



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 15, 2014 – 02:17 AM EDT

PDB ID : 4D1D  
Title : STRUCTURE OF MHP1, A NUCLEOBASE-CATION-SYMPORT-1FAMILY TRANSPORTER with the inhibitor 5-(2-naphthylmethyl)-L-hydantoin  
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Deposited on : 2014-05-01  
Resolution : 3.70 Å(reported)

This is a full wwPDB 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 <http://wwpdb.org/ValidationPDFNotes.html>

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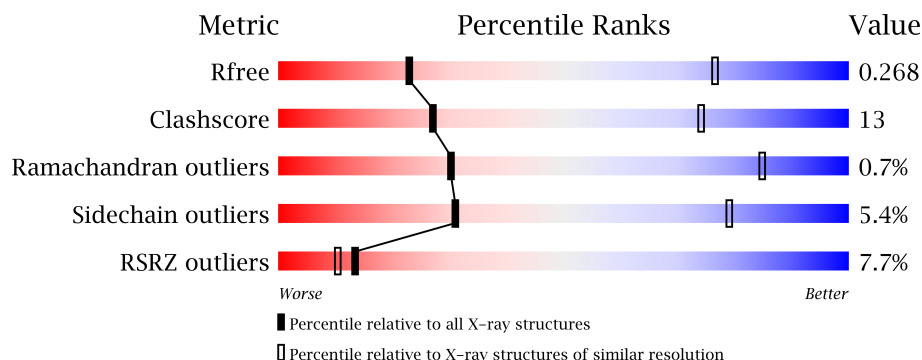
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.16 November 2013  
Xtriage (Phenix) : dev-1439  
EDS : stable23489  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable23489

# 1 Overall quality at a glance

The reported resolution of this entry is 3.70 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))
$R_{free}$	66092	1098 (4.00-3.40)
Clashscore	79885	1009 (3.94-3.46)
Ramachandran outliers	78287	1016 (3.98-3.42)
Sidechain outliers	78261	1014 (3.98-3.42)
RSRZ outliers	66119	1099 (4.00-3.40)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	495	

## 2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 3550 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

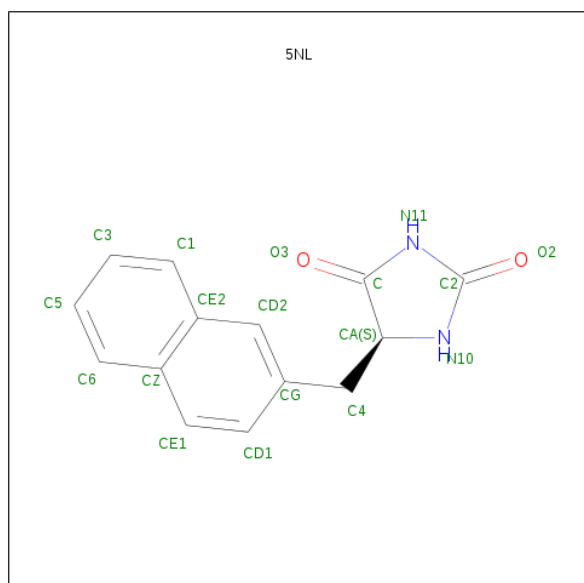
- Molecule 1 is a protein called HYDANTOIN TRANSPORT PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	456	3513	2336	563	592	22	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

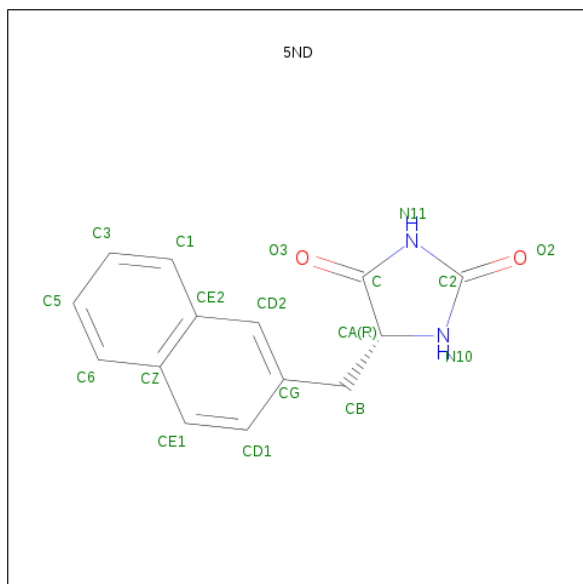
Chain	Residue	Modelled	Actual	Comment	Reference
A	488	GLY	-	EXPRESSION TAG	UNP D6R8X8
A	489	SER	-	EXPRESSION TAG	UNP D6R8X8
A	490	GLU	-	EXPRESSION TAG	UNP D6R8X8
A	491	ASN	-	EXPRESSION TAG	UNP D6R8X8
A	492	LEU	-	EXPRESSION TAG	UNP D6R8X8
A	493	TYR	-	EXPRESSION TAG	UNP D6R8X8
A	494	PHE	-	EXPRESSION TAG	UNP D6R8X8
A	495	GLN	-	EXPRESSION TAG	UNP D6R8X8

- Molecule 2 is 5-(2-NAPHTHYLMETHYL)-L-HYDANTOIN (three-letter code: 5NL) (formula: C<sub>14</sub>H<sub>12</sub>N<sub>2</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			18	14	2	2		

- Molecule 3 is 5-(2-NAPHTHYLMETHYL)-D-HYDANTOIN (three-letter code: 5ND) (formula:  $C_{14}H_{12}N_2O_2$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			18	14	2	2		

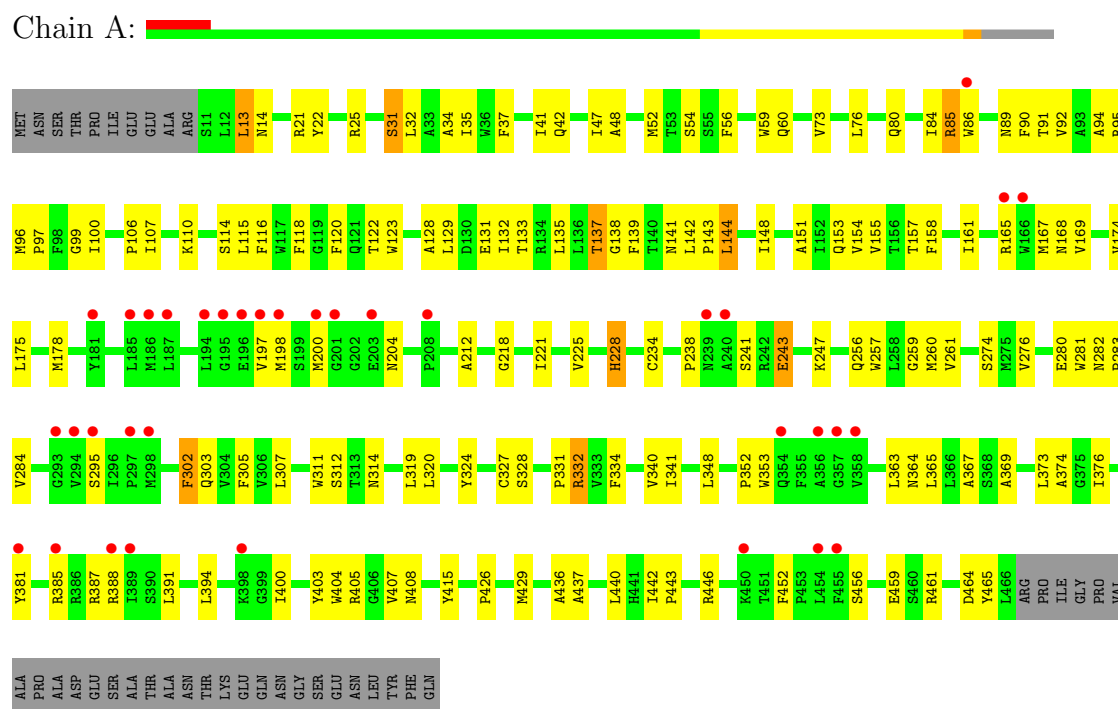
- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Na	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 errors 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: HYDANTOIN TRANSPORT PROTEIN



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	87.60Å 106.90Å 106.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.78 – 3.70 37.78 – 3.70	Depositor EDS
% Data completeness (in resolution range)	88.9 (37.78-3.70) 95.6 (37.78-3.70)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.13 (at 3.66Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.256 , 0.308 0.271 , 0.268	Depositor DCC
$R_{free}$ test set	1066 reflections (10.05%)	DCC
Wilson B-factor (Å <sup>2</sup> )	130.0	Xtriage
Anisotropy	0.714	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.20 , 65.5	EDS
Estimated twinning fraction	0.048 for -h,l,k	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.38$ , $\langle L^2 \rangle = 0.21$	Xtriage
Outliers	0 of 10722 reflections	Xtriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	3550	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	194.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.46% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NA, 5ND, 5NL

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	0.34	0/3610	0.60	0/4936

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3513	0	3604	93	0
2	A	18	0	0	0	0
3	A	18	0	0	0	0
4	A	1	0	0	0	0
All	All	3550	0	3604	93	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 13.

All (93) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:59:TRP:HB3	1:A:198:MET:HG3	1.73	0.71
1:A:32:LEU:HA	1:A:35:ILE:HD12	1.70	0.71
1:A:436:ALA:O	1:A:440:LEU:HG	1.97	0.63
1:A:13:LEU:HD12	1:A:14:ASN:N	2.13	0.63
1:A:324:TYR:O	1:A:328:SER:HB3	2.00	0.62
1:A:131:GLU:HB3	1:A:303:GLN:HG2	1.82	0.61
1:A:155:VAL:HA	1:A:158:PHE:CD2	2.37	0.59
1:A:48:ALA:O	1:A:52:MET:HG2	2.04	0.57
1:A:283:PRO:HG2	1:A:302:PHE:HZ	1.67	0.57
1:A:154:VAL:HG13	1:A:340:VAL:HG12	1.86	0.57
1:A:96:MET:HB2	1:A:97:PRO:HD3	1.87	0.56
1:A:369:ALA:O	1:A:415:TYR:OH	2.14	0.56
1:A:442:ILE:HB	1:A:443:PRO:HD3	1.87	0.55
1:A:385:ARG:NH2	1:A:403:TYR:OH	2.40	0.55
1:A:257:TRP:CE2	1:A:261:VAL:HG21	2.42	0.54
1:A:221:ILE:HG21	1:A:367:ALA:HB1	1.90	0.54
1:A:95:ARG:HG2	1:A:100:ILE:HA	1.89	0.54
1:A:131:GLU:O	1:A:135:LEU:HG	2.08	0.54
1:A:165:ARG:O	1:A:169:VAL:HG23	2.08	0.53
1:A:426:PRO:HA	1:A:429:MET:HG3	1.91	0.53
1:A:110:LYS:C	1:A:110:LYS:HD3	2.29	0.53
1:A:97:PRO:O	1:A:408:ASN:ND2	2.41	0.53
1:A:302:PHE:O	1:A:305:PHE:HB3	2.09	0.52
1:A:461:ARG:O	1:A:464:ASP:HB2	2.10	0.52
1:A:302:PHE:HD1	1:A:302:PHE:O	1.92	0.52
1:A:327:CYS:HA	1:A:334:PHE:HB2	1.92	0.52
1:A:22:TYR:OH	1:A:85:ARG:NH1	2.44	0.51
1:A:14:ASN:ND2	1:A:331:PRO:O	2.34	0.51
1:A:21:ARG:NH1	1:A:464:ASP:O	2.43	0.51
1:A:31:SER:O	1:A:35:ILE:HG13	2.10	0.51
1:A:34:ALA:O	1:A:168:ASN:HB3	2.11	0.50
1:A:157:THR:HG21	1:A:319:LEU:HD23	1.93	0.50
1:A:25:ARG:HD2	1:A:234:CYS:O	2.12	0.50
1:A:284:VAL:HA	1:A:302:PHE:CE2	2.46	0.50
1:A:388:ARG:NH1	1:A:459:GLU:OE2	2.45	0.49
1:A:256:GLN:O	1:A:260:MET:HG2	2.12	0.49
1:A:174:VAL:O	1:A:178:MET:HG3	2.13	0.48
1:A:178:MET:CE	1:A:305:PHE:HB2	2.43	0.48
1:A:52:MET:HE1	1:A:212:ALA:HB1	1.96	0.48
1:A:13:LEU:O	1:A:332:ARG:NH2	2.46	0.48
1:A:128:ALA:HA	1:A:303:GLN:HG3	1.96	0.48
1:A:76:LEU:O	1:A:80:GLN:HG2	2.14	0.48
1:A:37:PHE:CE1	1:A:41:ILE:HD11	2.49	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:142:LEU:HB3	1:A:143:PRO:HD3	1.95	0.47
1:A:37:PHE:HA	1:A:259:GLY:O	2.15	0.47
1:A:274:SER:HB3	1:A:280:GLU:O	2.15	0.47
1:A:106:PRO:HB2	1:A:373:LEU:HD13	1.97	0.47
1:A:54:SER:O	1:A:204:ASN:HB3	2.16	0.46
1:A:122:THR:HG21	1:A:348:LEU:HD21	1.97	0.46
1:A:352:PRO:HD2	1:A:353:TRP:CZ3	2.50	0.46
1:A:178:MET:HE2	1:A:305:PHE:HB2	1.97	0.46
1:A:89:ASN:HB3	1:A:92:VAL:H	1.81	0.45
1:A:129:LEU:HG	1:A:307:LEU:HD13	1.98	0.45
1:A:85:ARG:HD2	1:A:86:TRP:CE2	2.51	0.45
1:A:129:LEU:O	1:A:133:THR:HG23	2.17	0.45
1:A:218:GLY:HA2	1:A:221:ILE:HB	1.99	0.45
1:A:225:VAL:HG23	1:A:374:ALA:HB2	1.99	0.45
1:A:99:GLY:HA3	1:A:407:VAL:HA	1.98	0.45
1:A:25:ARG:NH1	1:A:84:ILE:O	2.44	0.45
1:A:151:ALA:O	1:A:155:VAL:HG23	2.17	0.44
1:A:118:PHE:HA	1:A:314:ASN:OD1	2.18	0.44
1:A:391:LEU:HA	1:A:394:LEU:HD12	1.99	0.44
1:A:153:GLN:O	1:A:157:THR:N	2.48	0.44
1:A:400:ILE:HD13	1:A:456:SER:HB2	2.00	0.43
1:A:404:TRP:CE2	1:A:452:PHE:HE2	2.36	0.43
1:A:73:VAL:HA	1:A:76:LEU:HD12	2.01	0.43
1:A:110:LYS:HD3	1:A:110:LYS:O	2.18	0.43
1:A:47:ILE:HG12	1:A:281:TRP:CE2	2.53	0.43
1:A:89:ASN:HB2	1:A:92:VAL:HB	2.00	0.43
1:A:132:ILE:CG1	1:A:303:GLN:HB3	2.49	0.43
1:A:22:TYR:CZ	1:A:238:PRO:HB3	2.53	0.43
1:A:144:LEU:HG	1:A:148:ILE:HD12	2.01	0.42
1:A:158:PHE:HZ	1:A:341:ILE:HD11	1.84	0.42
1:A:376:ILE:HG13	1:A:437:ALA:HB1	2.00	0.42
1:A:115:LEU:HA	1:A:115:LEU:HD23	1.84	0.42
1:A:282:ASN:HA	1:A:283:PRO:HD2	1.90	0.42
1:A:243:GLU:O	1:A:247:LYS:HG2	2.19	0.42
1:A:141:ASN:OD1	1:A:143:PRO:HD2	2.19	0.42
1:A:391:LEU:HD12	1:A:465:TYR:HB2	2.01	0.42
1:A:120:PHE:O	1:A:123:TRP:HB3	2.20	0.41
1:A:381:TYR:CE2	1:A:387:ARG:HG2	2.54	0.41
1:A:319:LEU:HD21	1:A:340:VAL:HG13	2.02	0.41
1:A:94:ALA:O	1:A:97:PRO:HD2	2.19	0.41
1:A:320:LEU:HA	1:A:320:LEU:HD23	1.82	0.41
1:A:56:PHE:HB3	1:A:60:GLN:OE1	2.20	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:91:THR:HG23	1:A:107:ILE:HD13	2.03	0.41
1:A:128:ALA:O	1:A:132:ILE:HG13	2.20	0.41
1:A:116:PHE:CE2	1:A:363:LEU:HD11	2.55	0.41
1:A:41:ILE:HD13	1:A:175:LEU:HB3	2.02	0.41
1:A:197:VAL:HA	1:A:200:MET:HG3	2.02	0.41
1:A:90:PHE:HB2	1:A:228:HIS:HB2	2.03	0.41
1:A:137:THR:C	1:A:139:PHE:H	2.24	0.41
1:A:440:LEU:O	1:A:443:PRO:HD2	2.22	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	454/495 (92%)	403 (89%)	48 (11%)	3 (1%)	30 85

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	228	HIS
1	A	137	THR
1	A	138	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	367/399 (92%)	347 (95%)	20 (5%)	31 79

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	LEU
1	A	31	SER
1	A	42	GLN
1	A	85	ARG
1	A	114	SER
1	A	144	LEU
1	A	161	ILE
1	A	167	MET
1	A	241	SER
1	A	243	GLU
1	A	276	VAL
1	A	295	SER
1	A	302	PHE
1	A	311	TRP
1	A	312	SER
1	A	332	ARG
1	A	364	ASN
1	A	365	LEU
1	A	405	ARG
1	A	446	ARG

Some 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 chains 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 3 ligands modelled in this entry, 1 is 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	5NL	A	1467	-	20,20,20	2.66	5 (25%)	28,28,28	1.58	4 (14%)
3	5ND	A	1468	-	20,20,20	2.65	4 (20%)	28,28,28	1.71	4 (14%)

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	5NL	A	1467	-	-	0/4/16/16	0/3/3/3
3	5ND	A	1468	-	-	0/4/16/16	0/3/3/3

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1467	5NL	C2-N10	7.38	1.45	1.35
3	A	1468	5ND	C2-N10	7.30	1.45	1.35
3	A	1468	5ND	CA-C	-6.63	1.47	1.52
2	A	1467	5NL	CA-C	-6.29	1.47	1.52
2	A	1467	5NL	C-N11	4.20	1.43	1.37
3	A	1468	5ND	C-N11	3.78	1.42	1.37
2	A	1467	5NL	C2-N11	3.46	1.46	1.39
3	A	1468	5ND	C2-N11	3.31	1.45	1.39
2	A	1467	5NL	CE1-CD1	2.04	1.40	1.36

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1468	5ND	C-CA-N10	5.57	108.04	100.99
2	A	1467	5NL	C-CA-N10	5.46	107.90	100.99
3	A	1468	5ND	CA-N10-C2	-4.29	107.88	112.92
2	A	1467	5NL	CA-N10-C2	-4.18	108.02	112.92
3	A	1468	5ND	CB-CA-N10	-3.69	109.92	114.29
3	A	1468	5ND	C-N11-C2	-3.03	108.03	111.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1467	5NL	C-N11-C2	-2.94	108.14	111.48
2	A	1467	5NL	C4-CA-N10	-2.25	111.63	114.29

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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	456/495 (92%)	0.32	35 (7%) 13 10	102, 185, 281, 399	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	293	GLY	6.3
1	A	196	GLU	5.8
1	A	294	VAL	5.3
1	A	194	LEU	4.6
1	A	388	ARG	4.6
1	A	200	MET	4.4
1	A	203	GLU	3.9
1	A	197	VAL	3.9
1	A	186	MET	3.4
1	A	185	LEU	3.4
1	A	381	TYR	3.1
1	A	398	LYS	3.1
1	A	358	VAL	3.0
1	A	450	LYS	2.8
1	A	201	GLY	2.7
1	A	239	ASN	2.7
1	A	389	ILE	2.7
1	A	357	GLY	2.6
1	A	454	LEU	2.6
1	A	208	PRO	2.5
1	A	297	PRO	2.5
1	A	356	ALA	2.4
1	A	354	GLN	2.4
1	A	86	TRP	2.3
1	A	295	SER	2.3
1	A	195	GLY	2.3
1	A	385	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	198	MET	2.2
1	A	165	ARG	2.2
1	A	181	TYR	2.1
1	A	455	PHE	2.1
1	A	240	ALA	2.1
1	A	187	LEU	2.1
1	A	298	MET	2.1
1	A	166	TRP	2.0

## 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. 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	5ND	A	1468	18/18	0.33	1.96	140,151,167,169	18
2	5NL	A	1467	18/18	0.31	1.68	142,154,170,171	18
4	NA	A	1471	1/1	0.16	-1.15	115,115,115,115	0

## 6.5 Other polymers

There are no such residues in this entry.