



# Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 10:27 pm BST

PDB ID : 6Q0V  
Title : Structure of DDB1-DDA1-DCAF15 complex bound to tasisulam and RBM39  
Authors : Faust, T.; Yoon, H.; Nowak, R.P.; Donovan, K.A.; Li, Z.; Cai, Q.; Eleuteri, N.A.; Zhang, T.; Gray, N.S.; Fischer, E.S.  
Deposited on : 2019-08-02  
Resolution : 2.90 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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
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) : 2.11

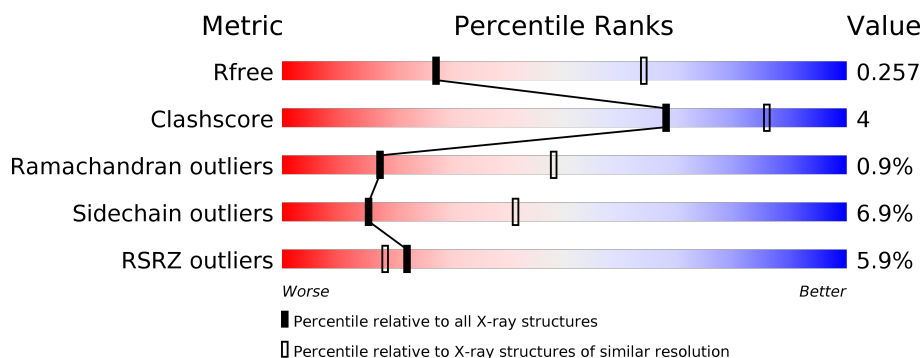
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.90 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	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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 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	864	<div> <div>6%</div> <div> <div></div> <div>78%</div> <div>10%</div> <div>11%</div> </div> </div>
2	B	276	<div> <div>3%</div> <div> <div></div> <div>63%</div> <div>12%</div> <div>25%</div> </div> </div>
3	C	263	<div> <div>3%</div> <div> <div></div> <div>59%</div> <div>12%</div> <div>27%</div> </div> </div>
4	D	107	<div> <div>2%</div> <div> <div></div> <div>57%</div> <div>16%</div> <div>26%</div> </div> </div>
5	E	126	<div> <div>4%</div> <div> <div></div> <div>37%</div> <div>9%</div> <div>51%</div> </div> </div>

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 10494 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 DNA damage-binding protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	772	Total	C	N	O	S	0	0	0
			6082	3862	1023	1163	34			

There are 34 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-27	MET	-	initiating methionine	UNP Q16531
A	-26	GLY	-	expression tag	UNP Q16531
A	-25	SER	-	expression tag	UNP Q16531
A	-24	SER	-	expression tag	UNP Q16531
A	-23	HIS	-	expression tag	UNP Q16531
A	-22	HIS	-	expression tag	UNP Q16531
A	-21	HIS	-	expression tag	UNP Q16531
A	-20	HIS	-	expression tag	UNP Q16531
A	-19	HIS	-	expression tag	UNP Q16531
A	-18	HIS	-	expression tag	UNP Q16531
A	-17	SER	-	expression tag	UNP Q16531
A	-16	ALA	-	expression tag	UNP Q16531
A	-15	ALA	-	expression tag	UNP Q16531
A	-14	HIS	-	expression tag	UNP Q16531
A	-13	ILE	-	expression tag	UNP Q16531
A	-12	VAL	-	expression tag	UNP Q16531
A	-11	MET	-	expression tag	UNP Q16531
A	-10	VAL	-	expression tag	UNP Q16531
A	-9	ASP	-	expression tag	UNP Q16531
A	-8	ALA	-	expression tag	UNP Q16531
A	-7	TYR	-	expression tag	UNP Q16531
A	-6	LYS	-	expression tag	UNP Q16531
A	-5	PRO	-	expression tag	UNP Q16531
A	-4	THR	-	expression tag	UNP Q16531
A	-3	LYS	-	expression tag	UNP Q16531
A	-2	GLY	-	expression tag	UNP Q16531
A	-1	GLY	-	expression tag	UNP Q16531

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Chain	Residue	Modelled	Actual	Comment	Reference
A	0	ARG	-	expression tag	UNP Q16531
A	700	GLY	-	linker	UNP Q16531
A	701	ASN	-	linker	UNP Q16531
A	702	GLY	-	linker	UNP Q16531
A	703	ASN	-	linker	UNP Q16531
A	704	SER	-	linker	UNP Q16531
A	705	GLY	-	linker	UNP Q16531

- Molecule 2 is a protein called DDB1- and CUL4-associated factor 15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	208	Total	C	N	O	S	0	0	0
			1690	1091	291	298	10			

There are 49 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-15	MET	-	initiating methionine	UNP Q66K64
B	-14	ASP	-	expression tag	UNP Q66K64
B	-13	TRP	-	expression tag	UNP Q66K64
B	-12	SER	-	expression tag	UNP Q66K64
B	-11	HIS	-	expression tag	UNP Q66K64
B	-10	PRO	-	expression tag	UNP Q66K64
B	-9	GLN	-	expression tag	UNP Q66K64
B	-8	PHE	-	expression tag	UNP Q66K64
B	-7	GLU	-	expression tag	UNP Q66K64
B	-6	LYS	-	expression tag	UNP Q66K64
B	-5	SER	-	expression tag	UNP Q66K64
B	-4	ALA	-	expression tag	UNP Q66K64
B	-3	VAL	-	expression tag	UNP Q66K64
B	-2	GLY	-	expression tag	UNP Q66K64
B	-1	LEU	-	expression tag	UNP Q66K64
B	0	ASN	-	expression tag	UNP Q66K64
B	1	ASP	-	expression tag	UNP Q66K64
B	2	ILE	-	expression tag	UNP Q66K64
B	3	PHE	-	expression tag	UNP Q66K64
B	4	GLU	-	expression tag	UNP Q66K64
B	5	ALA	-	expression tag	UNP Q66K64
B	6	GLN	-	expression tag	UNP Q66K64
B	7	LYS	-	expression tag	UNP Q66K64
B	8	ILE	-	expression tag	UNP Q66K64
B	9	GLU	-	expression tag	UNP Q66K64

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Chain	Residue	Modelled	Actual	Comment	Reference
B	10	TRP	-	expression tag	UNP Q66K64
B	11	HIS	-	expression tag	UNP Q66K64
B	12	GLU	-	expression tag	UNP Q66K64
B	13	GLY	-	expression tag	UNP Q66K64
B	14	GLY	-	expression tag	UNP Q66K64
B	15	GLY	-	expression tag	UNP Q66K64
B	16	GLY	-	expression tag	UNP Q66K64
B	17	SER	-	expression tag	UNP Q66K64
B	18	GLY	-	expression tag	UNP Q66K64
B	19	GLU	-	expression tag	UNP Q66K64
B	20	ASN	-	expression tag	UNP Q66K64
B	21	LEU	-	expression tag	UNP Q66K64
B	22	TYR	-	expression tag	UNP Q66K64
B	23	PHE	-	expression tag	UNP Q66K64
B	24	GLN	-	expression tag	UNP Q66K64
B	25	GLY	-	expression tag	UNP Q66K64
B	26	GLY	-	expression tag	UNP Q66K64
B	27	GLY	-	expression tag	UNP Q66K64
B	28	ARG	-	expression tag	UNP Q66K64
B	29	MET	-	expression tag	UNP Q66K64
B	30	GLY	-	expression tag	UNP Q66K64
B	31	ARG	-	expression tag	UNP Q66K64
B	32	ARG	-	expression tag	UNP Q66K64
B	33	ARG	-	expression tag	UNP Q66K64

- Molecule 3 is a protein called DDB1- and CUL4-associated factor 15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	192	Total	C	N	O	S	0	0	0
			1545	992	256	290	7			

There are 45 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	338	MET	-	initiating methionine	UNP Q66K64
C	339	ASP	-	expression tag	UNP Q66K64
C	340	TRP	-	expression tag	UNP Q66K64
C	341	SER	-	expression tag	UNP Q66K64
C	342	HIS	-	expression tag	UNP Q66K64
C	343	PRO	-	expression tag	UNP Q66K64
C	344	GLN	-	expression tag	UNP Q66K64
C	345	PHE	-	expression tag	UNP Q66K64

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Chain	Residue	Modelled	Actual	Comment	Reference
C	346	GLU	-	expression tag	UNP Q66K64
C	347	LYS	-	expression tag	UNP Q66K64
C	348	SER	-	expression tag	UNP Q66K64
C	349	ALA	-	expression tag	UNP Q66K64
C	350	VAL	-	expression tag	UNP Q66K64
C	351	GLY	-	expression tag	UNP Q66K64
C	352	LEU	-	expression tag	UNP Q66K64
C	353	ASN	-	expression tag	UNP Q66K64
C	354	ASP	-	expression tag	UNP Q66K64
C	355	ILE	-	expression tag	UNP Q66K64
C	356	PHE	-	expression tag	UNP Q66K64
C	357	GLU	-	expression tag	UNP Q66K64
C	358	ALA	-	expression tag	UNP Q66K64
C	359	GLN	-	expression tag	UNP Q66K64
C	360	LYS	-	expression tag	UNP Q66K64
C	361	ILE	-	expression tag	UNP Q66K64
C	362	GLU	-	expression tag	UNP Q66K64
C	363	TRP	-	expression tag	UNP Q66K64
C	364	HIS	-	expression tag	UNP Q66K64
C	365	GLU	-	expression tag	UNP Q66K64
C	366	GLY	-	expression tag	UNP Q66K64
C	367	GLY	-	expression tag	UNP Q66K64
C	368	GLY	-	expression tag	UNP Q66K64
C	369	GLY	-	expression tag	UNP Q66K64
C	370	SER	-	expression tag	UNP Q66K64
C	371	GLY	-	expression tag	UNP Q66K64
C	372	GLU	-	expression tag	UNP Q66K64
C	373	ASN	-	expression tag	UNP Q66K64
C	374	LEU	-	expression tag	UNP Q66K64
C	375	TYR	-	expression tag	UNP Q66K64
C	376	PHE	-	expression tag	UNP Q66K64
C	377	GLN	-	expression tag	UNP Q66K64
C	378	GLY	-	expression tag	UNP Q66K64
C	379	GLY	-	expression tag	UNP Q66K64
C	380	GLY	-	expression tag	UNP Q66K64
C	381	ARG	-	expression tag	UNP Q66K64
C	382	MET	-	expression tag	UNP Q66K64

- Molecule 4 is a protein called RNA-binding protein 39.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	79	Total	C	N	O	S	0	0	0
			619	392	106	115	6			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	226	MET	-	initiating methionine	UNP Q14498
D	227	GLY	-	expression tag	UNP Q14498
D	228	SER	-	expression tag	UNP Q14498
D	229	SER	-	expression tag	UNP Q14498
D	230	HIS	-	expression tag	UNP Q14498
D	231	HIS	-	expression tag	UNP Q14498
D	232	HIS	-	expression tag	UNP Q14498
D	233	HIS	-	expression tag	UNP Q14498
D	234	HIS	-	expression tag	UNP Q14498
D	235	HIS	-	expression tag	UNP Q14498
D	236	SER	-	expression tag	UNP Q14498
D	237	ALA	-	expression tag	UNP Q14498
D	238	VAL	-	expression tag	UNP Q14498
D	239	ASP	-	expression tag	UNP Q14498
D	240	GLU	-	expression tag	UNP Q14498
D	241	ASN	-	expression tag	UNP Q14498
D	242	LEU	-	expression tag	UNP Q14498
D	243	TYR	-	expression tag	UNP Q14498
D	244	PHE	-	expression tag	UNP Q14498
D	245	GLN	-	expression tag	UNP Q14498
D	246	GLY	-	expression tag	UNP Q14498
D	247	GLY	-	expression tag	UNP Q14498
D	248	GLY	-	expression tag	UNP Q14498
D	249	ARG	-	expression tag	UNP Q14498

- Molecule 5 is a protein called DET1- and DDB1-associated protein 1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	E	62	Total	C	N	O	0	0	0
			520	336	91	93			

There are 24 discrepancies between the modelled and reference sequences:

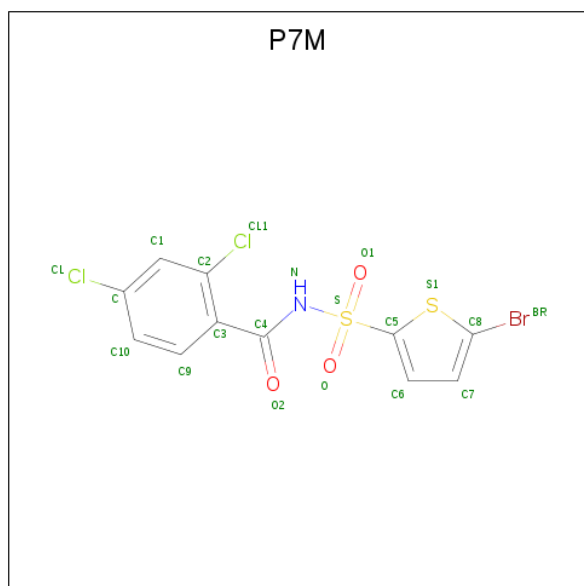
Chain	Residue	Modelled	Actual	Comment	Reference
E	-23	MET	-	initiating methionine	UNP Q9BW61
E	-22	GLY	-	expression tag	UNP Q9BW61
E	-21	SER	-	expression tag	UNP Q9BW61
E	-20	SER	-	expression tag	UNP Q9BW61
E	-19	HIS	-	expression tag	UNP Q9BW61
E	-18	HIS	-	expression tag	UNP Q9BW61
E	-17	HIS	-	expression tag	UNP Q9BW61

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-16	HIS	-	expression tag	UNP Q9BW61
E	-15	HIS	-	expression tag	UNP Q9BW61
E	-14	HIS	-	expression tag	UNP Q9BW61
E	-13	SER	-	expression tag	UNP Q9BW61
E	-12	ALA	-	expression tag	UNP Q9BW61
E	-11	VAL	-	expression tag	UNP Q9BW61
E	-10	ASP	-	expression tag	UNP Q9BW61
E	-9	GLU	-	expression tag	UNP Q9BW61
E	-8	ASN	-	expression tag	UNP Q9BW61
E	-7	LEU	-	expression tag	UNP Q9BW61
E	-6	TYR	-	expression tag	UNP Q9BW61
E	-5	PHE	-	expression tag	UNP Q9BW61
E	-4	GLN	-	expression tag	UNP Q9BW61
E	-3	GLY	-	expression tag	UNP Q9BW61
E	-2	GLY	-	expression tag	UNP Q9BW61
E	-1	GLY	-	expression tag	UNP Q9BW61
E	0	ARG	-	expression tag	UNP Q9BW61

- Molecule 6 is N-[(5-bromothiophen-2-yl)sulfonyl]-2,4-dichlorobenzamide (three-letter code: P7M) (formula:  $C_{11}H_6BrCl_2NO_3S_2$ ) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
			Total	Br	C	Cl	N	O	S		
6	B	1	20	1	11	2	1	3	2	0	0

- Molecule 7 is ZINC ION (three-letter code: ZN) (formula:  $Zn$ ).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	1	Total	Zn	0	0
			1	1		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	7	Total	O	0	0
			7	7		
8	B	6	Total	O	0	0
			6	6		
8	C	2	Total	O	0	0
			2	2		
8	D	1	Total	O	0	0
			1	1		
8	E	1	Total	O	0	0
			1	1		

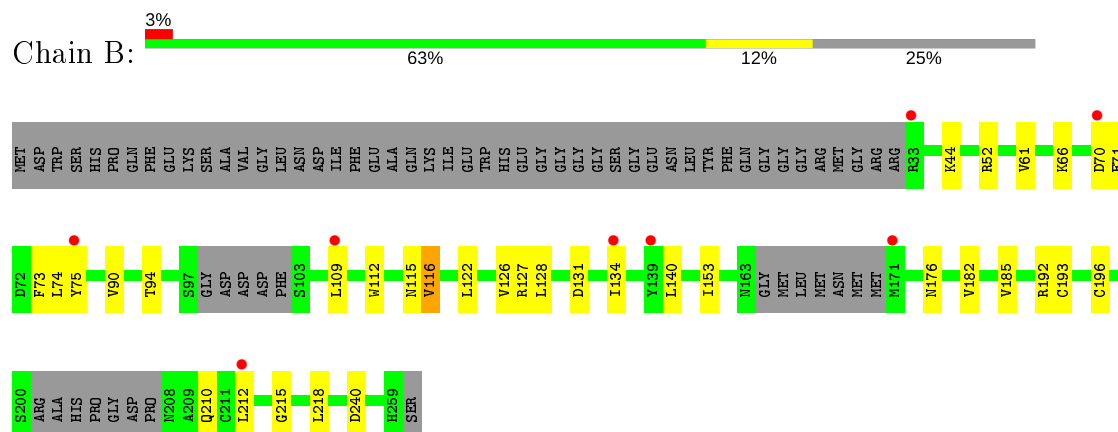
### 3 Residue-property plots

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: DNA damage-binding protein 1



- Molecule 2: DDB1- and CUL4-associated factor 15



Chain C:

3% 59% 12% 27%

Met ASP TRP SER HIS PRO GLN PHE LYS LEU ALA VAL GLY LEU ASP ASP ILE PHE GLU GLU ALA GLN LYS ILE GLU TRP HIS GLU GLY GLY GLY ARG MET E383 Y386 L392 Y393 Y394 Y395 L396 GLU SER GLY GLY GLY TRP

GLU PRO ASP ASP GLU LEU GLU ASP ASP LYS ILE S414 L415 G424 R425 R431 E432 R433 T434 A435 V436 Q437 G438 Q439 L441 Q445 L446 T447 Y452 Y456 V457 S472 D473 Y474 D475 L476 L492 G493 G494 L495 L496 T503 GLU GLU GLY GLN L508 P509 P510 Y511 Y512 Y513 K518 T530 V531 S532 V539 K540 G541 Q542 M558 V559 M560 P565 A579 L580 H581 L582 G583 S585 E593 R594 L600

Chain D:

Amino Acid	Frequency (%)
MET	2%
GLY	57%
GLY	16%
GLY	26%

Chain E:

Residue Type	Count
Met	1
Gly	1
Ser	1
Ser	1
His	1
His	1
His	1
His	1
His	1
His	1
Ser	1
Ser	1
Ala	1
Val	1
Alu	1
Asp	1
Glu	1
Asn	1
Leu	1
Tyr	1
Phe	1
Gln	1
Gly	1
Gly	1
Gly	1
Arg	1
Met	1
Met	1
Ala	1
D3	1
F4	1
L5	1
K6	1
G7	1
L8	1
K13	1
F19	1
H20	1
A21	1
ASP	1
Ser	1
Ser	1
Val	1
Cys	1
Lys	1
Ala	1
Ser	1
Ser	1
Asn	1
Arg	1
Arg	1
P32	1
Y35	1
L36	1
P37	1
T38	1
R39	1
E40	1
Y41	1
E44	1
E45	1
T49	1
I54	1
W63	1
D64	1
K65	1
K70	1
K71	1
Q74	1
Glu	1
Gln	1
Val	1
Glu	1
Leu	1
Gly	1
Gly	1
Gly	1
Gly	1
Ser	1
Ser	1
Ala	1
Pro	1
Pro	1
Pro	1
Arg	1
Lys	1
Val	1
Ala	1
Arg	1
Thr	1
Thr	1
Asp	1
Ser	1
Ser	1
Pro	1
Asp	1
Met	1
His	1
His	1
Glu	1
Asp	1
Thr	1

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	81.77Å 94.61Å 260.39Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.55 – 2.90 46.54 – 2.91	Depositor EDS
% Data completeness (in resolution range)	99.7 (46.55-2.90) 99.7 (46.54-2.91)	Depositor EDS
$R_{merge}$	0.22	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.46 (at 2.91Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, $R_{free}$	0.206 , 0.242 0.218 , 0.257	Depositor DCC
$R_{free}$ test set	2249 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	85.7	Xtriage
Anisotropy	0.597	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 84.4	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	10494	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	120.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.02% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, P7M

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	0.52	0/6189	0.74	0/8369
2	B	0.55	0/1734	0.72	0/2349
3	C	0.53	0/1579	0.72	0/2150
4	D	0.51	0/630	0.72	0/841
5	E	0.53	0/533	0.74	0/718
All	All	0.53	0/10665	0.73	0/14427

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 [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	6082	0	6066	47	0
2	B	1690	0	1665	11	0
3	C	1545	0	1520	15	0
4	D	619	0	609	6	0
5	E	520	0	517	11	0
6	B	20	0	0	2	0
7	B	1	0	0	0	0
8	A	7	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	B	6	0	0	0	0
8	C	2	0	0	1	0
8	D	1	0	0	0	0
8	E	1	0	0	0	0
All	All	10494	0	10377	80	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 (80) 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:207:TRP:HB3	1:A:242:GLY:HA2	1.71	0.72
1:A:55:VAL:HG21	1:A:1065:VAL:HG21	1.74	0.70
1:A:53:LYS:HG2	5:E:35:TYR:HB2	1.80	0.62
2:B:70:ASP:HB3	2:B:73:PHE:HD2	1.64	0.62
3:C:518:LYS:HB2	3:C:532:SER:HB3	1.83	0.60
1:A:57:MET:HG3	1:A:61:ILE:HD11	1.84	0.59
1:A:219:VAL:HG12	1:A:231:ILE:HG22	1.86	0.58
2:B:126:VAL:HG21	2:B:185:VAL:HG11	1.87	0.57
3:C:560:MET:HE1	4:D:260:ASN:HD22	1.69	0.57
1:A:843:PRO:HG2	1:A:869:ALA:HB2	1.88	0.56
1:A:755:SER:H	1:A:758:THR:HG22	1.70	0.56
1:A:113:GLY:HA2	8:C:701:HOH:O	2.07	0.55
6:B:301:P7M:CL1	3:C:559:VAL:HG11	2.44	0.55
2:B:193:CYS:HB3	2:B:196:CYS:HB2	1.89	0.55
1:A:374:GLN:HG2	1:A:391:ARG:HB3	1.88	0.54
1:A:793:ILE:HD13	1:A:803:HIS:HB3	1.90	0.54
6:B:301:P7M:CL1	6:B:301:P7M:O2	2.64	0.53
5:E:35:TYR:CE2	5:E:37:PRO:HG3	2.44	0.53
1:A:231:ILE:HG13	1:A:238:THR:OG1	2.10	0.51
1:A:374:GLN:HE21	1:A:391:ARG:HD3	1.77	0.51
1:A:312:GLU:HB2	1:A:327:ARG:HB2	1.93	0.50
1:A:358:PRO:HD2	1:A:380:GLY:HA2	1.94	0.50
1:A:928:ARG:HH22	2:B:115:ASN:HA	1.77	0.50
2:B:61:VAL:HG11	2:B:116:VAL:HG13	1.94	0.49
1:A:130:MET:HE3	1:A:142:VAL:HB	1.95	0.49
1:A:363:CYS:O	1:A:375:LEU:HD23	2.13	0.49
2:B:70:ASP:HB3	2:B:73:PHE:CD2	2.45	0.48
3:C:494:LEU:HD23	3:C:496:LEU:HD23	1.96	0.48
1:A:985:THR:HB	1:A:988:GLU:HG2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:888:VAL:HG22	1:A:905:HIS:HB3	1.95	0.47
1:A:385:GLY:HA3	1:A:719:GLU:O	2.14	0.47
1:A:793:ILE:HD11	1:A:858:LEU:HD22	1.96	0.47
1:A:1047:TRP:HZ3	1:A:1132:VAL:HG13	1.80	0.47
1:A:1136:LEU:O	1:A:1139:ILE:HG12	2.15	0.46
2:B:71:GLU:HA	2:B:74:LEU:HD13	1.97	0.46
1:A:114:ARG:HG2	3:C:565:PRO:HB2	1.97	0.46
1:A:791:LEU:HD23	1:A:858:LEU:HD21	1.97	0.46
1:A:230:ILE:HD11	1:A:285:LEU:HD21	1.98	0.46
1:A:1128:ASP:O	1:A:1131:LYS:HG3	2.15	0.46
1:A:69:PRO:HD2	1:A:72:GLU:HG3	1.97	0.45
3:C:539:VAL:HG13	3:C:542:GLN:HG3	1.98	0.45
4:D:298:PHE:HB2	4:D:304:ALA:HB2	1.97	0.45
5:E:6:LYS:HD3	5:E:6:LYS:H	1.82	0.45
1:A:239:TYR:HB3	1:A:246:LEU:HB2	1.98	0.44
1:A:1104:LYS:HE2	5:E:39:ARG:H	1.82	0.44
3:C:393:TYR:HD2	3:C:431:ARG:HA	1.82	0.44
1:A:167:VAL:HG23	1:A:180:PHE:HB3	1.99	0.44
1:A:88:ILE:HG12	1:A:104:ALA:HB3	1.99	0.44
1:A:21:GLY:HA3	1:A:66:LEU:HD13	1.99	0.44
1:A:45:THR:HG23	1:A:47:GLU:H	1.82	0.44
1:A:124:ILE:HG12	1:A:131:ILE:HG12	2.00	0.43
5:E:44:GLU:O	5:E:45:GLN:HB2	2.17	0.43
2:B:196:CYS:SG	2:B:210:GLN:HG3	2.59	0.43
3:C:476:ILE:HD12	3:C:492:ILE:HG12	2.00	0.43
3:C:474:TYR:HB3	3:C:494:LEU:HD12	2.00	0.43
1:A:250:PRO:HA	1:A:251:PRO:HD3	1.94	0.43
2:B:212:LEU:HD21	3:C:441:LEU:HB2	2.01	0.42
3:C:511:LYS:HB2	3:C:513:TYR:CE1	2.54	0.42
4:D:258:HIS:HB3	4:D:261:ILE:HG12	2.00	0.42
1:A:208:LYS:H	1:A:208:LYS:HD2	1.84	0.42
1:A:151:GLU:HG3	1:A:153:LYS:HE2	2.01	0.42
1:A:141:LYS:HZ1	5:E:49:THR:HG21	1.85	0.42
1:A:1063:LYS:HB2	5:E:37:PRO:HB2	2.02	0.41
1:A:252:ILE:HG13	1:A:252:ILE:H	1.55	0.41
1:A:218:MET:HG2	1:A:232:ILE:HB	2.03	0.41
1:A:141:LYS:NZ	5:E:49:THR:HG21	2.36	0.41
1:A:10:GLN:HB3	1:A:1037:ILE:HB	2.02	0.41
3:C:415:LEU:H	3:C:445:GLN:HE22	1.68	0.41
4:D:279:ILE:HG12	4:D:296:ILE:HG12	2.02	0.41
2:B:90:VAL:HG13	2:B:112:TRP:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:386:TYR:HB3	3:C:452:TYR:CD1	2.56	0.41
4:D:250:MET:HE2	4:D:304:ALA:HB3	2.02	0.41
1:A:740:ILE:N	1:A:740:ILE:HD12	2.36	0.41
5:E:13:LYS:HE2	5:E:13:LYS:H	1.86	0.40
1:A:1022:THR:HA	1:A:1023:PRO:HD3	1.94	0.40
3:C:457:VAL:HG12	3:C:530:THR:CG2	2.52	0.40
2:B:109:LEU:HB2	2:B:128:LEU:HD11	2.03	0.40
3:C:531:VAL:O	5:E:63:TRP:HB2	2.22	0.40
1:A:158:ARG:HB2	5:E:54:ILE:HD12	2.03	0.40
4:D:259:PHE:HB3	4:D:289:ARG:HD3	2.03	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	758/864 (88%)	726 (96%)	31 (4%)	1 (0%)	51	82
2	B	200/276 (72%)	186 (93%)	11 (6%)	3 (2%)	10	34
3	C	184/263 (70%)	162 (88%)	19 (10%)	3 (2%)	9	32
4	D	77/107 (72%)	73 (95%)	2 (3%)	2 (3%)	5	20
5	E	58/126 (46%)	50 (86%)	6 (10%)	2 (3%)	3	15
All	All	1277/1636 (78%)	1197 (94%)	69 (5%)	11 (1%)	17	48

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	436	VAL
4	D	288	GLY
4	D	317	ALA
5	E	39	ARG

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Mol	Chain	Res	Type
5	E	45	GLN
2	B	116	VAL
3	C	424	GLY
3	C	439	GLN
1	A	1023	PRO
2	B	176	ASN
2	B	215	GLY

### 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	677/749 (90%)	643 (95%)	34 (5%)	24	57
2	B	189/242 (78%)	174 (92%)	15 (8%)	12	34
3	C	174/232 (75%)	157 (90%)	17 (10%)	8	24
4	D	66/89 (74%)	59 (89%)	7 (11%)	6	20
5	E	57/112 (51%)	50 (88%)	7 (12%)	4	14
All	All	1163/1424 (82%)	1083 (93%)	80 (7%)	15	41

All (80) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	VAL
1	A	45	THR
1	A	53	LYS
1	A	54	GLU
1	A	97	SER
1	A	111	ARG
1	A	114	ARG
1	A	139	LEU
1	A	142	VAL
1	A	148	ASP
1	A	159	LEU
1	A	208	LYS

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Mol	Chain	Res	Type
1	A	252	ILE
1	A	315	THR
1	A	342	GLU
1	A	375	LEU
1	A	713	ARG
1	A	714	THR
1	A	758	THR
1	A	800	GLU
1	A	842	GLU
1	A	855	ASP
1	A	867	LYS
1	A	887	THR
1	A	888	VAL
1	A	928	ARG
1	A	931	LEU
1	A	939	GLU
1	A	963	ASP
1	A	969	GLU
1	A	993	GLN
1	A	1102	ARG
1	A	1131	LYS
1	A	1134	GLU
2	B	44	LYS
2	B	52	ARG
2	B	66	LYS
2	B	75	TYR
2	B	94	THR
2	B	122	LEU
2	B	127	ARG
2	B	131	ASP
2	B	134	ILE
2	B	140	LEU
2	B	153	ILE
2	B	182	VAL
2	B	192	ARG
2	B	218	LEU
2	B	240	ASP
3	C	392	LEU
3	C	395	VAL
3	C	431	ARG
3	C	433	ARG
3	C	437	GLN

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Mol	Chain	Res	Type
3	C	441	LEU
3	C	445	GLN
3	C	447	THR
3	C	456	GLU
3	C	472	SER
3	C	509	ARG
3	C	530	THR
3	C	532	SER
3	C	558	MET
3	C	559	VAL
3	C	593	GLU
3	C	594	ARG
4	D	250	MET
4	D	271	GLU
4	D	275	ARG
4	D	283	MET
4	D	286	GLU
4	D	306	LYS
4	D	319	ARG
5	E	5	LEU
5	E	6	LYS
5	E	8	LEU
5	E	13	LYS
5	E	19	PHE
5	E	41	TYR
5	E	71	LYS

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

Mol	Chain	Res	Type
1	A	85	ASN
1	A	209	GLN
1	A	319	ASN
1	A	374	GLN
1	A	852	GLN
1	A	859	GLN
2	B	39	GLN
2	B	78	HIS
4	D	260	ASN
4	D	325	HIS
5	E	61	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 1 is 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
6	P7M	B	301	-	19,21,21	3.40	1 (5%)	22,31,31	1.67	4 (18%)

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
6	P7M	B	301	-	-	2/9/15/15	0/2/2/2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	301	P7M	C5-S	-14.59	1.53	1.76

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	301	P7M	C5-S-N	-5.18	101.22	107.27
6	B	301	P7M	C2-C3-C4	-3.74	116.62	122.58
6	B	301	P7M	C4-N-S	-2.34	120.33	123.36
6	B	301	P7M	C9-C3-C4	2.31	124.61	118.43

There are no chirality outliers.

All (2) torsion outliers are listed below:

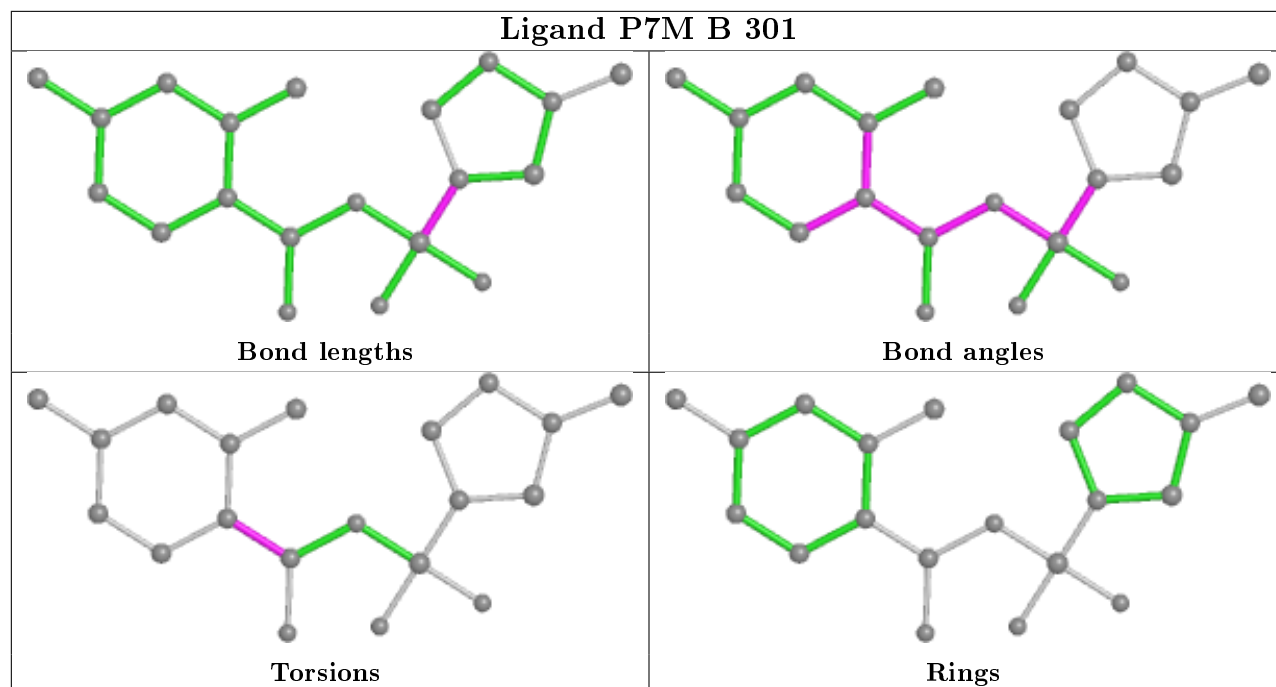
Mol	Chain	Res	Type	Atoms
6	B	301	P7M	C2-C3-C4-N
6	B	301	P7M	C9-C3-C4-N

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	301	P7M	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, 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	772/864 (89%)	0.41	55 (7%) 16 12	69, 120, 174, 190	0
2	B	208/276 (75%)	0.34	8 (3%) 40 36	67, 100, 156, 201	0
3	C	192/263 (73%)	0.17	7 (3%) 42 37	69, 102, 183, 208	0
4	D	79/107 (73%)	0.29	2 (2%) 57 55	89, 114, 145, 155	0
5	E	62/126 (49%)	0.42	5 (8%) 12 9	88, 152, 193, 223	0
All	All	1313/1636 (80%)	0.36	77 (5%) 22 18	67, 114, 174, 223	0

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	C	436	VAL	8.3
1	A	752	LEU	6.3
1	A	1050	LEU	5.5
1	A	1098	LEU	5.4
1	A	1132	VAL	5.1
1	A	1061	VAL	4.3
1	A	1129	LEU	4.0
1	A	794	ILE	3.9
1	A	766	SER	3.9
1	A	1047	TRP	3.8
1	A	246	LEU	3.7
2	B	109	LEU	3.7
2	B	75	TYR	3.6
1	A	821	LEU	3.6
5	E	21	ALA	3.6
1	A	374	GLN	3.5
1	A	745	THR	3.2
1	A	1046	SER	3.1
2	B	33	ARG	3.0
1	A	1054	MET	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	1097	PHE	3.0
2	B	212	LEU	2.9
1	A	919	ASP	2.9
1	A	1133	VAL	2.8
1	A	1102	ARG	2.8
1	A	710	LEU	2.8
1	A	1094	ILE	2.8
1	A	1029	LEU	2.7
1	A	274	GLY	2.7
1	A	1106	GLN	2.7
1	A	1139	ILE	2.7
3	C	425	ARG	2.7
5	E	70	LYS	2.7
1	A	1135	GLU	2.7
1	A	306	GLY	2.7
3	C	386	TYR	2.6
1	A	1039	LEU	2.6
1	A	300	LEU	2.6
1	A	1096	SER	2.6
1	A	836	VAL	2.6
1	A	1010	GLY	2.5
1	A	1140	HIS	2.5
3	C	435	ALA	2.5
3	C	440	TYR	2.5
1	A	253	ILE	2.5
1	A	1053	ASP	2.4
1	A	1057	ARG	2.4
2	B	70	ASP	2.4
1	A	801	VAL	2.4
4	D	250	MET	2.4
4	D	321	MET	2.4
1	A	799	PHE	2.3
1	A	765	VAL	2.3
2	B	171	MET	2.3
1	A	806	GLN	2.3
3	C	541	GLY	2.3
2	B	134	ILE	2.3
1	A	791	LEU	2.3
1	A	364	VAL	2.2
1	A	304	LEU	2.2
5	E	74	GLN	2.2
1	A	258	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
5	E	20	HIS	2.2
1	A	715	VAL	2.2
1	A	389	ILE	2.2
3	C	437	GLN	2.2
1	A	858	LEU	2.1
1	A	1127	ASP	2.1
1	A	1130	ILE	2.1
1	A	232	ILE	2.1
5	E	65	LYS	2.1
1	A	742	VAL	2.1
1	A	336	LEU	2.1
1	A	897	LYS	2.1
2	B	139	TYR	2.1
1	A	356	LEU	2.0
1	A	792	LEU	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](#)

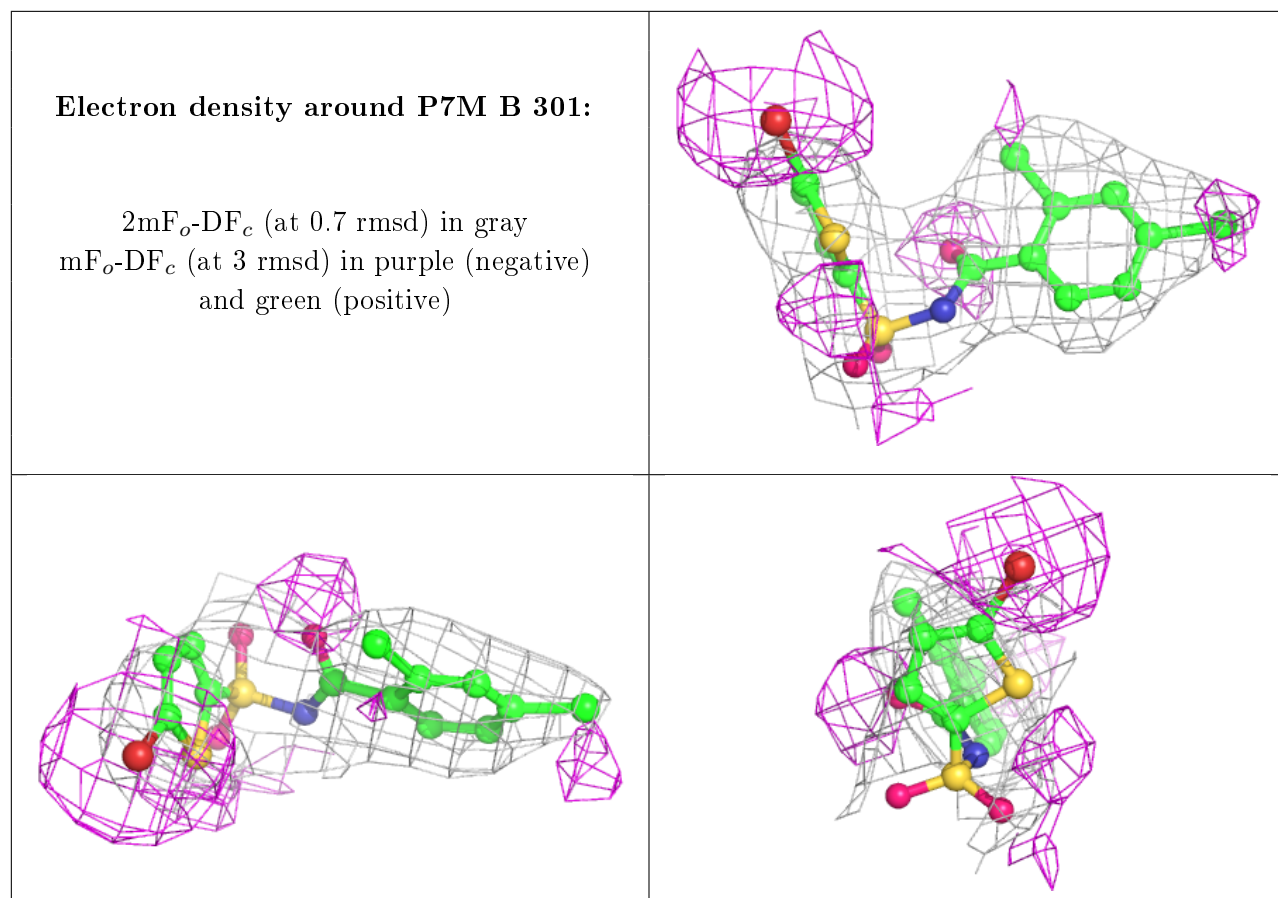
There are no carbohydrates in this entry.

## 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( $\text{\AA}^2$ )	Q<0.9
6	P7M	B	301	20/20	0.91	0.25	85,102,155,184	0
7	ZN	B	302	1/1	0.99	0.15	140,140,140,140	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.



## 6.5 Other polymers [i](#)

There are no such residues in this entry.