



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 16, 2021 – 02:29 PM EDT

PDB ID : 6V0O  
Title : PRMT5 bound to the PBM peptide from pICln  
Authors : McMillan, B.J.; Raymond, D.D.  
Deposited on : 2019-11-19  
Resolution : 2.86 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 : 2.23.1  
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) : 2.23.1

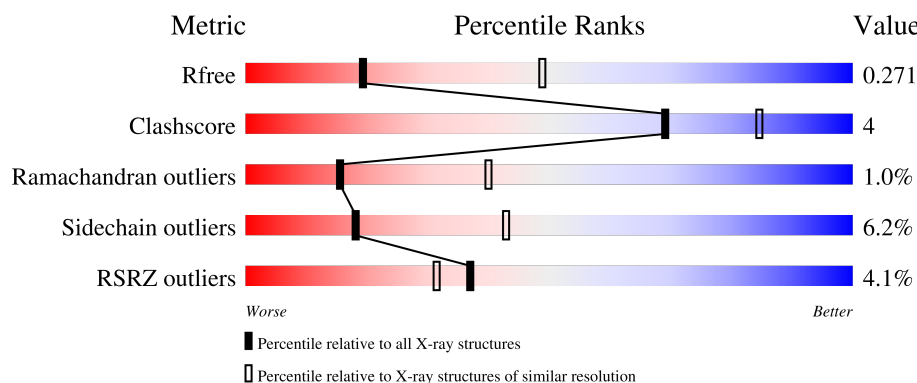
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.86 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	3168 (2.90-2.82)
Clashscore	141614	3438 (2.90-2.82)
Ramachandran outliers	138981	3348 (2.90-2.82)
Sidechain outliers	138945	3351 (2.90-2.82)
RSRZ outliers	127900	3103 (2.90-2.82)

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	637	<div> <div>2%</div> <div> <div></div> <div>85%</div> <div>13%</div> <div>..</div> </div> </div>
2	B	342	<div> <div>7%</div> <div> <div></div> <div>75%</div> <div>13%</div> <div>• 10%</div> </div> </div>
3	D	13	<div> <div></div> <div> <div>62%</div> <div>15%</div> <div>23%</div> </div> </div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7526 atoms, of which 23 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 Protein arginine N-methyltransferase 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	625	Total	C	N	O	S	0	1	0
			5069	3242	870	932	25			

- Molecule 2 is a protein called Methylosome protein 50.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	309	Total	C	N	O	S	0	0	0
			2331	1461	399	457	14			

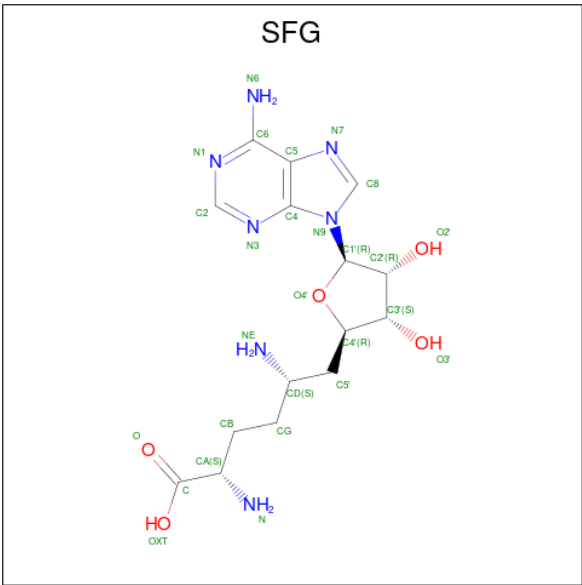
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	1	PRO	-	expression tag	UNP Q9BQA1

- Molecule 3 is a protein called PBM peptide.

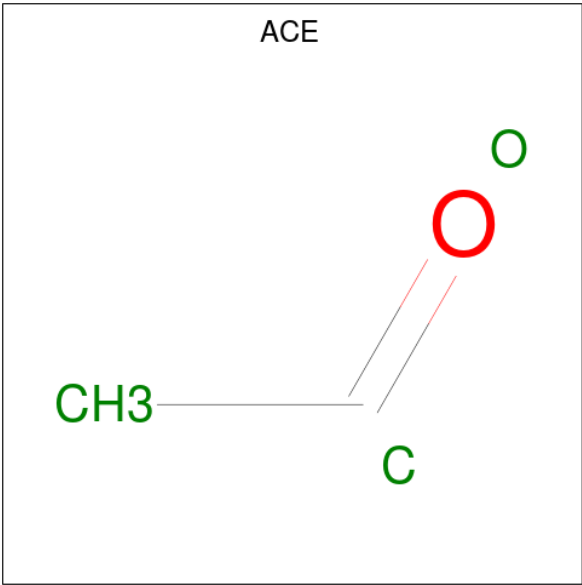
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	D	10	Total	C	N	O	0	0	0
			73	44	11	18			

- Molecule 4 is SINEFUNGIN (three-letter code: SFG) (formula: C<sub>15</sub>H<sub>23</sub>N<sub>7</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	H	N	O	0	0
			50	15	23	7	5		

- Molecule 5 is ACETYL GROUP (three-letter code: ACE) (formula: C<sub>2</sub>H<sub>4</sub>O).

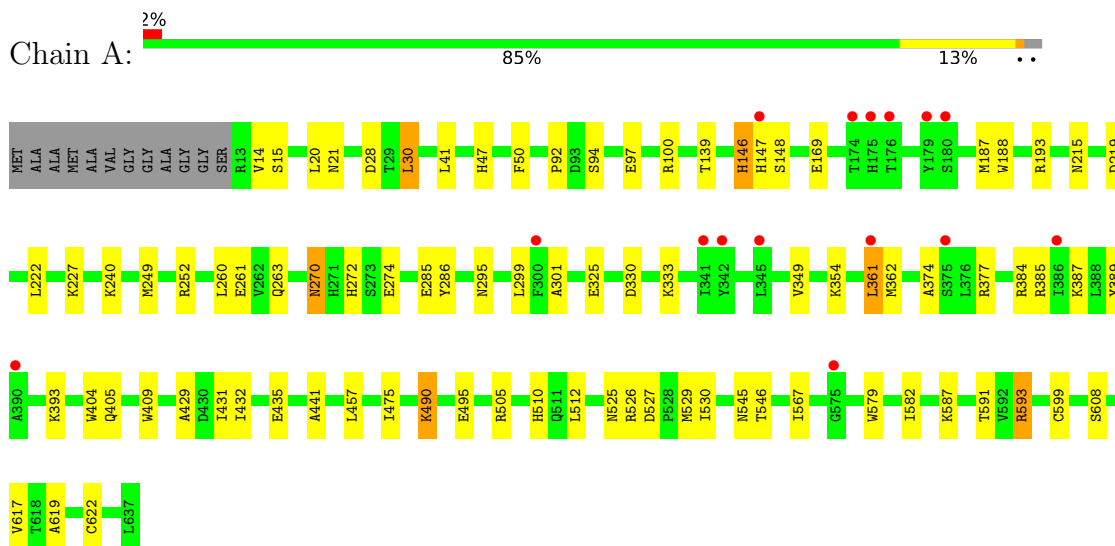


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	3	0
			3	2	1		

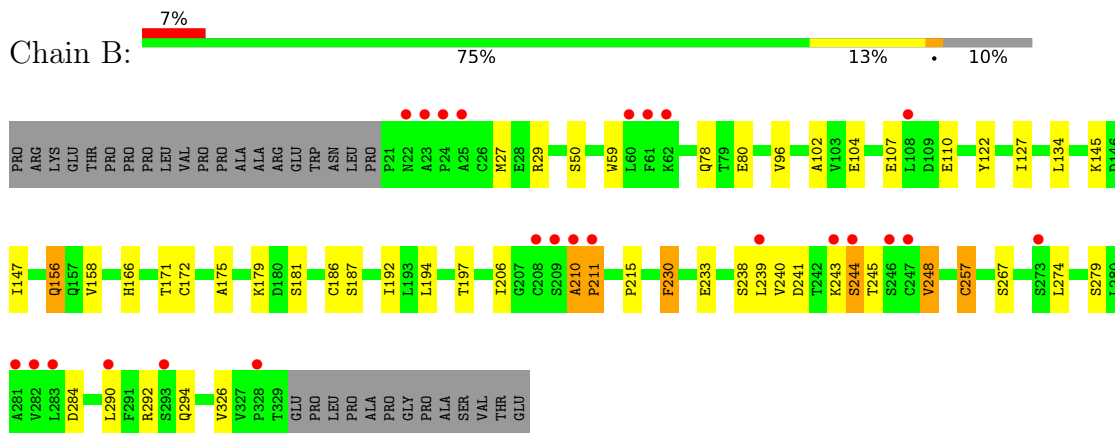
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Protein arginine N-methyltransferase 5



- Molecule 2: Methylosome protein 50



- Molecule 3: PBM peptide



## 4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	100.01 Å   136.40 Å   179.77 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	44.94 – 2.86 44.94 – 2.86	Depositor EDS
% Data completeness (in resolution range)	97.9 (44.94-2.86) 97.9 (44.94-2.86)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.01 (at 2.86 Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, $R_{free}$	0.211   ,   0.247 0.234   ,   0.271	Depositor DCC
$R_{free}$ test set	1410 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	92.6	Xtriage
Anisotropy	0.549	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 82.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7526	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	115.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.70% 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: SFG, ACE

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	0.53	0/5211	0.71	0/7088
2	B	0.53	0/2387	0.77	0/3261
3	D	0.71	0/73	0.64	0/98
All	All	0.53	0/7671	0.73	0/10447

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5069	0	4960	32	0
2	B	2331	0	2248	21	0
3	D	73	0	62	1	0
4	A	27	23	22	0	0
5	A	3	0	3	0	0
All	All	7503	23	7295	54	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 (54) 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)
2:B:241:ASP:HB3	2:B:244:SER:HB2	1.64	0.80
1:A:525:ASN:HD22	1:A:530:ILE:HG12	1.47	0.80
2:B:233:GLU:HA	2:B:257:CYS:HB2	1.65	0.79
2:B:194:LEU:HB2	2:B:206:ILE:HD11	1.78	0.66
1:A:94:SER:O	1:A:100:ARG:HD3	2.01	0.61
1:A:146:HIS:HD2	1:A:148:SER:H	1.47	0.61
1:A:222:LEU:HB3	1:A:510:HIS:HB2	1.83	0.61
1:A:187[B]:MET:HE1	1:A:188:TRP:HD1	1.67	0.58
2:B:210:ALA:HB1	2:B:211:PRO:CD	2.34	0.57
2:B:134:LEU:HD23	2:B:175:ALA:HB1	1.87	0.56
2:B:240:VAL:HG22	2:B:248:VAL:HG11	1.88	0.55
2:B:239:LEU:O	2:B:248:VAL:HB	2.06	0.55
2:B:127:ILE:HB	2:B:145:LYS:HD2	1.88	0.54
1:A:301:ALA:HB1	1:A:505:ARG:HG2	1.89	0.53
2:B:279:SER:HB3	2:B:294:GLN:HE21	1.73	0.53
1:A:47:HIS:HB3	1:A:50:PHE:HB2	1.92	0.51
1:A:15:SER:HB3	1:A:263:GLN:HG2	1.93	0.51
1:A:567:ILE:HG21	1:A:579:TRP:HB2	1.92	0.51
2:B:230:PHE:CE2	2:B:238:SER:HB2	2.46	0.50
1:A:219:ASP:O	1:A:222:LEU:HB2	2.10	0.50
1:A:20:LEU:HD12	1:A:41:LEU:HD11	1.94	0.49
1:A:432:ILE:HG12	1:A:457:LEU:HD13	1.95	0.49
2:B:102:ALA:HB2	2:B:122:TYR:CD1	2.48	0.49
1:A:512:LEU:HD22	1:A:546:THR:HG21	1.95	0.48
1:A:525:ASN:ND2	1:A:530:ILE:HG12	2.23	0.48
1:A:545:ASN:HB3	1:A:593:ARG:NH1	2.27	0.48
1:A:362:MET:HG2	1:A:389:TYR:HB2	1.96	0.48
2:B:166:HIS:ND1	2:B:187:SER:HB3	2.28	0.47
2:B:210:ALA:HB1	2:B:211:PRO:HD3	1.95	0.47
1:A:599:CYS:HB3	1:A:619:ALA:HB3	1.97	0.46
1:A:495:GLU:HB3	1:A:587:LYS:HE2	1.97	0.46
1:A:405:GLN:HA	1:A:409:TRP:HB2	1.98	0.46
1:A:330:ASP:OD2	1:A:333:LYS:HB2	2.16	0.45
1:A:490:LYS:H	1:A:490:LYS:HG2	1.48	0.45
2:B:27:MET:HB3	2:B:59:TRP:CZ2	2.52	0.45
1:A:617:VAL:O	1:A:622:CYS:HA	2.17	0.45
2:B:181:SER:HB2	2:B:197:THR:OG1	2.18	0.44
2:B:186:CYS:HB2	2:B:215:PRO:HG2	2.00	0.43
1:A:30:LEU:HD23	1:A:30:LEU:HA	1.86	0.43
3:D:2:VAL:O	3:D:5:GLN:HB2	2.19	0.43
1:A:361:LEU:HD11	1:A:431:ILE:HD12	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:227:LYS:HD3	1:A:227:LYS:HA	1.92	0.43
1:A:260:LEU:HD23	1:A:260:LEU:HA	1.92	0.43
2:B:284:ASP:HB3	2:B:290:LEU:HD11	2.00	0.43
2:B:210:ALA:CB	2:B:211:PRO:CD	2.97	0.42
2:B:96:VAL:HB	2:B:104:GLU:HB2	2.01	0.42
1:A:374:ALA:HA	1:A:377:ARG:NH1	2.34	0.42
1:A:295:ASN:O	1:A:299:LEU:HB2	2.19	0.42
1:A:362:MET:SD	1:A:429:ALA:HB2	2.60	0.42
1:A:349:VAL:HG12	1:A:384:ARG:HH11	1.85	0.41
2:B:172:CYS:HB3	2:B:186:CYS:SG	2.61	0.41
1:A:92:PRO:O	1:A:100:ARG:HG3	2.20	0.41
2:B:156:GLN:HB3	2:B:158:VAL:HG22	2.02	0.41
1:A:270:ASN:HD22	1:A:272:HIS:H	1.69	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	624/637 (98%)	600 (96%)	20 (3%)	4 (1%)	25	53
2	B	307/342 (90%)	288 (94%)	14 (5%)	5 (2%)	9	28
3	D	8/13 (62%)	7 (88%)	1 (12%)	0	100	100
All	All	939/992 (95%)	895 (95%)	35 (4%)	9 (1%)	15	40

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	147	ILE
2	B	210	ALA
2	B	211	PRO
1	A	14	VAL

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Mol	Chain	Res	Type
1	A	146	HIS
2	B	245	THR
1	A	441	ALA
1	A	354	LYS
2	B	248	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	559/562 (100%)	526 (94%)	33 (6%)	19	45
2	B	262/290 (90%)	244 (93%)	18 (7%)	15	38
3	D	7/10 (70%)	7 (100%)	0	100	100
All	All	828/862 (96%)	777 (94%)	51 (6%)	18	43

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	ASN
1	A	28	ASP
1	A	30	LEU
1	A	97	GLU
1	A	139	THR
1	A	147	HIS
1	A	169	GLU
1	A	193	ARG
1	A	215	ASN
1	A	240	LYS
1	A	249	MET
1	A	252	ARG
1	A	261	GLU
1	A	270	ASN
1	A	274	GLU
1	A	285	GLU
1	A	286	TYR

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Mol	Chain	Res	Type
1	A	325	GLU
1	A	361	LEU
1	A	385	ARG
1	A	387	LYS
1	A	393	LYS
1	A	404	TRP
1	A	435	GLU
1	A	475	ILE
1	A	490	LYS
1	A	526	ARG
1	A	527	ASP
1	A	529	MET
1	A	582	ILE
1	A	591	THR
1	A	593	ARG
1	A	608	SER
2	B	29	ARG
2	B	50	SER
2	B	78	GLN
2	B	80	GLU
2	B	107	GLU
2	B	110	GLU
2	B	156	GLN
2	B	171	THR
2	B	179	LYS
2	B	192	ILE
2	B	230	PHE
2	B	243	LYS
2	B	244	SER
2	B	257	CYS
2	B	267	SER
2	B	274	LEU
2	B	292	ARG
2	B	326	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	61	ASN
1	A	146	HIS
1	A	270	ASN
1	A	357	ASN

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Mol	Chain	Res	Type
1	A	525	ASN
1	A	588	GLN
2	B	294	GLN

### 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

2 ligands are 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	$\# Z  > 2$
4	SFG	A	701	-	22,29,29	0.59	0	18,42,42	0.80	1 (5%)
5	ACE	A	702	-	1,2,2	0.42	0	1,1,1	0.40	0

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
4	SFG	A	701	-	-	3/9/33/33	0/3/3/3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	701	SFG	C5-C6-N6	2.01	123.40	120.35

There are no chirality outliers.

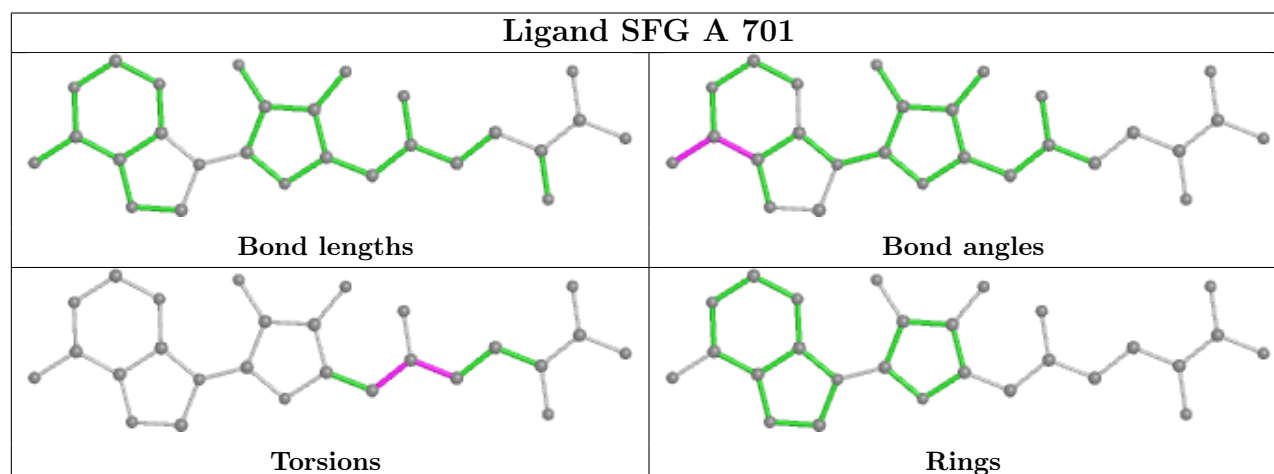
All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	701	SFG	NE-CD-CG-CB
4	A	701	SFG	C5'-CD-CG-CB
4	A	701	SFG	C4'-C5'-CD-NE

There are no ring outliers.

No monomer is involved in short contacts.

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	625/637 (98%)	0.08	15 (2%) 59 56	81, 108, 148, 184	0
2	B	309/342 (90%)	0.34	24 (7%) 13 9	91, 121, 153, 171	0
3	D	10/13 (76%)	-0.21	0 100 100	105, 111, 129, 151	0
All	All	944/992 (95%)	0.16	39 (4%) 37 31	81, 114, 150, 184	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	60	LEU	5.4
2	B	247	CYS	5.1
2	B	209	SER	3.9
1	A	175	HIS	3.6
2	B	282	VAL	3.5
1	A	386	ILE	3.3
2	B	208	CYS	3.3
2	B	290	LEU	3.2
1	A	147	HIS	3.1
2	B	25	ALA	3.1
2	B	211	PRO	3.1
2	B	246	SER	3.0
2	B	244	SER	3.0
2	B	273	SER	3.0
1	A	176	THR	2.9
1	A	345	LEU	2.8
2	B	243	LYS	2.8
2	B	24	PRO	2.7
1	A	390	ALA	2.7
2	B	283	LEU	2.7
2	B	23	ALA	2.7
2	B	239	LEU	2.6
1	A	300	PHE	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	180	SER	2.5
1	A	575	GLY	2.5
1	A	342	TYR	2.5
2	B	62	LYS	2.5
2	B	293	SER	2.4
1	A	341	ILE	2.4
2	B	22	ASN	2.3
1	A	179	TYR	2.3
1	A	174	THR	2.2
1	A	375	SER	2.2
2	B	61	PHE	2.2
1	A	361	LEU	2.1
2	B	281	ALA	2.1
2	B	328	PRO	2.0
2	B	210	ALA	2.0
2	B	108	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 monosaccharides in this entry.

## 6.4 Ligands [i](#)

LIGAND-RSR INFOmissingINFO

## 6.5 Other polymers [i](#)

There are no such residues in this entry.