1:B:167:GLU:OE2	2.35	0.48
1:A:230:ILE:HG21	1:A:250:VAL:HG21	1.96	0.48
1:B:7:LEU:HD23	1:B:254:LEU:HD12	1.96	0.47
1:A:215:GLY:O	1:A:216:HIS:HB3	2.15	0.47
1:A:273:LYS:HG2	1:A:291:PHE:CZ	2.49	0.47
1:A:26:ARG:NH2	1:A:314:MET:O	2.45	0.47
1:B:94:HIS:ND1	2:B:401:2Q0:H15	2.30	0.47
1:B:310:LEU:HD13	1:B:311:PRO:HD2	1.98	0.46
2:A:401:2Q0:H16	2:A:401:2Q0:H17	1.79	0.46
1:A:295:PHE:O	1:A:319:ASN:ND2	2.36	0.45
1:A:148:LYS:HA	1:A:149:ASN:HA	1.75	0.45
1:A:189:TYR:HA	1:A:190:ALA:HA	1.51	0.44
1:B:142:GLU:HA	1:B:143:SER:C	2.38	0.44
2:A:401:2Q0:OAC	2:A:401:2Q0:H2	2.18	0.44
1:A:13:SER:OG	1:A:14:ASP:OD2	2.33	0.43
1:B:192:ILE:HA	1:B:193:GLU:HA	1.73	0.43
1:A:139:TYR:HA	1:A:140:PRO:HD3	1.88	0.43
1:A:145:ALA:HA	1:A:146:LEU:HA	1.55	0.43
1:A:148:LYS:HG3	1:A:148:LYS:H	1.52	0.43
1:B:273:LYS:HG2	1:B:291:PHE:CZ	2.53	0.43
1:B:79:LYS:NZ	4:B:517:HOH:O	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:68:VAL:HG13	1:B:101:LEU:HD11	2.01	0.42
1:B:81:MET:HB3	1:B:87:VAL:HG21	2.01	0.42
1:B:10:LEU:HD13	1:B:45:ALA:HB2	2.02	0.42
1:B:142:GLU:HB3	1:B:145:ALA:HB3	2.03	0.41
1:A:193:GLU:CB	1:A:194:GLN:HA	2.51	0.41
1:A:78:LEU:HD12	1:A:78:LEU:HA	1.89	0.41
1:A:226:GLN:HA	1:A:227:PRO:HA	1.89	0.41
1:B:215:GLY:O	1:B:216:HIS:HB3	2.20	0.41
1:A:97:LYS:HE3	1:A:97:LYS:HB2	1.85	0.41
1:A:275:LEU:HB3	1:A:277:TYR:CE2	2.56	0.40
1:B:152:ASP:O	1:B:156:PHE:N	2.49	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	330/335 (98%)	306 (93%)	23 (7%)	1 (0%)	43	53
1	B	319/335 (95%)	299 (94%)	19 (6%)	1 (0%)	43	53
All	All	649/670 (97%)	605 (93%)	42 (6%)	2 (0%)	43	53

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	144	GLU
1	B	312	ASP

### 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	279/297 (94%)	270 (97%)	9 (3%)	42	58
1	B	261/297 (88%)	254 (97%)	7 (3%)	48	65
All	All	540/594 (91%)	524 (97%)	16 (3%)	44	60

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	71	LEU
1	A	78	LEU
1	A	142	GLU
1	A	148	LYS
1	A	149	ASN
1	A	186	LEU
1	A	197	GLU
1	A	261	ARG
1	A	314	MET
1	B	71	LEU
1	B	81	MET
1	B	102	PHE
1	B	141	ASP
1	B	142	GLU
1	B	226	GLN
1	B	256	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	149	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 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$
2	2Q0	A	401	-	20,20,20	2.54	7 (35%)	28,28,28	2.75	10 (35%)
2	2Q0	B	401	-	20,20,20	2.34	7 (35%)	28,28,28	2.54	8 (28%)

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	2Q0	A	401	-	-	2/8/24/24	0/2/2/2
2	2Q0	B	401	-	-	0/8/24/24	0/2/2/2

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	2Q0	CAO-CAQ	-7.63	1.33	1.48
2	A	401	2Q0	CAO-CAQ	-7.35	1.34	1.48
2	A	401	2Q0	CAP-SAL	-5.73	1.62	1.74
2	B	401	2Q0	CAP-SAL	-3.95	1.66	1.74
2	A	401	2Q0	CAQ-SAL	-3.47	1.66	1.73
2	B	401	2Q0	CAN-CAF	-3.20	1.40	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	2Q0	CAN-CAF	-3.00	1.40	1.46
2	B	401	2Q0	CAP-SAE	2.69	1.73	1.66
2	A	401	2Q0	CAP-SAE	2.56	1.73	1.66
2	B	401	2Q0	CAQ-SAL	-2.51	1.68	1.73
2	A	401	2Q0	CAK-NAS	2.49	1.51	1.46
2	B	401	2Q0	CAO-NAS	-2.15	1.34	1.39
2	A	401	2Q0	CAP-NAS	-2.00	1.34	1.37
2	B	401	2Q0	CAP-NAS	-2.00	1.34	1.37

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	2Q0	CAK-NAS-CAP	-8.41	113.23	122.41
2	B	401	2Q0	CAK-NAS-CAP	8.38	131.55	122.41
2	B	401	2Q0	CAQ-CAO-NAS	6.00	116.71	110.14
2	A	401	2Q0	CAK-NAS-CAO	5.63	135.46	121.49
2	A	401	2Q0	CAQ-CAO-NAS	4.97	115.58	110.14
2	A	401	2Q0	CAP-NAS-CAO	-4.27	111.30	116.72
2	A	401	2Q0	CAN-CAF-CAQ	-4.07	125.55	131.01
2	B	401	2Q0	CAN-CAF-CAQ	-4.00	125.64	131.01
2	A	401	2Q0	OAC-CAO-CAQ	-3.77	120.46	126.44
2	B	401	2Q0	CAF-CAQ-SAL	3.38	133.66	129.25
2	B	401	2Q0	CAP-NAS-CAO	-3.37	112.44	116.72
2	A	401	2Q0	CAR-CAK-NAS	3.35	118.00	112.83
2	B	401	2Q0	CAO-CAQ-SAL	-3.00	106.84	110.58
2	B	401	2Q0	OAC-CAO-CAQ	-2.84	121.95	126.44
2	A	401	2Q0	CAO-CAQ-SAL	-2.59	107.35	110.58
2	A	401	2Q0	CAF-CAQ-SAL	2.32	132.27	129.25
2	B	401	2Q0	CAK-NAS-CAO	-2.22	115.99	121.49
2	A	401	2Q0	CAP-SAL-CAQ	2.12	94.91	92.69

There are no chirality outliers.

All (2) torsion outliers are listed below:

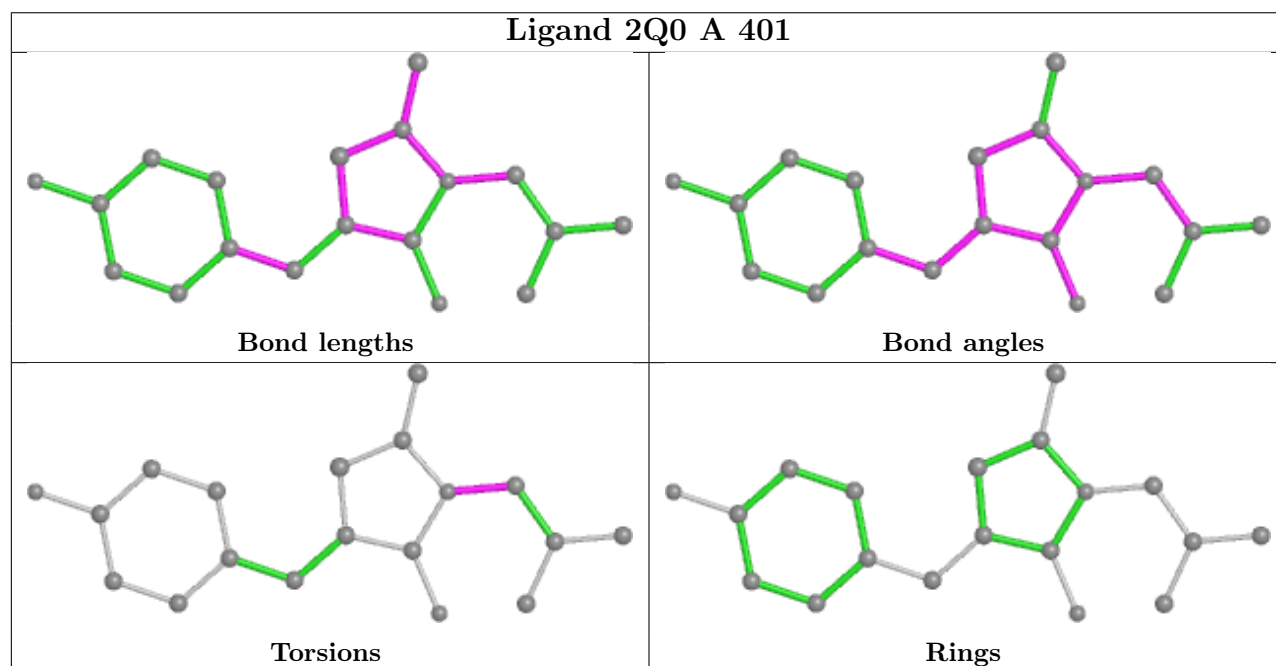
Mol	Chain	Res	Type	Atoms
2	A	401	2Q0	CAR-CAK-NAS-CAP
2	A	401	2Q0	CAR-CAK-NAS-CAO

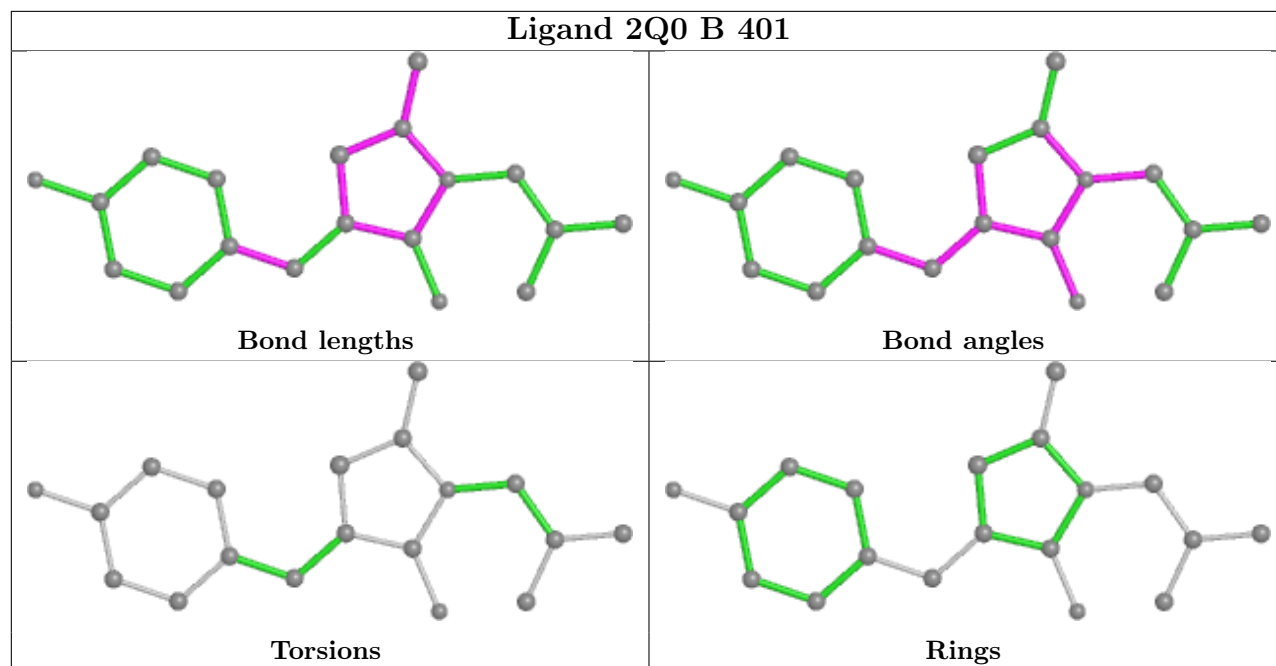
There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	2Q0	3	0
2	B	401	2Q0	3	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	331/335 (98%)	0.61	41 (12%) 4 6	20, 40, 110, 186	0
1	B	321/335 (95%)	0.87	43 (13%) 3 4	21, 44, 113, 208	0
All	All	652/670 (97%)	0.74	84 (12%) 3 5	20, 42, 116, 208	0

All (84) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	187	ALA	15.1
1	B	189	TYR	14.9
1	B	188	GLY	13.7
1	B	192	ILE	13.0
1	B	190	ALA	12.5
1	A	143	SER	12.2
1	B	143	SER	12.2
1	A	145	ALA	10.3
1	A	194	GLN	9.9
1	B	196	ARG	9.7
1	A	146	LEU	9.7
1	B	195	GLY	9.6
1	A	195	GLY	8.4
1	B	147	ARG	8.1
1	B	191	GLY	8.0
1	B	193	GLU	7.0
1	A	191	GLY	6.5
1	A	144	GLU	6.2
1	B	146	LEU	5.9
1	B	144	GLU	5.6
1	B	194	GLN	5.4
1	B	197	GLU	5.2
1	A	190	ALA	5.1
1	A	192	ILE	5.0

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Mol	Chain	Res	Type	RSRZ
1	B	54	LEU	4.3
1	A	196	ARG	4.3
1	A	189	TYR	3.9
1	A	147	ARG	3.8
1	A	256	ARG	3.8
1	A	54	LEU	3.6
1	B	148	LYS	3.6
1	A	169	LEU	3.5
1	B	186	LEU	3.5
1	B	12	THR	3.4
1	B	56	THR	3.4
1	A	193	GLU	3.4
1	B	150	GLU	3.3
1	A	197	GLU	3.3
1	B	213	ALA	3.2
1	B	89	VAL	3.2
1	A	56	THR	3.1
1	B	10	LEU	3.1
1	A	55	LEU	3.0
1	B	198	ILE	3.0
1	B	314	MET	3.0
1	B	13	SER	2.8
1	A	151	GLY	2.7
1	B	11	HIS	2.6
1	A	149	ASN	2.6
1	A	257	GLY	2.6
1	A	153	PHE	2.5
1	A	12	THR	2.5
1	B	90	LEU	2.5
1	B	9	ILE	2.5
1	B	179	GLY	2.4
1	B	309	ILE	2.4
1	A	88	VAL	2.4
1	B	88	VAL	2.4
1	A	188	GLY	2.4
1	B	232	PRO	2.4
1	A	96	TRP	2.3
1	A	93	ASN	2.3
1	B	169	LEU	2.3
1	A	13	SER	2.3
1	A	142	GLU	2.2
1	B	53	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	150	GLU	2.2
1	B	178	MET	2.2
1	A	53	ILE	2.2
1	B	142	GLU	2.2
1	A	87	VAL	2.1
1	A	141	ASP	2.1
1	B	145	ALA	2.1
1	A	9	ILE	2.1
1	A	261	ARG	2.1
1	B	215	GLY	2.1
1	A	11	HIS	2.1
1	A	213	ALA	2.1
1	A	148	LYS	2.1
1	A	89	VAL	2.1
1	B	15	TRP	2.1
1	B	55	LEU	2.0
1	B	141	ASP	2.0
1	A	283	SER	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 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	MN	B	403	1/1	0.75	0.34	46,46,46,46	1
3	MN	A	402	1/1	0.81	0.22	60,60,60,60	1
2	2Q0	A	401	19/19	0.84	0.23	53,75,86,88	0
3	MN	A	403	1/1	0.86	0.21	54,54,54,54	1
2	2Q0	B	401	19/19	0.89	0.19	49,55,79,80	0

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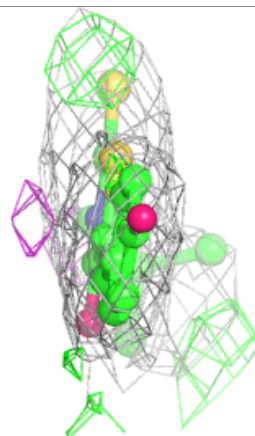
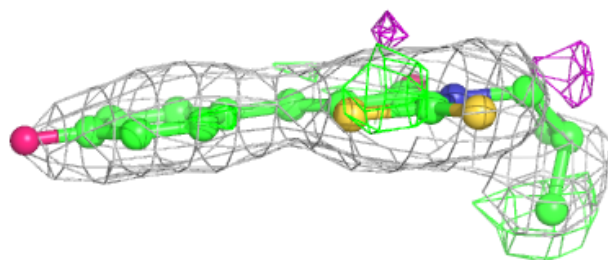
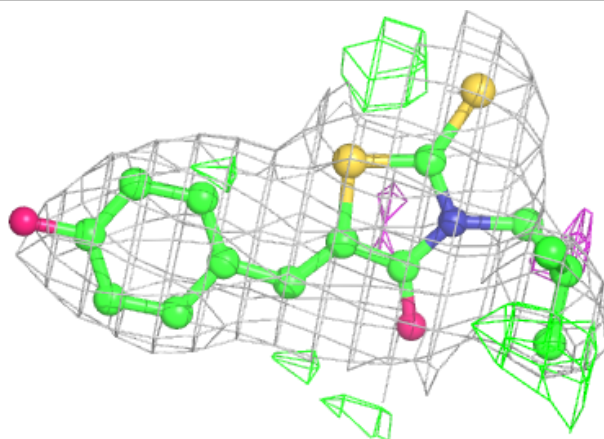
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	MN	B	402	1/1	0.96	0.38	60,60,60,60	1

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.

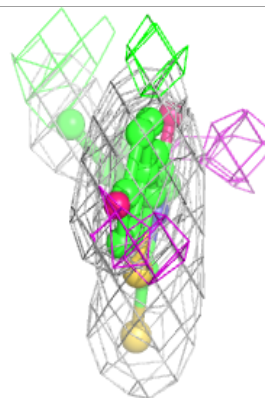
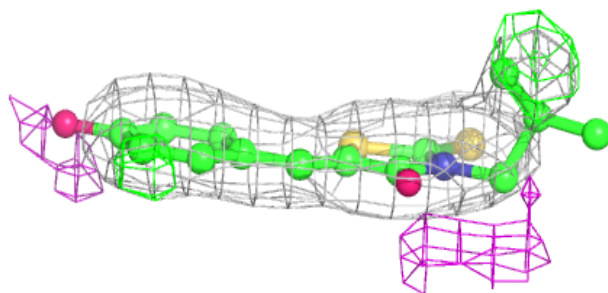
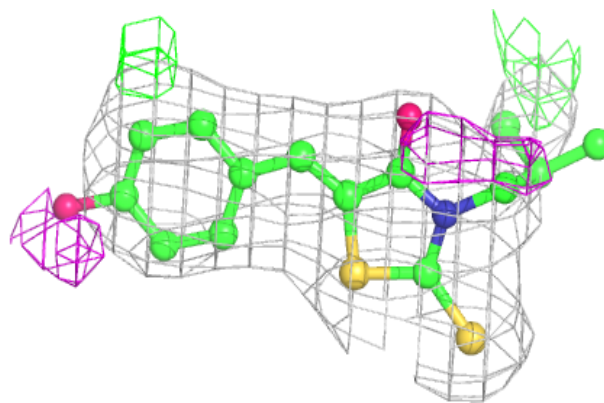
**Electron density around 2Q0 A 401:**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around 2Q0 B 401:**

$2mF_o - DF_c$  (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.