



# Full wwPDB X-ray Structure Validation Report ⓘ

Apr 20, 2021 – 12:15 AM JST

PDB ID : 7DQ5  
Title : Crystal structure of HitB in complex with (S)-beta-phenylalanine sulfamoyladenine  
Authors : Kudo, F.; Takahashi, S.; Miyanaga, A.; Nakazawa, Y.; Eguchi, T.  
Deposited on : 2020-12-22  
Resolution : 2.45 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	:	2.18
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)	:	2.18

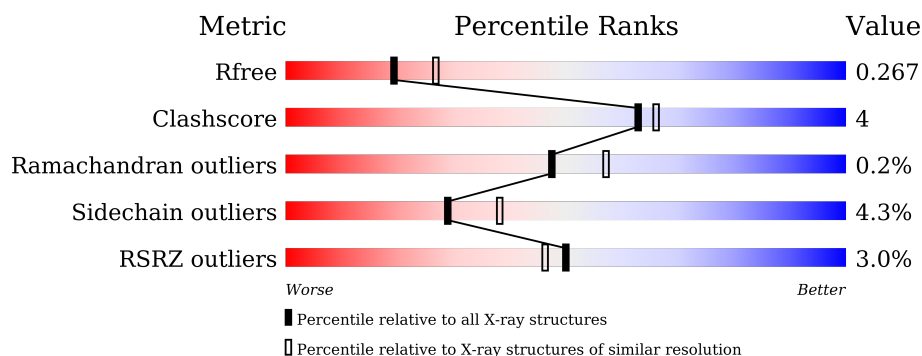
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.45 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	1544 (2.48-2.44)
Clashscore	141614	1613 (2.48-2.44)
Ramachandran outliers	138981	1598 (2.48-2.44)
Sidechain outliers	138945	1598 (2.48-2.44)
RSRZ outliers	127900	1523 (2.48-2.44)

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  $\geq 3$ , 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	549	<div> <div>2%</div> <div> <div></div> <div>76%</div> <div>13%</div> <div>•</div> <div>11%</div> </div> </div>
1	B	549	<div> <div>3%</div> <div> <div></div> <div>69%</div> <div>10%</div> <div>•</div> <div>20%</div> </div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7316 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 Putative ATP-dependent b-aminoacyl-ACP synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	490	Total	C	N	O	S	0	0	0
			3753	2380	674	690	9			
1	B	441	Total	C	N	O	S	0	0	0
			3382	2140	612	623	7			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-15	MET	-	initiating methionine	UNP A0A0F7R6G7
A	-14	ASN	-	expression tag	UNP A0A0F7R6G7
A	-13	HIS	-	expression tag	UNP A0A0F7R6G7
A	-12	LYS	-	expression tag	UNP A0A0F7R6G7
A	-11	VAL	-	expression tag	UNP A0A0F7R6G7
A	-10	HIS	-	expression tag	UNP A0A0F7R6G7
A	-9	HIS	-	expression tag	UNP A0A0F7R6G7
A	-8	HIS	-	expression tag	UNP A0A0F7R6G7
A	-7	HIS	-	expression tag	UNP A0A0F7R6G7
A	-6	HIS	-	expression tag	UNP A0A0F7R6G7
A	-5	HIS	-	expression tag	UNP A0A0F7R6G7
A	-4	ILE	-	expression tag	UNP A0A0F7R6G7
A	-3	GLU	-	expression tag	UNP A0A0F7R6G7
A	-2	GLY	-	expression tag	UNP A0A0F7R6G7
A	-1	ARG	-	expression tag	UNP A0A0F7R6G7
A	0	HIS	-	expression tag	UNP A0A0F7R6G7
B	-15	MET	-	initiating methionine	UNP A0A0F7R6G7
B	-14	ASN	-	expression tag	UNP A0A0F7R6G7
B	-13	HIS	-	expression tag	UNP A0A0F7R6G7
B	-12	LYS	-	expression tag	UNP A0A0F7R6G7
B	-11	VAL	-	expression tag	UNP A0A0F7R6G7
B	-10	HIS	-	expression tag	UNP A0A0F7R6G7
B	-9	HIS	-	expression tag	UNP A0A0F7R6G7
B	-8	HIS	-	expression tag	UNP A0A0F7R6G7
B	-7	HIS	-	expression tag	UNP A0A0F7R6G7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-6	HIS	-	expression tag	UNP A0A0F7R6G7
B	-5	HIS	-	expression tag	UNP A0A0F7R6G7
B	-4	ILE	-	expression tag	UNP A0A0F7R6G7
B	-3	GLU	-	expression tag	UNP A0A0F7R6G7
B	-2	GLY	-	expression tag	UNP A0A0F7R6G7
B	-1	ARG	-	expression tag	UNP A0A0F7R6G7
B	0	HIS	-	expression tag	UNP A0A0F7R6G7

- [illegible]



WORLD WIDE  
PDB  
PROTEIN DATA BANK

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	62	Total 62	O 62	0	0
4	B	49	Total 49	O 49	0	0



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	67.68Å 93.64Å 165.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.48 – 2.45 47.44 – 2.45	Depositor EDS
% Data completeness (in resolution range)	99.9 (47.48-2.45) 99.9 (47.44-2.45)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.70 (at 2.45Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, $R_{free}$	0.210 , 0.260 0.223 , 0.267	Depositor DCC
$R_{free}$ test set	2002 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	42.5	Xtriage
Anisotropy	0.308	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 37.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	7316	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.51% 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: CA, 8PZ

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	0.78	0/3833	0.95	1/5218 (0.0%)
1	B	0.75	1/3455 (0.0%)	0.93	0/4704
All	All	0.77	1/7288 (0.0%)	0.94	1/9922 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	164	GLU	CD-OE1	7.53	1.33	1.25

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	198	ARG	NE-CZ-NH1	5.31	122.96	120.30

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	3753	0	3760	34	0
1	B	3382	0	3378	28	0
2	A	34	0	0	1	0
2	B	34	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	62	0	0	0	0
4	B	49	0	0	1	0
All	All	7316	0	7138	61	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 (61) 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:499:GLY:HA2	1:A:502:ILE:HD12	1.76	0.66
1:A:331:VAL:HG12	1:A:342:LEU:HD21	1.83	0.59
1:B:180:THR:HG23	1:B:182:ARG:H	1.66	0.59
1:B:18:ASP:HA	4:B:702:HOH:O	2.03	0.59
1:A:442:GLY:O	1:A:446:ARG:HB2	2.02	0.58
1:B:221:ASP:OD1	2:B:601:8PZ:N3	2.37	0.58
1:B:196:LEU:HD22	1:B:324:MET:SD	2.45	0.56
1:B:73:ASP:O	1:B:75:ARG:NH1	2.40	0.55
1:A:196:LEU:HD22	1:A:324:MET:SD	2.48	0.54
1:A:58:VAL:HG22	1:A:88:ALA:HA	1.90	0.53
1:A:126:GLN:O	1:A:143:ARG:HA	2.09	0.52
1:B:70:LEU:HA	1:B:158:ARG:HD2	1.91	0.52
1:A:271:ARG:HB3	1:A:272:PRO:HD3	1.93	0.51
1:B:128:GLU:OE1	1:B:150:ARG:NH2	2.30	0.50
1:A:51:TYR:OH	1:A:231:LEU:HA	2.12	0.50
1:A:473:ALA:O	1:A:506:ILE:HA	2.13	0.49
1:A:405:ARG:HH11	1:A:405:ARG:HB3	1.78	0.48
1:A:411:GLY:O	1:A:428:VAL:HG13	2.14	0.48
1:B:75:ARG:HG3	1:B:99:PRO:HG2	1.96	0.48
1:B:126:GLN:O	1:B:143:ARG:HA	2.13	0.47
1:B:51:TYR:OH	1:B:231:LEU:HA	2.14	0.47
1:A:447:ARG:HH21	1:A:450:GLU:HG3	1.80	0.47
1:A:453:GLY:O	1:A:477:VAL:HA	2.15	0.47
1:B:58:VAL:HG22	1:B:88:ALA:HA	1.95	0.47
1:B:200:ILE:HD12	1:B:203:GLN:HG3	1.96	0.47
1:A:379:MET:HG2	1:A:394:LEU:HD11	1.97	0.46
1:B:46:VAL:O	1:B:46:VAL:HG13	2.14	0.46
1:A:262:GLN:HA	1:A:289:GLY:O	2.15	0.46
1:A:70:LEU:HA	1:A:158:ARG:HD2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:PRO:HB3	1:A:170:THR:HG22	1.96	0.46
1:A:347:PRO:CG	1:A:353:VAL:HG23	2.46	0.46
1:B:271:ARG:HB3	1:B:272:PRO:HD3	1.96	0.46
1:A:175:PHE:HA	1:A:184:LYS:O	2.17	0.45
1:B:118:THR:HG22	1:B:384:TRP:CD1	2.51	0.45
1:A:73:ASP:OD2	1:B:400:ASP:HB2	2.16	0.45
1:A:221:ASP:OD1	2:A:601:8PZ:N3	2.51	0.44
1:A:369:ALA:HA	1:A:414:ALA:O	2.18	0.43
1:B:302:LEU:CD2	1:B:342:LEU:HD11	2.48	0.43
1:A:206:ILE:HG22	1:A:233:THR:HG21	2.00	0.43
1:B:68:LEU:HD21	1:B:151:VAL:HG21	2.01	0.43
1:B:175:PHE:HA	1:B:184:LYS:O	2.19	0.43
1:A:221:ASP:OD2	1:A:321:THR:HA	2.19	0.43
1:A:341:ARG:NH1	1:A:415:TYR:OH	2.51	0.43
1:B:379:MET:HG2	1:B:394:LEU:HD11	2.00	0.43
1:A:133:ALA:O	1:A:135:VAL:HG23	2.18	0.43
1:B:369:ALA:HA	1:B:414:ALA:O	2.19	0.43
1:A:405:ARG:HB3	1:A:405:ARG:NH1	2.34	0.42
1:A:196:LEU:HD11	1:A:325:ALA:HB3	2.02	0.42
1:B:262:GLN:HA	1:B:289:GLY:O	2.20	0.42
1:A:222:PHE:CE2	1:A:293:THR:HG22	2.54	0.42
1:B:103:VAL:HG11	1:B:112:LEU:HD13	2.02	0.42
1:B:186:VAL:HG11	1:B:321:THR:HG22	2.02	0.41
1:B:222:PHE:CE2	1:B:293:THR:HG22	2.55	0.41
1:A:241:PRO:HD2	1:A:244:GLU:HG3	2.02	0.41
1:B:178:GLY:O	1:B:180:THR:O	2.38	0.41
1:B:221:ASP:OD2	1:B:321:THR:HA	2.20	0.41
1:A:252:LEU:HD21	1:A:273:VAL:HG11	2.03	0.41
1:B:266:VAL:HG23	1:B:268:SER:HB2	2.02	0.41
1:A:79:GLU:HA	1:A:103:VAL:O	2.21	0.40
1:A:371:GLN:HG2	1:A:373:HIS:CE1	2.57	0.40
1:A:314:ILE:HB	1:A:331:VAL:HG22	2.04	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	478/549 (87%)	456 (95%)	21 (4%)	1 (0%)	47	57
1	B	431/549 (78%)	413 (96%)	17 (4%)	1 (0%)	47	57
All	All	909/1098 (83%)	869 (96%)	38 (4%)	2 (0%)	47	57

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	324	MET
1	B	324	MET

### 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	392/438 (90%)	373 (95%)	19 (5%)	25	33
1	B	353/438 (81%)	340 (96%)	13 (4%)	34	45
All	All	745/876 (85%)	713 (96%)	32 (4%)	29	38

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	ARG
1	A	30	SER
1	A	55	ARG
1	A	67	GLU
1	A	196	LEU
1	A	222	PHE
1	A	297	PHE
1	A	338	ASP
1	A	358	GLU
1	A	371	GLN

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Mol	Chain	Res	Type
1	A	396	SER
1	A	405	ARG
1	A	421	GLU
1	A	427	ARG
1	A	428	VAL
1	A	440	GLU
1	A	472	HIS
1	A	485	ASP
1	A	522	ARG
1	B	9	ARG
1	B	30	SER
1	B	57	ARG
1	B	67	GLU
1	B	156	ARG
1	B	196	LEU
1	B	222	PHE
1	B	297	PHE
1	B	358	GLU
1	B	365	GLU
1	B	405	ARG
1	B	421	GLU
1	B	427	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry

Of 4 ligands modelled in this entry, 2 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	8PZ	B	601	-	34,37,37	0.77	1 (2%)	36,54,54	0.97	3 (8%)
2	8PZ	A	601	-	34,37,37	0.91	3 (8%)	36,54,54	0.91	2 (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	8PZ	B	601	-	-	3/18/48/48	0/4/4/4
2	8PZ	A	601	-	-	2/18/48/48	0/4/4/4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	8PZ	C13-N4	-2.67	1.33	1.38
2	A	601	8PZ	C13-N4	-2.33	1.34	1.38
2	A	601	8PZ	O3-S1	-2.19	1.40	1.42
2	A	601	8PZ	S1-N4	2.10	1.63	1.59

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	8PZ	C2-C3-N7	2.62	124.34	120.35
2	B	601	8PZ	C13-N4-S1	-2.42	120.38	124.30
2	A	601	8PZ	O6-C16-C15	-2.19	104.71	111.05
2	B	601	8PZ	C11-C12-C13	2.09	118.76	112.73
2	A	601	8PZ	C1-C2-N6	2.05	111.53	109.40

There are no chirality outliers.

All (5) torsion outliers are listed below:

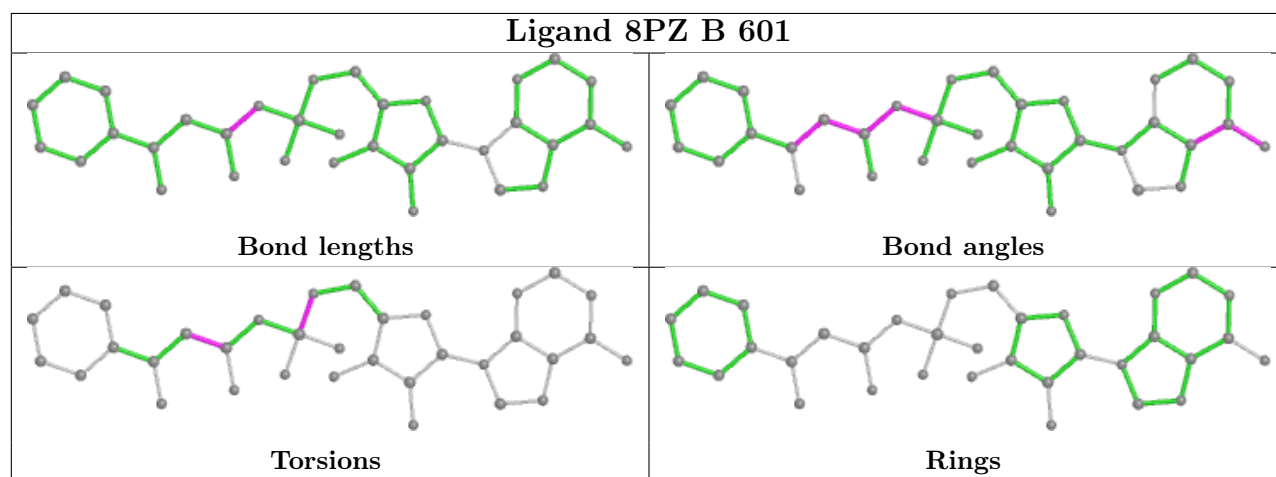
Mol	Chain	Res	Type	Atoms
2	B	601	8PZ	C11-C12-C13-O1
2	B	601	8PZ	C11-C12-C13-N4
2	A	601	8PZ	C11-C12-C13-N4
2	B	601	8PZ	C14-O4-S1-N4
2	A	601	8PZ	C11-C12-C13-O1

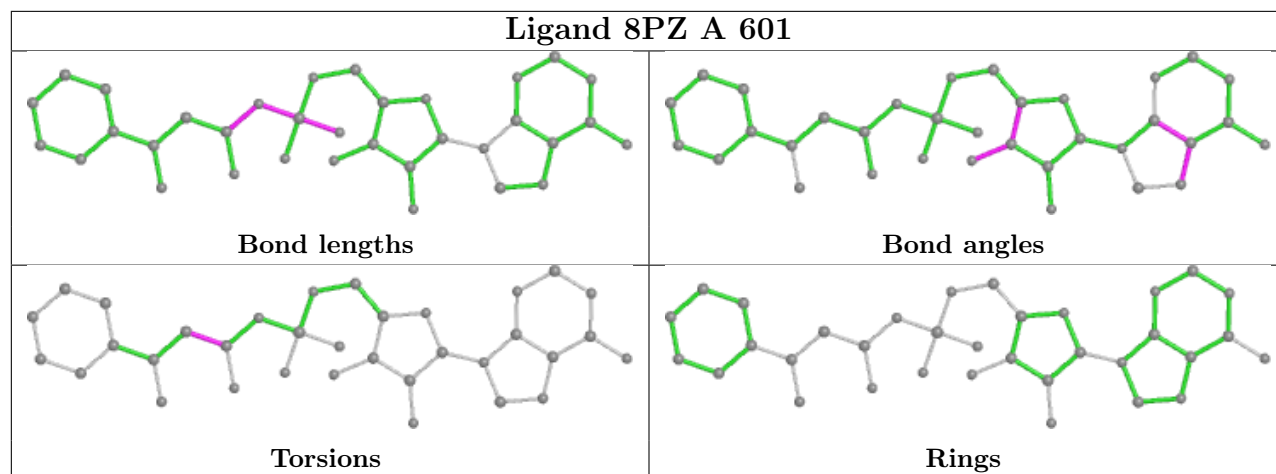
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	8PZ	1	0
2	A	601	8PZ	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, 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	490/549 (89%)	-0.01	12 (2%) 59 54	33, 46, 82, 103	0
1	B	441/549 (80%)	0.11	16 (3%) 42 39	36, 52, 77, 89	0
All	All	931/1098 (84%)	0.05	28 (3%) 50 46	33, 49, 79, 103	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	487	ALA	4.8
1	A	500	TYR	4.7
1	B	460	LEU	4.1
1	B	472	HIS	4.1
1	B	473	ALA	3.7
1	A	472	HIS	3.6
1	B	461	LEU	3.2
1	B	47	ARG	3.1
1	B	280	LEU	3.1
1	A	495	ASP	3.1
1	A	488	LYS	2.9
1	B	146	ALA	2.8
1	A	486	LYS	2.7
1	B	340	GLU	2.7
1	A	491	ALA	2.6
1	A	470	VAL	2.4
1	B	252	LEU	2.4
1	B	363	VAL	2.2
1	B	281	LEU	2.2
1	A	493	CYS	2.2
1	B	279	GLU	2.1
1	B	370	GLY	2.1
1	A	474	PHE	2.1
1	B	474	PHE	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	477	VAL	2.1
1	A	504	ALA	2.1
1	B	366	ILE	2.1
1	B	512	ILE	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](#)

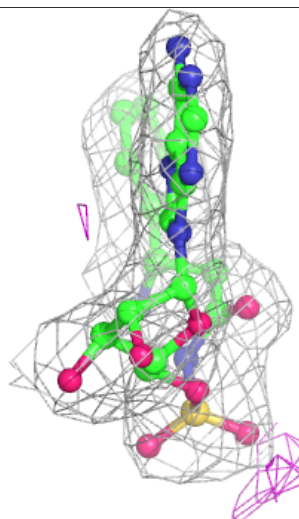
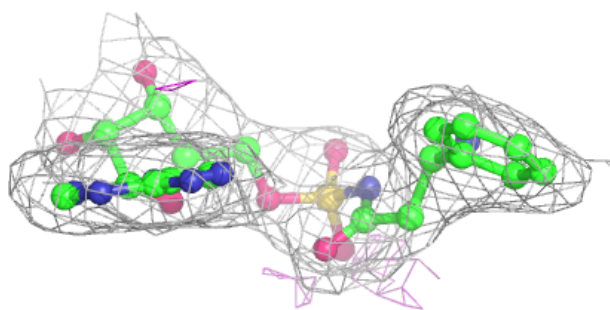
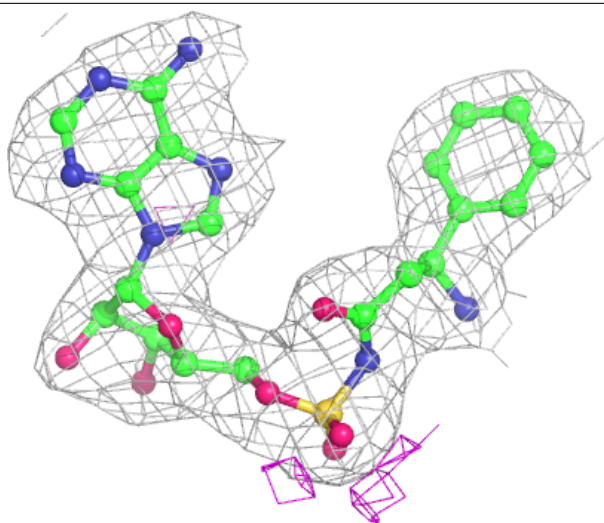
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 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
3	CA	A	602	1/1	0.94	0.10	62,62,62,62	0
3	CA	B	602	1/1	0.94	0.18	67,67,67,67	0
2	8PZ	A	601	34/34	0.97	0.12	32,36,38,39	0
2	8PZ	B	601	34/34	0.97	0.12	37,43,47,48	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.

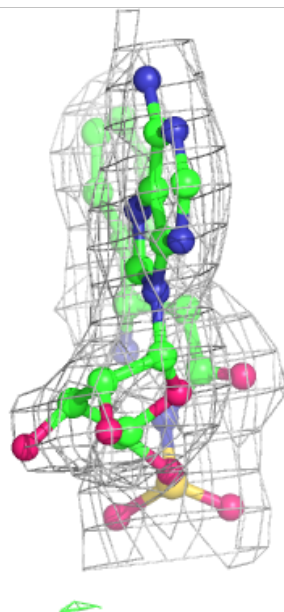
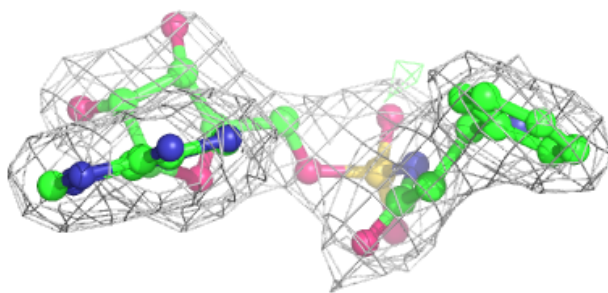
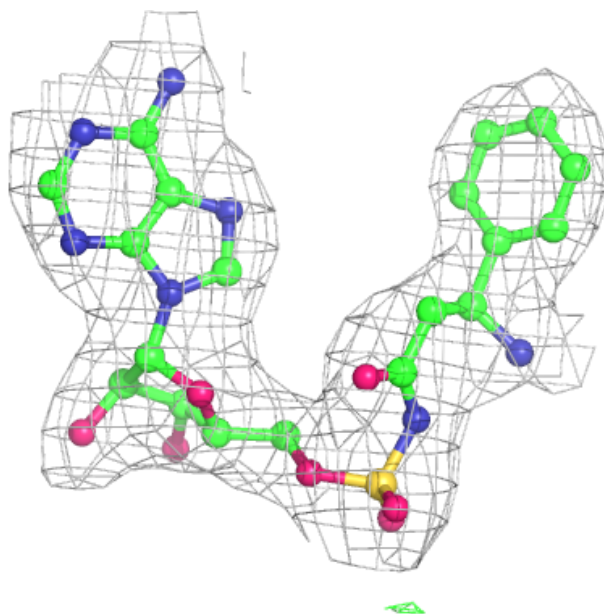
**Electron density around 8PZ A 601:**

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



**Electron density around 8PZ B 601:**

$2mF_o-DF_c$  (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.