



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 05:54 PM GMT

PDB ID : 4JSP  
Title : structure of mTORDeltaN-mLST8-ATPgammaS-Mg complex  
Authors : Pavletich, N.P.; Yang, H.  
Deposited on : 2013-03-22  
Resolution : 3.30 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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  
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

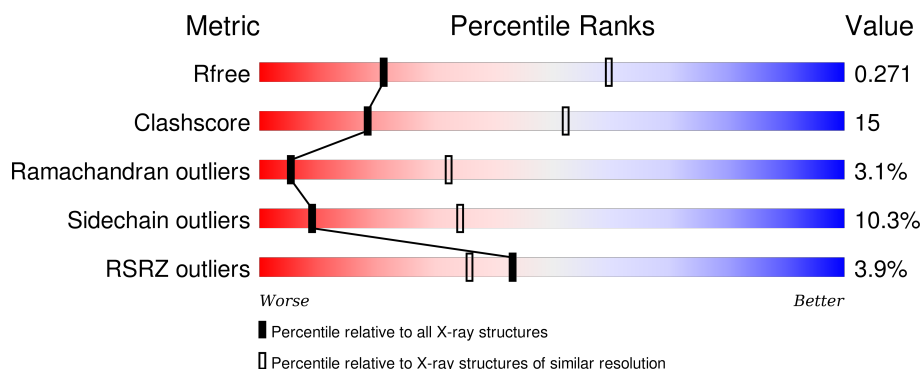
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.30 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))
$R_{free}$	91344	2060 (3.40-3.20)
Clashscore	102246	1058 (3.38-3.22)
Ramachandran outliers	100387	1038 (3.38-3.22)
Sidechain outliers	100360	1037 (3.38-3.22)
RSRZ outliers	91569	2070 (3.40-3.20)

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	1174	<div> <div>5%</div> <div>60% 26% • 10%</div> </div>
1	B	1174	<div> <div>3%</div> <div>60% 26% • 10%</div> </div>
2	C	326	<div> <div>2%</div> <div>53% 36% 7% • •</div> </div>
2	D	326	<div> <div>%</div> <div>51% 37% 8% • •</div> </div>

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 22194 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.

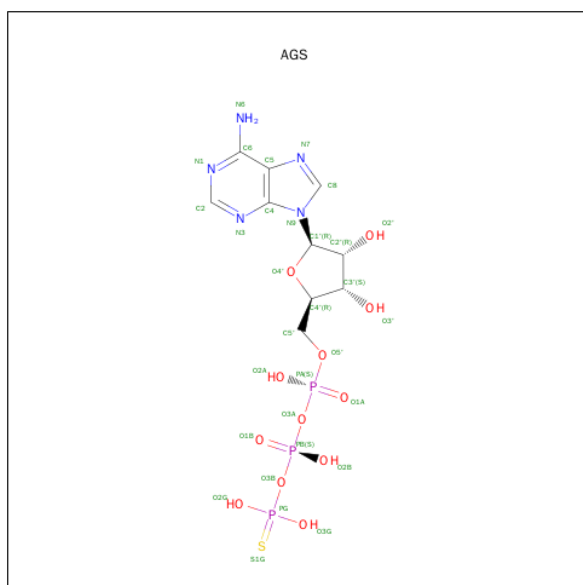
- Molecule 1 is a protein called Serine/threonine-protein kinase mTOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	1058	Total	C	N	O	S	0	0	0
			8608	5472	1521	1552	63			
1	A	1058	Total	C	N	O	S	0	0	0
			8608	5472	1521	1552	63			

- Molecule 2 is a protein called Target of rapamycin complex subunit LST8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	317	Total	C	N	O	S	0	0	0
			2456	1526	436	476	18			
2	C	317	Total	C	N	O	S	0	0	0
			2456	1526	436	476	18			

- Molecule 3 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (three-letter code: AGS) (formula:  $C_{10}H_{16}N_5O_{12}P_3S$ ).

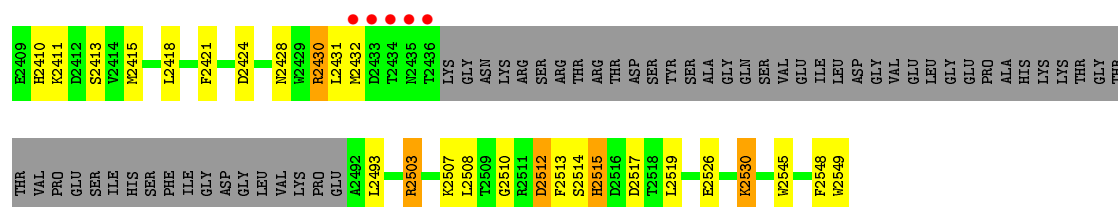


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	B	1	Total	C	N	O	P	S	0	0
			31	10	5	12	3	1		
3	A	1	Total	C	N	O	P	S	0	0
			31	10	5	12	3	1		

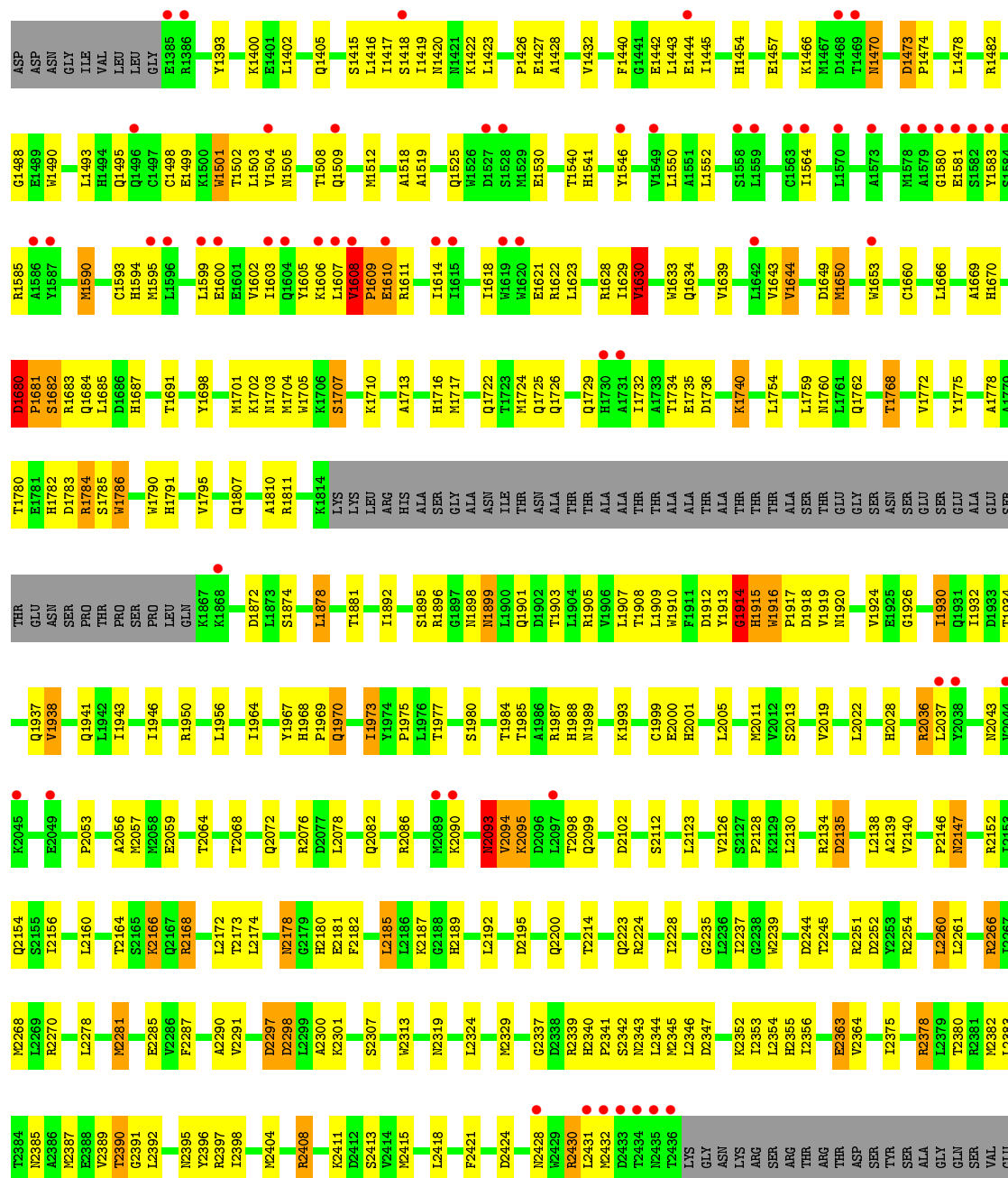
- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

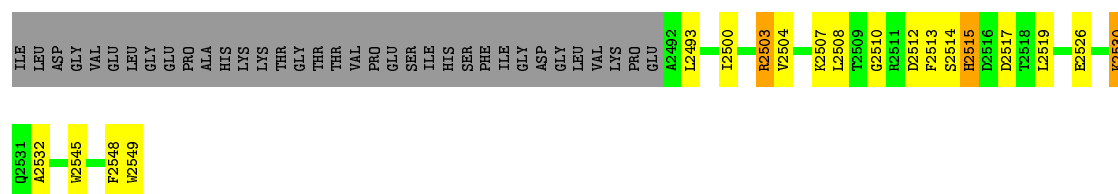
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	2	Total	Mg	0	0
			2	2		
4	A	2	Total	Mg	0	0
			2	2		



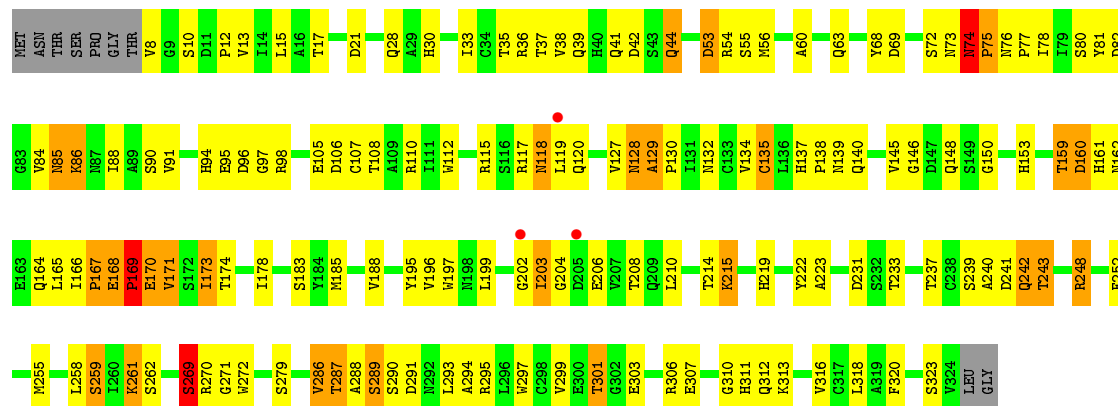


• Molecule 1: Serine/threonine-protein kinase mTOR

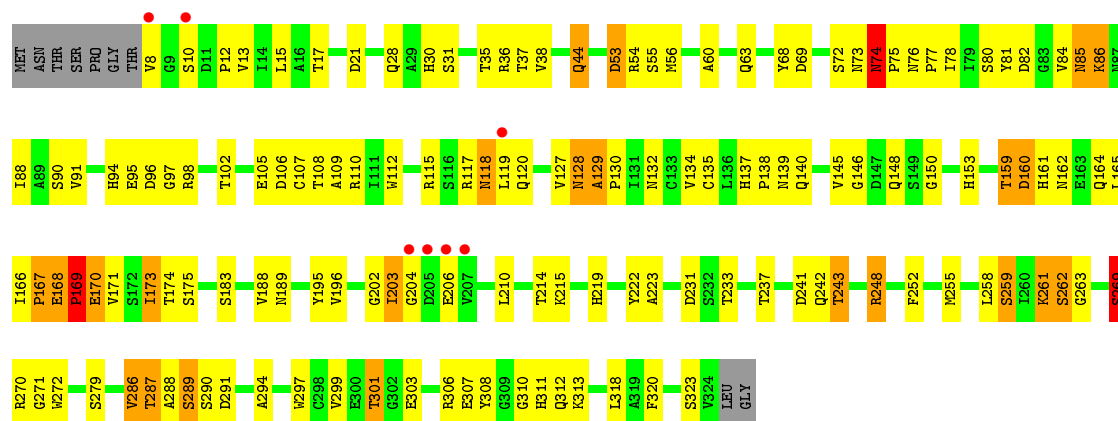




- Molecule 2: Target of rapamycin complex subunit LST8



- Molecule 2: Target of rapamycin complex subunit LST8



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 2 <sub>1</sub> 2 <sub>1</sub> 2 <sub>1</sub>	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	139.40 Å   163.20 Å   207.80 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	100.00 – 3.30 74.20 – 3.19	Depositor EDS
% Data completeness (in resolution range)	89.9 (100.00-3.30) 87.4 (74.20-3.19)	Depositor EDS
$R_{merge}$	0.15	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.69 (at 3.19 Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, $R_{free}$	0.233   ,   0.268 0.234   ,   0.271	Depositor DCC
$R_{free}$ test set	1770 reflections (2.81%)	DCC
Wilson B-factor (Å <sup>2</sup> )	51.6	Xtriage
Anisotropy	0.559	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 33.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	4 of 77327 reflections (0.005%)	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	22194	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 40.83 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 2.5835e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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, 0.375 respectively for untwinned datasets, and 0.333, 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: MG, AGS

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	0.35	0/8805	0.60	2/11920 (0.0%)
1	B	0.36	0/8805	0.60	1/11920 (0.0%)
2	C	0.38	0/2514	0.66	0/3426
2	D	0.43	0/2514	0.68	0/3426
All	All	0.37	0/22638	0.62	3/30692 (0.0%)

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	1
1	B	0	1
2	C	0	1
2	D	0	1
All	All	0	4

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1915	HIS	N-CA-C	5.96	127.09	111.00
1	B	1915	HIS	N-CA-C	5.88	126.89	111.00
1	A	1610	GLU	N-CA-C	5.77	126.58	111.00

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1914	GLY	Peptide
1	B	1914	GLY	Peptide
2	C	169	PRO	Peptide
2	D	169	PRO	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	8608	0	8593	237	6
1	B	8608	0	8593	233	0
2	C	2456	0	2341	110	0
2	D	2456	0	2341	119	0
3	A	31	0	12	1	0
3	B	31	0	12	1	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
All	All	22194	0	21892	683	6

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 15.

The worst 5 of 683 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:2503:ARG:HH11	1:A:2507:LYS:HE2	1.11	1.13
1:B:2503:ARG:HH11	1:B:2507:LYS:HE2	1.10	1.07
2:C:76:ASN:HB3	2:C:77:PRO:HD2	1.38	1.06
2:C:231:ASP:HB3	2:C:233:THR:OG1	1.59	1.02
2:D:231:ASP:HB3	2:D:233:THR:OG1	1.61	1.00

The worst 5 of 6 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:1607:LEU:N	1:A:1609:PRO:O[2_554]	1.39	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1607:LEU:CA	1:A:1609:PRO:O[2_554]	1.77	0.43
1:A:1608:VAL:O	1:A:1608:VAL:O[2_554]	1.84	0.36
1:A:1606:LYS:C	1:A:1609:PRO:O[2_554]	1.92	0.28
1:A:1607:LEU:N	1:A:1609:PRO:C[2_554]	2.13	0.07

## 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	1052/1174 (90%)	938 (89%)	85 (8%)	29 (3%)	6	34
1	B	1052/1174 (90%)	940 (89%)	84 (8%)	28 (3%)	6	35
2	C	315/326 (97%)	270 (86%)	31 (10%)	14 (4%)	3	22
2	D	315/326 (97%)	273 (87%)	27 (9%)	15 (5%)	3	20
All	All	2734/3000 (91%)	2421 (89%)	227 (8%)	86 (3%)	5	32

5 of 86 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1630	VAL
1	B	1650	MET
1	B	1937	GLN
1	B	1970	GLN
1	B	2094	VAL

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	931/1024 (91%)	848 (91%)	83 (9%)	12	43
1	B	931/1024 (91%)	845 (91%)	86 (9%)	11	40
2	C	269/276 (98%)	230 (86%)	39 (14%)	4	18
2	D	269/276 (98%)	229 (85%)	40 (15%)	4	17
All	All	2400/2600 (92%)	2152 (90%)	248 (10%)	9	34

5 of 248 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	214	THR
1	A	1608	VAL
2	C	169	PRO
2	D	243	THR
2	D	312	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 81 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	161	HIS
1	A	1719	HIS
2	C	137	HIS
2	D	198	ASN
1	A	1594	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

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
3	AGS	A	3000	4	24,33,33	2.30	3 (12%)	28,52,52	2.21	5 (17%)
3	AGS	B	3000	4	24,33,33	2.33	4 (16%)	28,52,52	1.95	5 (17%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	AGS	A	3000	4	-	0/15/38/38	0/3/3/3
3	AGS	B	3000	4	-	0/15/38/38	0/3/3/3

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	3000	AGS	O4'-C1'	2.23	1.44	1.41
3	B	3000	AGS	PG-O2G	2.25	1.63	1.55
3	A	3000	AGS	PG-O2G	2.27	1.63	1.55
3	A	3000	AGS	C5-C4	2.96	1.47	1.40
3	B	3000	AGS	C5-C4	3.02	1.47	1.40

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	3000	AGS	N3-C2-N1	-7.78	122.94	128.89
3	B	3000	AGS	N3-C2-N1	-7.09	123.46	128.89
3	A	3000	AGS	PA-O3A-PB	-4.95	118.84	132.73
3	A	3000	AGS	PB-O3B-PG	-3.56	120.73	132.67
3	B	3000	AGS	PA-O3A-PB	-3.23	123.66	132.73

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	3000	AGS	1	0
3	B	3000	AGS	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	1058/1174 (90%)	0.21	62 (5%) 26 20	30, 64, 156, 230	0
1	B	1058/1174 (90%)	0.11	35 (3%) 50 43	25, 54, 134, 177	0
2	C	317/326 (97%)	0.08	7 (2%) 65 59	36, 63, 113, 157	0
2	D	317/326 (97%)	-0.01	3 (0%) 85 82	27, 43, 94, 127	0
All	All	2750/3000 (91%)	0.13	107 (3%) 43 36	25, 57, 143, 230	0

The worst 5 of 107 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1580	GLY	6.8
1	A	1599	LEU	6.5
1	B	2433	ASP	5.9
1	A	1385	GLU	5.8
1	B	2434	THR	5.6

### 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	AGS	B	3000	31/31	0.92	0.21	-0.25	50,56,79,84	0
3	AGS	A	3000	31/31	0.92	0.19	-1.01	51,60,81,85	0
4	MG	A	3002	1/1	0.82	0.21	-	72,72,72,72	0
4	MG	B	3001	1/1	0.87	0.25	-	63,63,63,63	0
4	MG	B	3002	1/1	0.88	0.10	-	69,69,69,69	0
4	MG	A	3001	1/1	0.91	0.16	-	66,66,66,66	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.