



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:08 AM GMT

PDB ID : 3HCD  
Title : Crystal Structure of hPNMT in Complex With Noradrenaline and AdoHcy  
Authors : Drinkwater, N.; Martin, J.L.  
Deposited on : 2009-05-06  
Resolution : 2.39 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  
<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

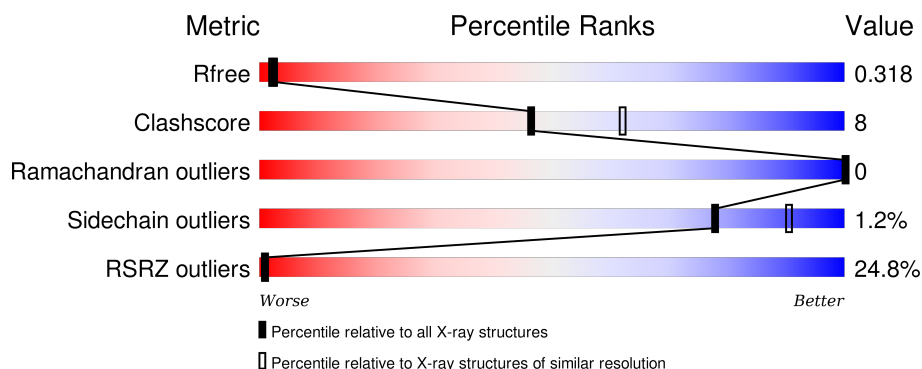
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.39 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	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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. 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	289	
1	B	289	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	LNR	A	2001	-	-	-	X
3	LNR	B	2002	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4421 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.

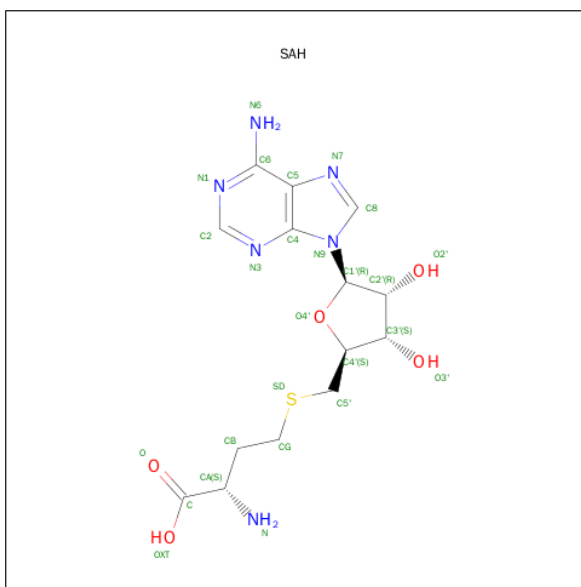
- Molecule 1 is a protein called Phenylethanolamine N-methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	257	Total	C	N	O	S	1	0	0
			2016	1280	358	369	9			
1	B	268	Total	C	N	O	S	0	1	0
			2089	1324	371	385	9			

There are 14 discrepancies between the modelled and reference sequences:

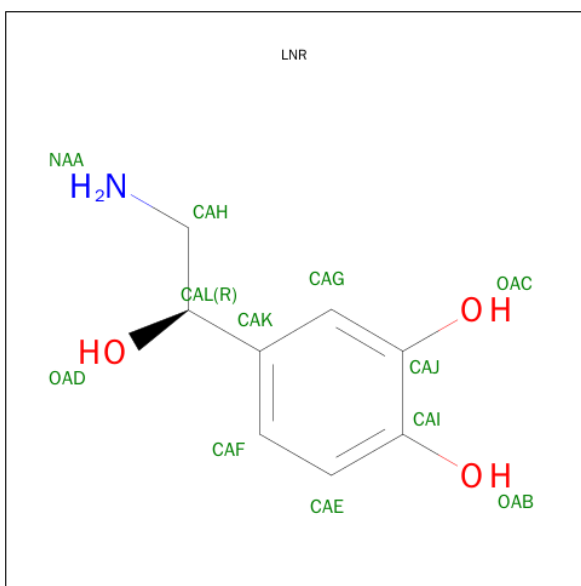
Chain	Residue	Modelled	Actual	Comment	Reference
A	283	GLU	-	EXPRESSION TAG	UNP P11086
A	284	HIS	-	EXPRESSION TAG	UNP P11086
A	285	HIS	-	EXPRESSION TAG	UNP P11086
A	286	HIS	-	EXPRESSION TAG	UNP P11086
A	287	HIS	-	EXPRESSION TAG	UNP P11086
A	288	HIS	-	EXPRESSION TAG	UNP P11086
A	289	HIS	-	EXPRESSION TAG	UNP P11086
B	283	GLU	-	EXPRESSION TAG	UNP P11086
B	284	HIS	-	EXPRESSION TAG	UNP P11086
B	285	HIS	-	EXPRESSION TAG	UNP P11086
B	286	HIS	-	EXPRESSION TAG	UNP P11086
B	287	HIS	-	EXPRESSION TAG	UNP P11086
B	288	HIS	-	EXPRESSION TAG	UNP P11086
B	289	HIS	-	EXPRESSION TAG	UNP P11086

- Molecule 2 is S-ADENOSYL-L-HOMOCYSTEINE (three-letter code: SAH) (formula: C<sub>14</sub>H<sub>20</sub>N<sub>6</sub>O<sub>5</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 26	C 14	N 6	O 5	S 1	0	0
2	B	1	Total 26	C 14	N 6	O 5	S 1	0	0

- Molecule 3 is L-NOREPINEPHRINE (three-letter code: LNR) (formula:  $C_8H_{11}NO_3$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total 12	C 8	N 1	O 3	0	0
3	B	1	Total 12	C 8	N 1	O 3	0	0

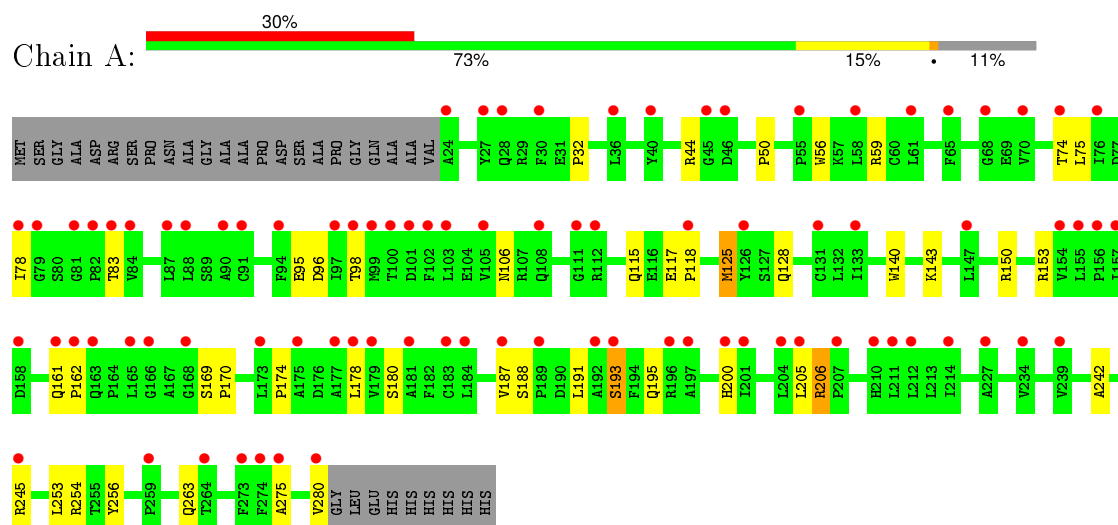
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	114	Total 114	O 114	0	0
4	B	126	Total 126	O 126	0	0

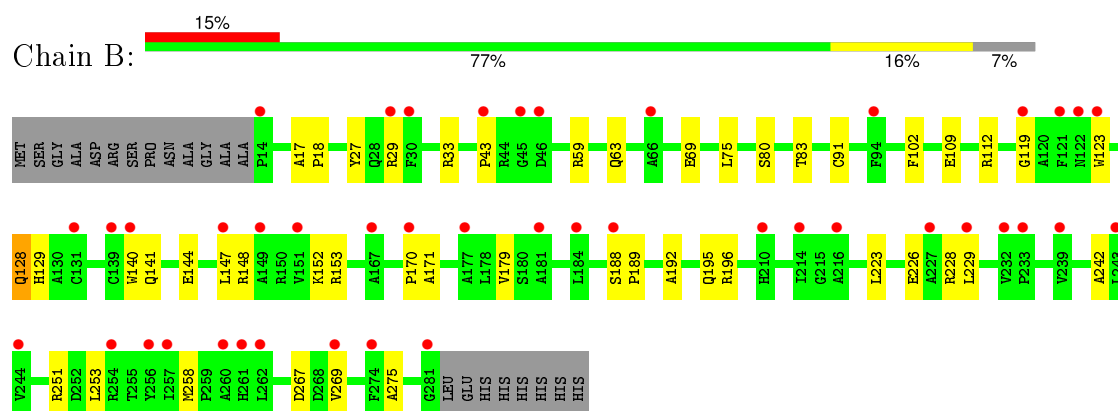
### 3 Residue-property plots [i](#)

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: Phenylethanolamine N-methyltransferase



#### • Molecule 1: Phenylethanolamine N-methyltransferase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	93.65Å 93.65Å 187.29Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.78 – 2.39 66.22 – 2.39	Depositor EDS
% Data completeness (in resolution range)	91.2 (34.78-2.39) 99.7 (66.22-2.39)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.32 (at 2.40Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, $R_{free}$	0.181 , 0.230 0.320 , 0.318	Depositor DCC
$R_{free}$ test set	3362 reflections (11.07%)	DCC
Wilson B-factor (Å <sup>2</sup> )	44.7	Xtriage
Anisotropy	0.449	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 34.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	1 of 33902 reflections (0.003%)	Xtriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	4421	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 4.01% 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, 0.375 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: SAH, LNR

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	0.46	0/2067	0.59	0/2813
1	B	0.53	0/2145	0.62	0/2920
All	All	0.50	0/4212	0.60	0/5733

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	2016	0	1983	34	0
1	B	2089	0	2053	32	0
2	A	26	0	19	2	0
2	B	26	0	20	2	0
3	A	12	0	11	1	0
3	B	12	0	11	1	0
4	A	114	0	0	6	0
4	B	126	0	0	3	0
All	All	4421	0	4097	63	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 8.

All (63) 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:125:MET:HE2	1:B:141:GLN:HE22	1.17	1.07
1:A:125:MET:CE	1:B:141:GLN:HE22	1.86	0.89
1:B:29:ARG:HH21	1:B:226:GLU:HB3	1.41	0.85
1:A:125:MET:HB2	4:A:400:HOH:O	1.76	0.84
1:B:75:LEU:HD11	1:B:179:VAL:HG23	1.66	0.77
1:B:195:GLN:HE22	1:B:242:ALA:HA	1.50	0.75
1:B:29:ARG:NH2	1:B:226:GLU:HB3	2.05	0.71
1:A:125:MET:HE2	1:B:141:GLN:NE2	2.00	0.69
1:A:254:ARG:NH2	4:A:504:HOH:O	2.36	0.58
1:A:115:GLN:HB2	1:A:117:GLU:HG3	1.86	0.57
1:A:143:LYS:HD3	4:A:320:HOH:O	2.04	0.56
1:A:98:THR:HG23	1:A:153:ARG:HG3	1.87	0.56
1:A:125:MET:CE	1:B:141:GLN:NE2	2.61	0.56
1:B:69:GLU:OE1	1:B:251:ARG:NH2	2.38	0.56
1:A:83:THR:OG1	2:A:3001:SAH:HA	2.08	0.54
1:B:112:ARG:HH21	1:B:119:GLY:HA3	1.72	0.54
1:A:263:GLN:HG2	4:A:337:HOH:O	2.08	0.53
1:A:50:PRO:O	1:A:59:ARG:NH2	2.41	0.52
1:A:195:GLN:HE22	1:A:242:ALA:HA	1.75	0.51
1:B:17:ALA:HB3	1:B:18:PRO:HD3	1.93	0.50
1:B:253:LEU:HD13	1:B:275:ALA:HB2	1.94	0.50
1:A:253:LEU:HD13	1:A:275:ALA:HB2	1.94	0.50
1:B:128[A]:GLN:HE21	1:B:128[A]:GLN:HA	1.76	0.49
1:B:128[B]:GLN:HG2	1:B:140:TRP:CD1	2.47	0.48
1:B:148:ARG:HD2	4:B:414:HOH:O	2.12	0.48
1:A:161:GLN:HA	1:A:161:GLN:OE1	2.12	0.48
1:A:32:PRO:HG3	1:A:106:ASN:ND2	2.29	0.47
1:B:91:CYS:HB3	1:B:147:LEU:HD13	1.96	0.47
1:A:188:SER:HB3	1:A:193:SER:HB2	1.96	0.46
1:B:83:THR:HA	1:B:123:TRP:CZ2	2.51	0.46
1:A:280:VAL:HG13	1:A:280:VAL:O	2.15	0.46
1:B:129:HIS:ND1	4:B:445:HOH:O	2.35	0.46
1:B:170:PRO:O	1:B:171:ALA:C	2.54	0.46
1:B:43:PRO:HD2	4:B:426:HOH:O	2.14	0.46
1:A:187:VAL:HG11	2:A:3001:SAH:C5	2.45	0.45
1:B:102:PHE:HB2	2:B:3002:SAH:C4	2.45	0.45
1:A:74:THR:HG22	1:A:96:ASP:HB3	1.98	0.45
1:B:27:TYR:CE2	1:B:229:LEU:HD22	2.52	0.45
1:B:258:MET:HE3	3:B:2002:LNR:HAE	2.00	0.44
1:A:174:PRO:HG2	1:A:206:ARG:HB2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:245:ARG:HB2	1:A:245:ARG:HE	1.62	0.43
1:A:195:GLN:NE2	1:A:245:ARG:HD2	2.34	0.43
1:B:59:ARG:HG2	1:B:63:GLN:NE2	2.33	0.43
1:B:188:SER:HA	1:B:189:PRO:HD3	1.90	0.43
1:B:192:ALA:O	1:B:196:ARG:HG3	2.18	0.43
1:A:56:TRP:CE2	1:A:256:TYR:HB2	2.54	0.43
1:A:128:GLN:HG2	1:A:140:TRP:CD1	2.54	0.43
1:A:178:LEU:HG	1:A:205:LEU:HD13	2.00	0.43
1:B:33:ARG:NH2	1:B:109:GLU:OE2	2.51	0.43
1:A:44:ARG:HG3	4:A:294:HOH:O	2.18	0.43
1:A:117:GLU:HB3	1:A:118:PRO:CD	2.50	0.42
1:A:75:LEU:C	1:A:75:LEU:HD23	2.39	0.42
1:A:162:PRO:HA	1:A:200:HIS:CD2	2.54	0.41
1:A:78:ILE:HB	1:A:180:SER:HB2	2.03	0.41
3:A:2001:LNR:HAHA	3:A:2001:LNR:HAG	1.81	0.41
1:A:169:SER:HA	1:A:170:PRO:HD3	1.94	0.41
1:B:267:ASP:OD2	1:B:269:VAL:HG12	2.21	0.41
1:B:223:LEU:HD21	1:B:228:ARG:HD2	2.01	0.41
1:A:95:GLU:HA	1:A:150:ARG:HD3	2.03	0.41
1:B:152:LYS:O	1:B:153:ARG:HB3	2.19	0.41
1:B:80:SER:O	2:B:3002:SAH:HA	2.20	0.41
1:A:125:MET:HG3	4:A:441:HOH:O	2.21	0.40
1:B:144:GLU:O	1:B:148:ARG:HG3	2.21	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	255/289 (88%)	247 (97%)	8 (3%)	0	100	100
1	B	267/289 (92%)	262 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	522/578 (90%)	509 (98%)	13 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	212/233 (91%)	208 (98%)	4 (2%)	65	83
1	B	219/233 (94%)	217 (99%)	2 (1%)	84	93
All	All	431/466 (92%)	425 (99%)	6 (1%)	78	88

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	125	MET
1	A	191	LEU
1	A	193	SER
1	A	206	ARG
1	B	128[A]	GLN
1	B	128[B]	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	106	ASN
1	A	195	GLN
1	B	106	ASN
1	B	141	GLN
1	B	195	GLN

### 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 ⓘ

4 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$
3	LNR	A	2001	-	12,12,12	1.08	1 (8%)	15,16,16	1.01	0
2	SAH	A	3001	-	20,28,28	1.91	7 (35%)	19,40,40	3.69	5 (26%)
3	LNR	B	2002	-	12,12,12	1.01	0	15,16,16	0.90	0
2	SAH	B	3002	-	20,28,28	1.96	6 (30%)	19,40,40	3.11	8 (42%)

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	LNR	A	2001	-	-	0/6/6/6	0/1/1/1
2	SAH	A	3001	-	-	0/7/31/31	0/3/3/3
3	LNR	B	2002	-	-	0/6/6/6	0/1/1/1
2	SAH	B	3002	-	-	0/7/31/31	0/3/3/3

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	3001	SAH	C2'-C3'	-5.36	1.38	1.53
2	B	3002	SAH	C2'-C3'	-4.85	1.40	1.53
2	A	3001	SAH	C5-C4	-2.94	1.33	1.40
2	A	3001	SAH	O4'-C4'	-2.82	1.38	1.45
2	B	3002	SAH	O4'-C4'	-2.26	1.39	1.45
2	B	3002	SAH	O4'-C1'	-2.25	1.38	1.41
2	A	3001	SAH	O4'-C1'	-2.19	1.38	1.41
2	A	3001	SAH	C2-N3	2.07	1.35	1.32
2	B	3002	SAH	C2-N1	2.13	1.38	1.33
2	A	3001	SAH	C8-N7	2.16	1.38	1.34
3	A	2001	LNR	OAC-CAJ	2.24	1.41	1.36
2	B	3002	SAH	C2-N3	2.59	1.36	1.32
2	A	3001	SAH	C6-N6	2.85	1.43	1.34
2	B	3002	SAH	C6-N6	4.48	1.48	1.34

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	3001	SAH	N3-C2-N1	-13.62	118.47	128.89
2	B	3002	SAH	N3-C2-N1	-11.00	120.47	128.89
2	A	3001	SAH	C4'-O4'-C1'	-7.05	101.97	109.72
2	B	3002	SAH	C4-C5-N7	-3.52	106.24	109.48
2	B	3002	SAH	C4'-O4'-C1'	-3.08	106.34	109.72
2	A	3001	SAH	O4'-C4'-C5'	-2.91	100.92	108.85
2	B	3002	SAH	O3'-C3'-C4'	-2.06	104.88	111.05
2	B	3002	SAH	C2-N1-C6	2.02	122.38	118.77
2	A	3001	SAH	O2'-C2'-C3'	2.03	118.44	111.83
2	A	3001	SAH	CB-CG-SD	2.05	117.52	113.57
2	B	3002	SAH	C2'-C1'-N9	2.16	117.60	114.29
2	B	3002	SAH	CB-CA-N	2.76	118.36	110.52
2	B	3002	SAH	C4'-C5'-SD	2.83	122.27	113.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	2001	LNR	1	0
2	A	3001	SAH	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	2002	LNR	1	0
2	B	3002	SAH	2	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

### 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	257/289 (88%)	1.72	87 (33%) 0 0	33, 52, 82, 113	4 (1%)
1	B	268/289 (92%)	1.31	43 (16%) 3 2	31, 46, 72, 112	5 (1%)
All	All	525/578 (90%)	1.51	130 (24%) 1 1	31, 48, 78, 113	9 (1%)

All (130) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	281	GLY	6.2
1	A	184	LEU	5.3
1	A	76	ILE	5.1
1	A	178	LEU	5.0
1	A	181	ALA	4.7
1	A	175	ALA	4.5
1	A	189	PRO	4.4
1	A	103	LEU	4.4
1	A	192	ALA	4.0
1	A	111	GLY	3.9
1	A	61	LEU	3.9
1	A	105	VAL	3.9
1	A	187	VAL	3.9
1	A	88	LEU	3.8
1	A	40	TYR	3.6
1	A	274	PHE	3.6
1	A	78	ILE	3.6
1	A	65	PHE	3.5
1	A	204	LEU	3.5
1	A	58	LEU	3.5
1	A	87	LEU	3.5
1	A	245	ARG	3.4
1	A	165	LEU	3.4
1	B	43	PRO	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	98	THR	3.3
1	A	211	LEU	3.3
1	A	90	ALA	3.3
1	A	168	GLY	3.3
1	A	157	ILE	3.2
1	A	24	ALA	3.2
1	B	262	LEU	3.2
1	B	94	PHE	3.2
1	B	269	VAL	3.2
1	A	200	HIS	3.2
1	B	29	ARG	3.2
1	A	28	GLN	3.1
1	A	147	LEU	3.1
1	A	91	CYS	3.1
1	A	207	PRO	3.1
1	A	83	THR	3.1
1	A	79	GLY	3.1
1	A	102	PHE	3.1
1	A	214	ILE	3.0
1	A	205	LEU	3.0
1	A	36	LEU	3.0
1	A	156	PRO	3.0
1	A	162	PRO	3.0
1	A	126	TYR	3.0
1	B	170	PRO	2.9
1	B	227	ALA	2.9
1	A	273	PHE	2.9
1	A	45	GLY	2.9
1	A	275	ALA	2.9
1	A	212	LEU	2.9
1	A	81	GLY	2.8
1	B	123	TRP	2.8
1	B	261	HIS	2.8
1	A	82	PRO	2.8
1	B	214	ILE	2.7
1	B	46	ASP	2.7
1	A	133	ILE	2.7
1	A	101	ASP	2.6
1	A	177	ALA	2.6
1	B	66	ALA	2.6
1	A	179	VAL	2.6
1	A	239	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	254	ARG	2.5
1	B	122	ASN	2.5
1	A	70	VAL	2.5
1	B	244	VAL	2.5
1	B	243	LEU	2.5
1	A	118	PRO	2.5
1	B	181	ALA	2.4
1	A	100	THR	2.4
1	A	227	ALA	2.4
1	A	183	CYS	2.4
1	B	140	TRP	2.4
1	B	257	ILE	2.4
1	A	108	GLN	2.4
1	B	216	ALA	2.4
1	A	155	LEU	2.4
1	A	234	VAL	2.4
1	A	112	ARG	2.4
1	B	151	VAL	2.4
1	B	232	VAL	2.4
1	A	99	MET	2.4
1	A	163	GLN	2.4
1	A	173	LEU	2.4
1	B	121	PHE	2.4
1	B	177	ALA	2.4
1	A	210	HIS	2.3
1	A	30	PHE	2.3
1	A	197	ALA	2.3
1	B	167	ALA	2.3
1	A	193	SER	2.3
1	B	149	ALA	2.3
1	A	259	PRO	2.3
1	A	280	VAL	2.3
1	A	27	TYR	2.3
1	B	229	LEU	2.3
1	A	68	GLY	2.2
1	A	46	ASP	2.2
1	B	131	CYS	2.2
1	B	210	HIS	2.2
1	A	158	ASP	2.2
1	A	264	THR	2.2
1	A	196	ARG	2.1
1	A	55	PRO	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	30	PHE	2.1
1	A	94	PHE	2.1
1	B	274	PHE	2.1
1	B	14	PRO	2.1
1	A	161	GLN	2.1
1	A	97	ILE	2.1
1	A	201	ILE	2.1
1	A	131	CYS	2.1
1	A	74	THR	2.1
1	A	166	GLY	2.1
1	B	188	SER	2.1
1	B	233	PRO	2.1
1	A	154	VAL	2.1
1	B	119	GLY	2.0
1	B	139	CYS	2.0
1	B	260	ALA	2.0
1	A	84	VAL	2.0
1	B	239	VAL	2.0
1	B	147	LEU	2.0
1	B	184	LEU	2.0
1	B	45	GLY	2.0
1	B	256	TYR	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 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	LNR	B	2002	12/12	0.75	0.31	3.07	48,52,53,54	0
3	LNR	A	2001	12/12	0.71	0.35	2.97	46,49,53,54	0
2	SAH	A	3001	26/26	0.82	0.26	-0.25	41,54,59,62	0
2	SAH	B	3002	26/26	0.93	0.16	-1.04	30,40,47,47	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.