



# Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 12:18 am BST

PDB ID : 3SGI  
Title : Crystal structure of DNA ligase A BRCT domain deleted mutant of Mycobacterium tuberculosis  
Authors : Kukshal, V.; Ravishankar, R.  
Deposited on : 2011-06-15  
Resolution : 3.50 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

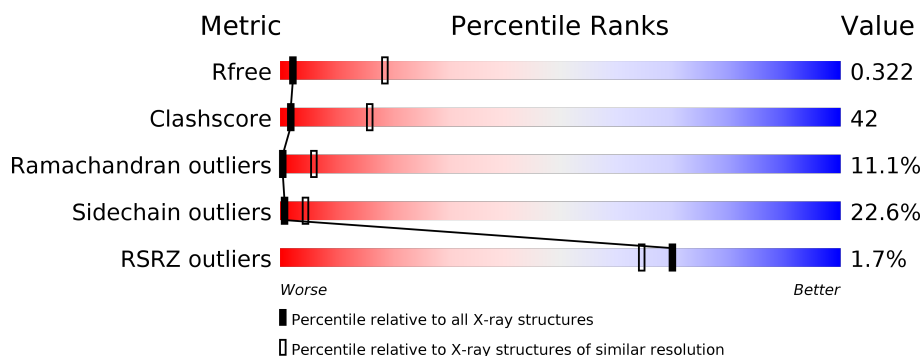
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.50 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	1659 (3.60-3.40)
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)
RSRZ outliers	127900	1559 (3.60-3.40)

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	615	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3221 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 ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	408	3176	1993	578	599	6	0	0	0

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	VAL	-	EXPRESSION TAG	UNP P63973
A	606	GLY	-	EXPRESSION TAG	UNP P63973
A	607	SER	-	EXPRESSION TAG	UNP P63973
A	608	ARG	-	EXPRESSION TAG	UNP P63973
A	609	SER	-	EXPRESSION TAG	UNP P63973
A	610	HIS	-	EXPRESSION TAG	UNP P63973
A	611	HIS	-	EXPRESSION TAG	UNP P63973
A	612	HIS	-	EXPRESSION TAG	UNP P63973
A	613	HIS	-	EXPRESSION TAG	UNP P63973
A	614	HIS	-	EXPRESSION TAG	UNP P63973
A	615	HIS	-	EXPRESSION TAG	UNP P63973

- Molecule 2 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: C<sub>10</sub>H<sub>14</sub>N<sub>5</sub>O<sub>7</sub>P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			22	10	5	6	1		

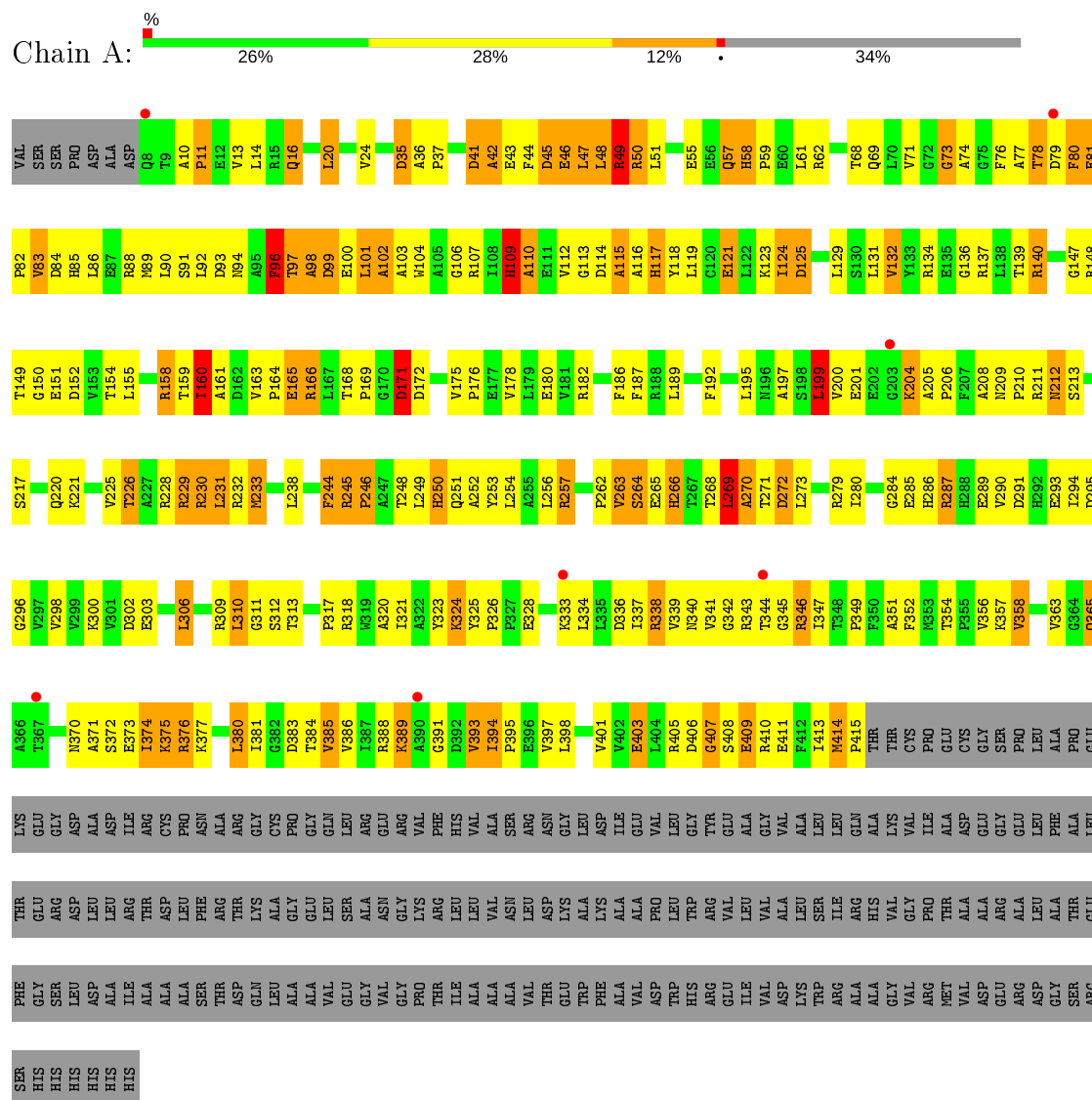
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	23	Total	O	0	0
			23	23		

### 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 ligase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	52.44Å 99.56Å 144.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.78 – 3.50 49.78 – 3.50	Depositor EDS
% Data completeness (in resolution range)	89.3 (49.78-3.50) 89.3 (49.78-3.50)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.24	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.24 (at 3.48Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.311 , 0.322 0.310 , 0.322	Depositor DCC
$R_{free}$ test set	435 reflections (4.85%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	66.1	Xtriage
Anisotropy	0.387	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 90.5	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	0.77	EDS
Total number of atoms	3221	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.24% 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: AMP

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	0.54	0/3243	0.82	6/4411 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	199	LEU	CA-CB-CG	6.46	130.15	115.30
1	A	171	ASP	CB-CG-OD2	6.10	123.79	118.30
1	A	269	LEU	CA-CB-CG	5.42	127.77	115.30
1	A	250	HIS	N-CA-C	5.34	125.42	111.00
1	A	171	ASP	CB-CG-OD1	-5.28	113.55	118.30
1	A	123	LYS	CD-CE-NZ	5.08	123.38	111.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	45	ASP	Peptide
1	A	96	PHE	Peptide

## 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	3176	0	3117	264	1
2	A	22	0	12	2	0
3	A	23	0	0	2	0
All	All	3221	0	3129	265	1

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 42.

All (265) 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:48:LEU:N	1:A:49:ARG:HB3	1.35	1.39
1:A:248:THR:OG1	1:A:251:GLN:HG3	1.44	1.16
1:A:48:LEU:H	1:A:49:ARG:CB	1.58	1.16
1:A:49:ARG:HG3	1:A:50:ARG:H	1.07	1.13
1:A:346:ARG:HH21	1:A:346:ARG:HG2	1.12	1.12
1:A:269:LEU:HA	1:A:270:ALA:HB3	1.24	1.12
1:A:80:PHE:HB2	1:A:151:GLU:HB3	1.25	1.12
1:A:46:GLU:HA	1:A:49:ARG:HD2	1.29	1.09
1:A:97:THR:HG23	1:A:98:ALA:HB3	1.32	1.07
1:A:160:ILE:HB	1:A:161:ALA:HA	1.08	1.06
1:A:264:SER:CB	1:A:265:GLU:HA	1.86	1.03
1:A:160:ILE:CB	1:A:161:ALA:HA	1.88	1.03
1:A:49:ARG:CG	1:A:50:ARG:H	1.72	1.03
1:A:264:SER:OG	1:A:265:GLU:HA	1.60	1.02
1:A:265:GLU:HB2	1:A:266:HIS:HB2	1.46	0.97
1:A:284:GLY:H	1:A:287:ARG:HB3	1.27	0.96
1:A:269:LEU:HA	1:A:270:ALA:CB	1.95	0.96
1:A:248:THR:OG1	1:A:251:GLN:CG	2.15	0.95
1:A:77:ALA:N	1:A:78:THR:HA	1.81	0.94
1:A:45:ASP:HB3	1:A:46:GLU:O	1.67	0.94
1:A:195:LEU:HD11	1:A:229:ARG:HD2	1.50	0.92
1:A:264:SER:HB3	1:A:265:GLU:HG3	1.51	0.91
1:A:339:VAL:HG12	1:A:340:ASN:H	1.35	0.91
1:A:49:ARG:HG3	1:A:50:ARG:N	1.82	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77:ALA:H	1:A:78:THR:HA	1.35	0.90
1:A:265:GLU:CB	1:A:266:HIS:HB2	2.03	0.88
1:A:160:ILE:HB	1:A:161:ALA:CA	2.00	0.85
1:A:46:GLU:CA	1:A:49:ARG:HD2	2.07	0.84
1:A:106:GLY:O	1:A:109:HIS:HB2	1.79	0.83
1:A:89:MET:HG3	1:A:89:MET:O	1.78	0.83
1:A:334:LEU:HD11	1:A:351:ALA:HB1	1.62	0.81
1:A:45:ASP:HB3	1:A:46:GLU:C	2.01	0.80
1:A:77:ALA:H	1:A:78:THR:CA	1.94	0.78
1:A:265:GLU:HB2	1:A:266:HIS:CB	2.13	0.78
1:A:346:ARG:NH2	1:A:346:ARG:HG2	1.82	0.77
1:A:83:VAL:HG22	1:A:152:ASP:HB2	1.68	0.76
1:A:97:THR:HG23	1:A:98:ALA:CB	2.12	0.75
1:A:346:ARG:CG	1:A:346:ARG:HH21	1.98	0.75
1:A:20:LEU:O	1:A:24:VAL:HG23	1.87	0.75
1:A:48:LEU:N	1:A:49:ARG:CB	2.32	0.74
1:A:80:PHE:CB	1:A:151:GLU:HB3	2.14	0.73
1:A:209:ASN:OD1	1:A:212:ASN:HB3	1.87	0.73
1:A:13:VAL:HA	1:A:16:GLN:HG2	1.69	0.73
1:A:134:ARG:HH11	1:A:140:ARG:NH2	1.86	0.73
1:A:118:TYR:O	1:A:270:ALA:HB3	1.89	0.72
1:A:265:GLU:CB	1:A:266:HIS:CB	2.68	0.72
1:A:121:GLU:OE2	1:A:300:LYS:HD2	1.90	0.72
1:A:97:THR:CG2	1:A:98:ALA:HB3	2.15	0.72
1:A:372:SER:O	1:A:376:ARG:HG2	1.90	0.71
1:A:77:ALA:H	1:A:79:ASP:N	1.88	0.71
1:A:264:SER:CB	1:A:265:GLU:CA	2.67	0.71
1:A:77:ALA:H	1:A:79:ASP:H	1.38	0.71
1:A:374:ILE:O	1:A:376:ARG:N	2.25	0.70
1:A:74:ALA:N	1:A:80:PHE:CZ	2.59	0.69
1:A:373:GLU:O	1:A:374:ILE:O	2.11	0.69
1:A:125:ASP:OD2	1:A:295:ASP:OD1	2.11	0.69
1:A:195:LEU:CD1	1:A:229:ARG:HD2	2.20	0.69
1:A:48:LEU:H	1:A:49:ARG:HB3	0.66	0.68
1:A:257:ARG:CZ	1:A:257:ARG:HB3	2.24	0.68
1:A:284:GLY:N	1:A:287:ARG:HB3	2.05	0.67
1:A:248:THR:O	1:A:251:GLN:HB2	1.94	0.67
1:A:73:GLY:O	1:A:80:PHE:HZ	1.78	0.67
1:A:393:VAL:HG13	1:A:394:ILE:H	1.59	0.67
1:A:380:LEU:CD1	1:A:409:GLU:HG2	2.25	0.66
1:A:339:VAL:HG11	1:A:347:ILE:HD13	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:381:ILE:O	1:A:409:GLU:HB2	1.95	0.66
1:A:246:PRO:HG2	1:A:252:ALA:HB2	1.78	0.66
1:A:250:HIS:O	1:A:250:HIS:CG	2.48	0.66
1:A:20:LEU:HD22	1:A:51:LEU:HB2	1.78	0.65
1:A:205:ALA:HB1	1:A:206:PRO:HD2	1.77	0.65
1:A:91:SER:OG	1:A:92:LEU:N	2.30	0.64
1:A:339:VAL:HG12	1:A:340:ASN:N	2.10	0.64
1:A:160:ILE:CB	1:A:161:ALA:CA	2.68	0.64
1:A:77:ALA:HB3	1:A:221:LYS:HG3	1.79	0.64
1:A:303:GLU:HB2	1:A:306:LEU:HD23	1.79	0.64
1:A:336:ASP:HB3	1:A:338:ARG:HH11	1.62	0.64
1:A:287:ARG:HB2	1:A:294:ILE:HD11	1.79	0.64
1:A:336:ASP:HB3	1:A:338:ARG:NH1	2.12	0.64
1:A:49:ARG:CG	1:A:50:ARG:N	2.47	0.64
1:A:312:SER:CB	1:A:317:PRO:HA	2.28	0.63
1:A:49:ARG:HG3	1:A:50:ARG:HD2	1.79	0.63
1:A:160:ILE:HG22	1:A:161:ALA:C	2.19	0.63
1:A:264:SER:HB3	1:A:265:GLU:HA	1.77	0.63
1:A:269:LEU:CA	1:A:270:ALA:CB	2.74	0.63
1:A:77:ALA:N	1:A:78:THR:CA	2.54	0.62
1:A:55:GLU:O	1:A:59:PRO:HA	2.00	0.62
1:A:187:PHE:HA	1:A:230:ARG:NH1	2.14	0.62
1:A:134:ARG:HE	1:A:140:ARG:HH21	1.49	0.61
1:A:265:GLU:HB2	1:A:266:HIS:CA	2.31	0.61
1:A:46:GLU:HA	1:A:49:ARG:CD	2.20	0.61
1:A:328:GLU:OE1	1:A:388:ARG:NH1	2.34	0.60
1:A:47:LEU:HA	1:A:49:ARG:HG2	1.82	0.60
1:A:58:HIS:ND1	1:A:58:HIS:N	2.50	0.60
1:A:306:LEU:HA	1:A:309:ARG:HB3	1.85	0.59
1:A:363:VAL:HG21	1:A:395:PRO:HG2	1.85	0.59
1:A:134:ARG:HH11	1:A:140:ARG:HH22	1.50	0.58
1:A:118:TYR:O	1:A:270:ALA:CB	2.51	0.58
1:A:264:SER:HB3	1:A:265:GLU:CG	2.29	0.58
1:A:57:GLN:HA	1:A:59:PRO:HD3	1.85	0.58
1:A:102:ALA:O	1:A:106:GLY:N	2.32	0.58
1:A:265:GLU:HB3	1:A:266:HIS:HB2	1.84	0.58
1:A:220:GLN:NE2	1:A:225:VAL:HG11	2.19	0.57
1:A:199:LEU:O	1:A:200:VAL:HB	2.04	0.57
1:A:233:MET:O	1:A:262:PRO:HB2	2.05	0.57
1:A:257:ARG:NH1	1:A:257:ARG:HB3	2.20	0.57
1:A:339:VAL:CG1	1:A:340:ASN:H	2.15	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:311:GLY:O	1:A:318:ARG:HB2	2.05	0.57
1:A:41:ASP:HB3	1:A:44:PHE:O	2.04	0.57
1:A:46:GLU:C	1:A:49:ARG:HD2	2.24	0.57
1:A:13:VAL:HG12	1:A:61:LEU:HD11	1.88	0.56
1:A:76:PHE:HA	1:A:80:PHE:H	1.71	0.56
1:A:101:LEU:O	1:A:103:ALA:N	2.35	0.56
1:A:217:SER:O	1:A:226:THR:HG23	2.07	0.55
1:A:116:ALA:O	1:A:117:HIS:HB2	2.06	0.55
1:A:200:VAL:O	1:A:205:ALA:HA	2.06	0.55
1:A:113:GLY:O	1:A:115:ALA:N	2.39	0.55
1:A:264:SER:HB3	1:A:265:GLU:CA	2.36	0.55
1:A:374:ILE:HG22	1:A:375:LYS:H	1.72	0.55
1:A:42:ALA:HA	1:A:43:GLU:C	2.26	0.55
1:A:76:PHE:HB3	1:A:81:GLU:HB3	1.88	0.55
1:A:204:LYS:N	3:A:628:HOH:O	2.31	0.55
1:A:336:ASP:OD1	1:A:338:ARG:HD2	2.07	0.55
1:A:48:LEU:CA	1:A:49:ARG:HB3	2.32	0.55
1:A:98:ALA:O	1:A:99:ASP:CG	2.45	0.55
1:A:325:TYR:HB3	1:A:326:PRO:CD	2.36	0.55
1:A:265:GLU:HB3	1:A:266:HIS:CD2	2.42	0.54
1:A:13:VAL:HA	1:A:16:GLN:CG	2.38	0.54
1:A:265:GLU:HB3	1:A:266:HIS:CG	2.43	0.54
1:A:101:LEU:HD12	1:A:102:ALA:H	1.73	0.54
1:A:165:GLU:HB2	1:A:166:ARG:HE	1.72	0.54
1:A:112:VAL:HG23	1:A:310:LEU:HD13	1.90	0.53
1:A:225:VAL:O	1:A:228:ARG:HG2	2.07	0.53
2:A:616:AMP:N3	2:A:616:AMP:H2'	2.23	0.53
1:A:200:VAL:HG12	1:A:201:GLU:HG2	1.90	0.53
1:A:78:THR:O	1:A:220:GLN:O	2.27	0.53
1:A:158:ARG:HH12	1:A:160:ILE:HD11	1.74	0.53
1:A:233:MET:HA	1:A:233:MET:HE3	1.90	0.53
1:A:96:PHE:HD2	1:A:99:ASP:OD1	1.92	0.53
1:A:107:ARG:HH11	1:A:110:ALA:HB2	1.74	0.53
1:A:265:GLU:HB2	1:A:266:HIS:C	2.29	0.53
1:A:85:HIS:CD2	1:A:147:GLY:O	2.62	0.53
1:A:349:PRO:HG3	1:A:374:ILE:HD11	1.89	0.53
1:A:380:LEU:O	1:A:383:ASP:HB2	2.09	0.53
1:A:158:ARG:NH1	1:A:165:GLU:CD	2.63	0.52
1:A:244:PHE:CG	1:A:245:ARG:N	2.77	0.52
1:A:325:TYR:HB3	1:A:326:PRO:HD2	1.91	0.52
1:A:82:PRO:HA	1:A:150:GLY:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:220:GLN:HE21	1:A:225:VAL:HG11	1.75	0.51
1:A:77:ALA:H	1:A:78:THR:C	2.13	0.51
1:A:139:THR:O	1:A:154:THR:HG21	2.11	0.51
1:A:391:GLY:HA3	1:A:393:VAL:N	2.25	0.51
1:A:83:VAL:CG2	1:A:152:ASP:HB2	2.39	0.51
1:A:197:ALA:HA	1:A:200:VAL:HG23	1.93	0.51
1:A:406:ASP:C	1:A:408:SER:H	2.14	0.50
1:A:132:VAL:HG23	1:A:140:ARG:O	2.11	0.50
1:A:47:LEU:O	1:A:48:LEU:HB2	2.10	0.50
1:A:333:LYS:HD3	1:A:384:THR:HG23	1.93	0.50
1:A:112:VAL:HG23	1:A:310:LEU:CD1	2.42	0.50
1:A:94:ASN:ND2	1:A:324:LYS:HE2	2.27	0.50
1:A:100:GLU:HA	1:A:101:LEU:HB3	1.93	0.50
1:A:337:ILE:HA	1:A:351:ALA:HA	1.93	0.50
1:A:78:THR:O	1:A:221:LYS:HA	2.12	0.49
1:A:116:ALA:O	1:A:117:HIS:ND1	2.44	0.49
1:A:116:ALA:O	1:A:117:HIS:CB	2.59	0.49
1:A:370:ASN:O	1:A:374:ILE:HG13	2.12	0.49
1:A:101:LEU:C	1:A:103:ALA:H	2.15	0.49
1:A:11:PRO:HD2	1:A:13:VAL:HG23	1.95	0.49
1:A:296:GLY:HA2	1:A:325:TYR:CD2	2.47	0.49
1:A:45:ASP:HA	1:A:46:GLU:HG2	1.95	0.49
1:A:129:LEU:CD1	1:A:131:LEU:HG	2.44	0.48
1:A:210:PRO:HA	1:A:213:SER:HB3	1.95	0.48
1:A:77:ALA:N	1:A:79:ASP:H	2.07	0.48
1:A:199:LEU:CD1	1:A:200:VAL:H	2.26	0.48
1:A:230:ARG:HE	1:A:231:LEU:H	1.61	0.48
1:A:125:ASP:HB2	1:A:293:GLU:HG2	1.95	0.48
1:A:136:GLY:O	1:A:166:ARG:HA	2.14	0.48
1:A:45:ASP:CB	1:A:46:GLU:O	2.49	0.48
1:A:48:LEU:O	1:A:48:LEU:HG	2.13	0.48
1:A:250:HIS:H	1:A:251:GLN:HB2	1.79	0.47
1:A:97:THR:O	1:A:323:TYR:CZ	2.67	0.47
1:A:101:LEU:CG	1:A:102:ALA:H	2.27	0.47
1:A:125:ASP:OD1	1:A:211:ARG:HB2	2.14	0.47
1:A:265:GLU:HB3	1:A:266:HIS:CB	2.39	0.47
1:A:217:SER:OG	1:A:229:ARG:NH1	2.48	0.47
1:A:248:THR:HB	1:A:302:ASP:CG	2.33	0.47
1:A:96:PHE:HB2	1:A:99:ASP:OD1	2.14	0.47
1:A:226:THR:HG22	1:A:231:LEU:HD11	1.96	0.47
1:A:405:ARG:C	1:A:407:GLY:H	2.18	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:339:VAL:HG11	1:A:347:ILE:CD1	2.43	0.47
1:A:101:LEU:CD1	1:A:102:ALA:H	2.28	0.47
1:A:101:LEU:C	1:A:103:ALA:N	2.68	0.47
1:A:380:LEU:HD13	1:A:409:GLU:HG2	1.96	0.46
1:A:312:SER:HB3	1:A:317:PRO:HA	1.98	0.46
1:A:92:LEU:HD13	1:A:298:VAL:HG21	1.97	0.46
1:A:403:GLU:CD	1:A:403:GLU:H	2.18	0.46
1:A:385:VAL:HG13	1:A:397:VAL:HG13	1.98	0.46
1:A:132:VAL:HG21	1:A:140:ARG:HD2	1.96	0.46
1:A:186:PHE:CE1	1:A:232:ARG:HB2	2.51	0.46
1:A:342:GLY:HA2	1:A:343:ARG:NH1	2.31	0.46
1:A:374:ILE:O	1:A:375:LYS:C	2.54	0.46
1:A:393:VAL:HG13	1:A:394:ILE:N	2.27	0.46
1:A:211:ARG:O	1:A:211:ARG:HD2	2.16	0.45
1:A:13:VAL:CA	1:A:16:GLN:HG2	2.45	0.45
1:A:168:THR:HA	1:A:169:PRO:HD3	1.72	0.45
1:A:298:VAL:HG11	2:A:616:AMP:C6	2.51	0.45
1:A:104:TRP:CZ2	1:A:320:ALA:HA	2.52	0.45
1:A:74:ALA:N	1:A:80:PHE:HZ	2.11	0.45
1:A:257:ARG:HH12	1:A:263:VAL:H	1.65	0.45
1:A:257:ARG:NH1	1:A:263:VAL:H	2.15	0.44
1:A:86:LEU:HD12	1:A:180:GLU:HB2	1.99	0.44
1:A:250:HIS:HB3	3:A:618:HOH:O	2.16	0.44
1:A:101:LEU:HG	1:A:102:ALA:H	1.81	0.44
1:A:230:ARG:HH12	1:A:232:ARG:HG2	1.83	0.44
1:A:10:ALA:HA	1:A:11:PRO:HD3	1.71	0.44
1:A:175:VAL:HA	1:A:176:PRO:HD3	1.93	0.43
1:A:287:ARG:NH1	1:A:325:TYR:HB3	2.33	0.43
1:A:73:GLY:C	1:A:80:PHE:HZ	2.20	0.43
1:A:246:PRO:HB3	1:A:251:GLN:HB3	2.00	0.43
1:A:104:TRP:HZ2	1:A:320:ALA:HA	1.83	0.43
1:A:160:ILE:HG12	1:A:160:ILE:H	1.51	0.43
1:A:230:ARG:NE	1:A:231:LEU:H	2.16	0.43
1:A:414:MET:HA	1:A:415:PRO:HD3	1.76	0.43
1:A:265:GLU:CB	1:A:266:HIS:CA	2.95	0.43
1:A:338:ARG:HG2	1:A:352:PHE:CD2	2.54	0.43
1:A:339:VAL:HG21	1:A:414:MET:HG2	2.01	0.43
1:A:131:LEU:HD21	1:A:163:VAL:HG21	2.00	0.43
1:A:36:ALA:N	1:A:37:PRO:HD3	2.34	0.42
1:A:414:MET:SD	1:A:415:PRO:HD2	2.58	0.42
1:A:79:ASP:O	1:A:80:PHE:HB3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:100:GLU:H	1:A:100:GLU:HG2	1.59	0.42
1:A:104:TRP:CD1	1:A:321:ILE:HG23	2.54	0.42
1:A:347:ILE:HG13	1:A:347:ILE:H	1.70	0.42
1:A:287:ARG:HB2	1:A:294:ILE:CD1	2.47	0.42
1:A:386:VAL:HG23	1:A:398:LEU:HB2	2.02	0.42
1:A:257:ARG:HD2	1:A:263:VAL:HG22	2.02	0.42
1:A:230:ARG:CZ	1:A:230:ARG:HB2	2.49	0.42
1:A:73:GLY:HA3	1:A:74:ALA:HA	1.76	0.42
1:A:124:ILE:H	1:A:124:ILE:HG12	1.39	0.42
1:A:217:SER:O	1:A:226:THR:CG2	2.68	0.42
1:A:373:GLU:C	1:A:374:ILE:O	2.58	0.42
1:A:391:GLY:HA3	1:A:393:VAL:H	1.83	0.42
1:A:164:PRO:HB2	1:A:166:ARG:O	2.19	0.42
1:A:104:TRP:CD2	1:A:321:ILE:HG13	2.55	0.42
1:A:163:VAL:HA	1:A:164:PRO:HD3	1.96	0.42
1:A:182:ARG:HB3	1:A:182:ARG:CZ	2.50	0.42
1:A:250:HIS:HD2	1:A:253:TYR:HB2	1.85	0.42
1:A:272:ASP:OD2	1:A:273:LEU:N	2.52	0.41
1:A:280:ILE:HG23	1:A:323:TYR:CE2	2.54	0.41
1:A:286:HIS:O	1:A:289:GLU:HG2	2.20	0.41
1:A:293:GLU:HG3	1:A:328:GLU:OE2	2.19	0.41
1:A:406:ASP:O	1:A:408:SER:N	2.53	0.41
1:A:248:THR:HB	1:A:302:ASP:OD2	2.20	0.41
1:A:371:ALA:HA	1:A:374:ILE:HD12	2.03	0.41
1:A:375:LYS:C	1:A:377:LYS:H	2.24	0.41
1:A:89:MET:HB3	1:A:147:GLY:O	2.20	0.41
1:A:226:THR:CG2	1:A:231:LEU:HD11	2.51	0.40
1:A:90:LEU:HD13	1:A:313:THR:O	2.21	0.40
1:A:134:ARG:HD2	1:A:139:THR:HG21	2.03	0.40
1:A:204:LYS:HB3	1:A:205:ALA:H	1.63	0.40
1:A:233:MET:HA	1:A:233:MET:CE	2.51	0.40
1:A:358:VAL:HG13	1:A:389:LYS:NZ	2.36	0.40
1:A:248:THR:OG1	1:A:251:GLN:HG2	2.10	0.40
1:A:312:SER:HA	1:A:318:ARG:H	1.86	0.40
1:A:35:ASP:OD1	1:A:35:ASP:N	2.54	0.40
1:A:363:VAL:HG22	1:A:365:GLN:H	1.87	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:140:ARG:CZ	1:A:171:ASP:OD1[4_455]	2.15	0.05

## 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	406/615 (66%)	304 (75%)	57 (14%)	45 (11%)	<b>0</b> <b>6</b>

All (45) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	41	ASP
1	A	46	GLU
1	A	47	LEU
1	A	48	LEU
1	A	49	ARG
1	A	88	ARG
1	A	99	ASP
1	A	114	ASP
1	A	115	ALA
1	A	117	HIS
1	A	160	ILE
1	A	171	ASP
1	A	172	ASP
1	A	245	ARG
1	A	270	ALA
1	A	291	ASP
1	A	374	ILE
1	A	375	LYS
1	A	393	VAL
1	A	414	MET
1	A	11	PRO
1	A	57	GLN
1	A	69	GLN

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Mol	Chain	Res	Type
1	A	73	GLY
1	A	101	LEU
1	A	269	LEU
1	A	413	ILE
1	A	42	ALA
1	A	109	HIS
1	A	204	LYS
1	A	208	ALA
1	A	244	PHE
1	A	246	PRO
1	A	345	GLY
1	A	376	ARG
1	A	407	GLY
1	A	80	PHE
1	A	83	VAL
1	A	98	ALA
1	A	159	THR
1	A	231	LEU
1	A	344	THR
1	A	102	ALA
1	A	110	ALA
1	A	71	VAL

### 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	328/492 (67%)	254 (77%)	74 (23%)	<b>1</b> <b>4</b>

All (74) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	LEU
1	A	16	GLN
1	A	20	LEU
1	A	35	ASP

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Mol	Chain	Res	Type
1	A	49	ARG
1	A	50	ARG
1	A	58	HIS
1	A	62	ARG
1	A	68	THR
1	A	78	THR
1	A	81	GLU
1	A	84	ASP
1	A	93	ASP
1	A	96	PHE
1	A	97	THR
1	A	109	HIS
1	A	119	LEU
1	A	121	GLU
1	A	124	ILE
1	A	125	ASP
1	A	132	VAL
1	A	137	ARG
1	A	140	ARG
1	A	148	ARG
1	A	149	THR
1	A	155	LEU
1	A	158	ARG
1	A	160	ILE
1	A	165	GLU
1	A	166	ARG
1	A	178	VAL
1	A	189	LEU
1	A	192	PHE
1	A	199	LEU
1	A	212	ASN
1	A	226	THR
1	A	229	ARG
1	A	230	ARG
1	A	233	MET
1	A	238	LEU
1	A	249	LEU
1	A	254	LEU
1	A	256	LEU
1	A	257	ARG
1	A	263	VAL
1	A	264	SER

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Mol	Chain	Res	Type
1	A	266	HIS
1	A	268	THR
1	A	271	THR
1	A	272	ASP
1	A	279	ARG
1	A	285	GLU
1	A	287	ARG
1	A	290	VAL
1	A	306	LEU
1	A	310	LEU
1	A	324	LYS
1	A	338	ARG
1	A	341	VAL
1	A	346	ARG
1	A	354	THR
1	A	356	VAL
1	A	357	LYS
1	A	358	VAL
1	A	365	GLN
1	A	380	LEU
1	A	385	VAL
1	A	389	LYS
1	A	394	ILE
1	A	401	VAL
1	A	403	GLU
1	A	409	GLU
1	A	410	ARG
1	A	411	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	GLN
1	A	212	ASN
1	A	220	GLN
1	A	236	HIS
1	A	240	HIS
1	A	250	HIS
1	A	266	HIS
1	A	340	ASN

### 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 ⓘ

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
2	AMP	A	616	1	19,24,25	1.54	5 (26%)	17,35,38	1.82	6 (35%)

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	AMP	A	616	1	-	0/3/25/26	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	616	AMP	C2'-C1'	-2.70	1.49	1.53
2	A	616	AMP	C5-N7	-2.36	1.31	1.39
2	A	616	AMP	P-O5'	-2.33	1.56	1.62
2	A	616	AMP	O4'-C4'	-2.28	1.39	1.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	616	AMP	C3'-C4'	-2.23	1.47	1.53

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	616	AMP	N3-C2-N1	-3.42	123.33	128.68
2	A	616	AMP	O3'-C3'-C4'	-2.64	103.41	111.05
2	A	616	AMP	C3'-C2'-C1'	2.50	104.74	100.98
2	A	616	AMP	C4-C5-N7	-2.23	107.07	109.40
2	A	616	AMP	O2'-C2'-C3'	-2.19	104.75	111.82
2	A	616	AMP	O4'-C4'-C3'	-2.12	100.92	105.11

There are no chirality outliers.

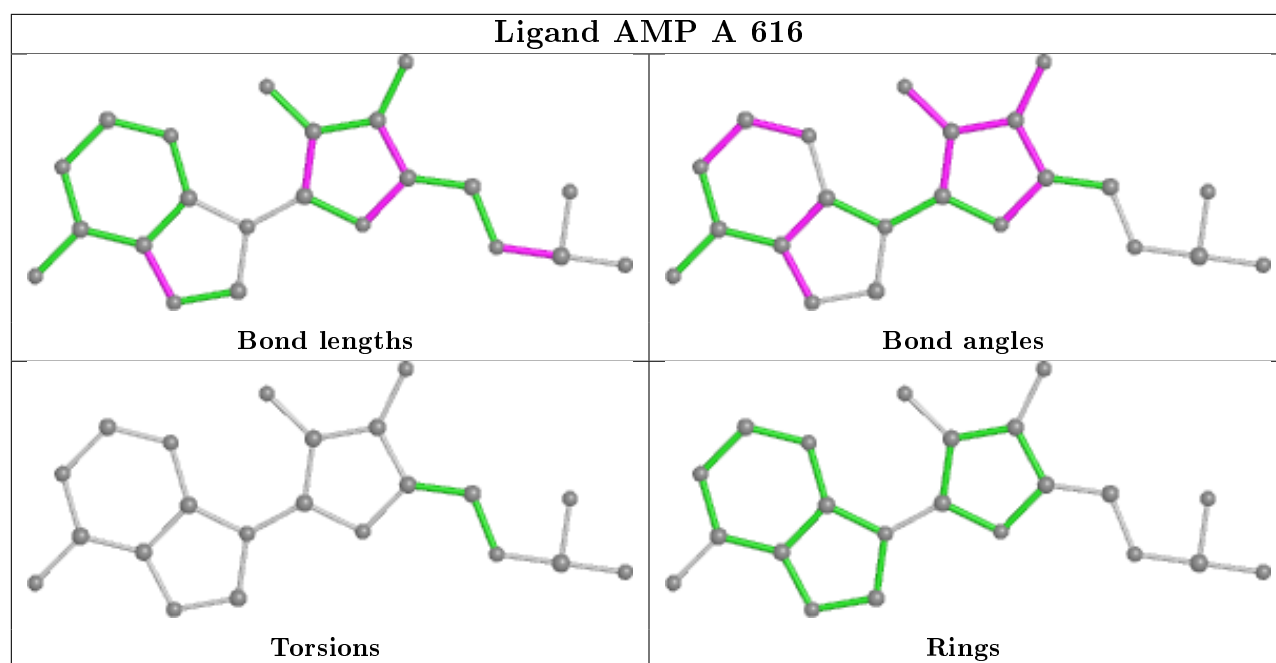
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	616	AMP	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	408/615 (66%)	-0.07	7 (1%) 70 64	23, 52, 74, 78	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	367	THR	3.0
1	A	79	ASP	2.9
1	A	8	GLN	2.5
1	A	390	ALA	2.5
1	A	203	GLY	2.4
1	A	333	LYS	2.3
1	A	344	THR	2.3

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

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

### 6.3 Carbohydrates ⓘ

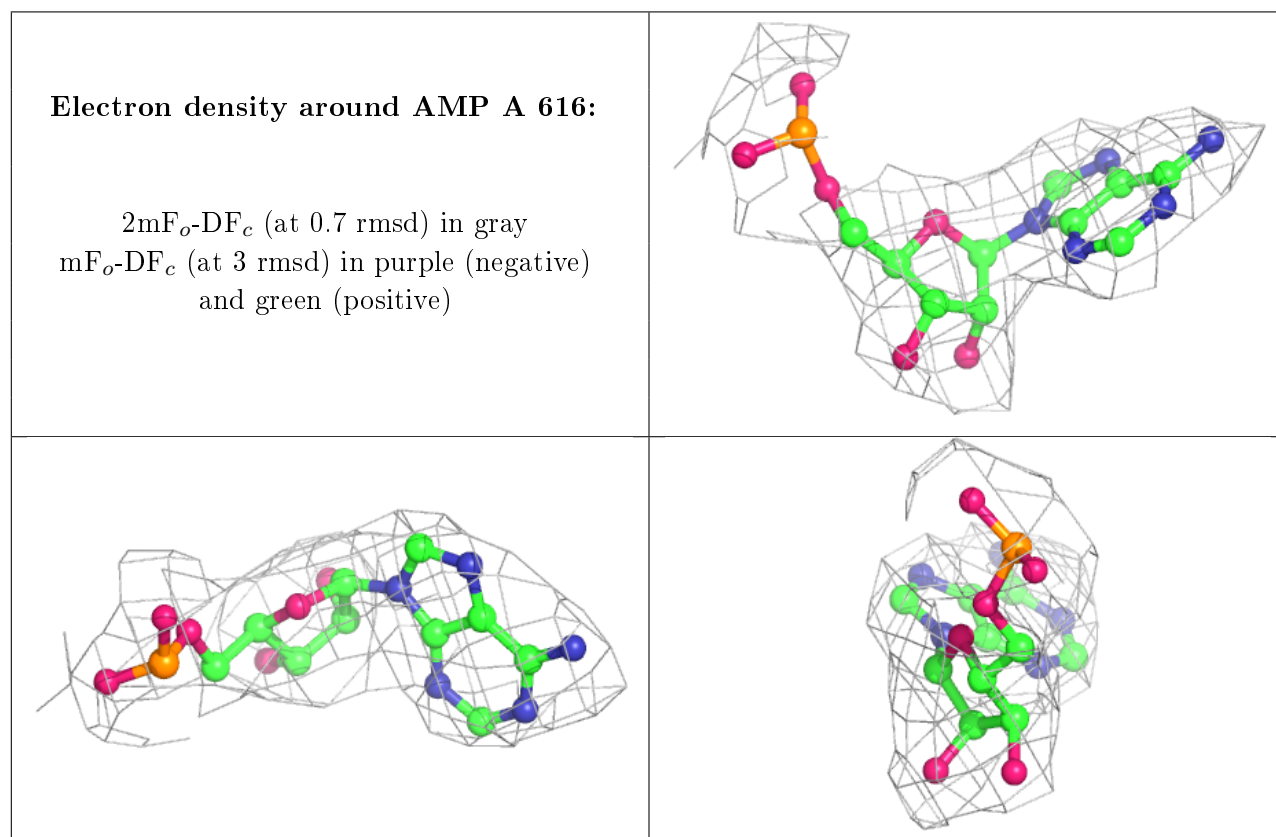
There are no carbohydrates in this entry.

### 6.4 Ligands ⓘ

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
2	AMP	A	616	22/23	0.95	0.18	45,49,55,56	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.