



# Full wwPDB X-ray Structure Validation Report ⓘ

May 24, 2020 – 03:33 pm BST

PDB ID : 2GN6  
Title : Crystal structure of UDP-GlcNAc inverting 4,6-dehydratase in complex with NADP and UDP-GlcNAc  
Authors : Ishiyama, N.; Creuzenet, C.; Lam, J.S.; Berghuis, A.M.  
Deposited on : 2006-04-09  
Resolution : 2.70 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

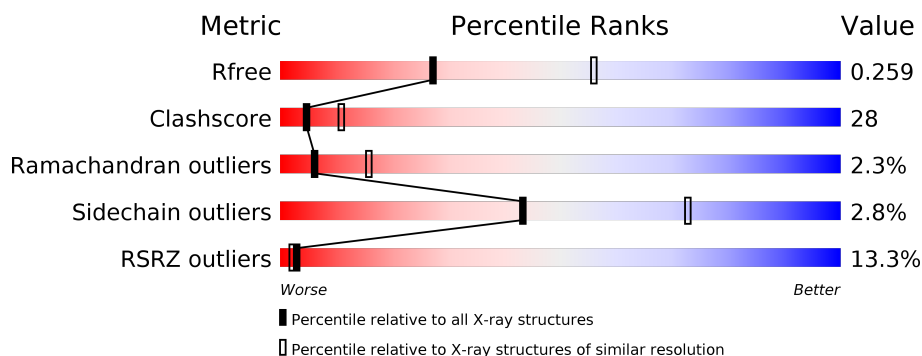
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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))
$R_{free}$	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	344	<div> <div>15%</div> <div>51%</div> <div>42%</div> <div>• •</div> </div>
1	B	344	<div> <div>10%</div> <div>56%</div> <div>36%</div> <div>• 5%</div> </div>

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
4	MES	B	336	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5517 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 UDP-GlcNAc C6 dehydratase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	329	Total	C	N	O	S	0	0	0
			2590	1656	440	479	15			
1	B	327	Total	C	N	O	S	0	0	0
			2573	1647	436	475	15			

There are 22 discrepancies between the modelled and reference sequences:

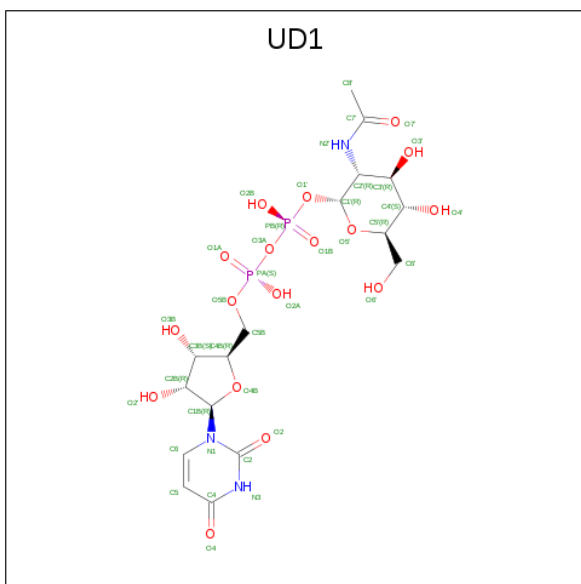
Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	MET	-	cloning artifact	UNP O25511
A	-9	HIS	-	EXPRESSION TAG	UNP O25511
A	-8	HIS	-	EXPRESSION TAG	UNP O25511
A	-7	HIS	-	EXPRESSION TAG	UNP O25511
A	-6	HIS	-	EXPRESSION TAG	UNP O25511
A	-5	HIS	-	EXPRESSION TAG	UNP O25511
A	-4	HIS	-	EXPRESSION TAG	UNP O25511
A	-3	GLY	-	cloning artifact	UNP O25511
A	-2	SER	-	cloning artifact	UNP O25511
A	-1	MET	-	cloning artifact	UNP O25511
A	0	SER	-	cloning artifact	UNP O25511
B	-10	MET	-	cloning artifact	UNP O25511
B	-9	HIS	-	EXPRESSION TAG	UNP O25511
B	-8	HIS	-	EXPRESSION TAG	UNP O25511
B	-7	HIS	-	EXPRESSION TAG	UNP O25511
B	-6	HIS	-	EXPRESSION TAG	UNP O25511
B	-5	HIS	-	EXPRESSION TAG	UNP O25511
B	-4	HIS	-	EXPRESSION TAG	UNP O25511
B	-3	GLY	-	cloning artifact	UNP O25511
B	-2	SER	-	cloning artifact	UNP O25511
B	-1	MET	-	cloning artifact	UNP O25511
B	0	SER	-	cloning artifact	UNP O25511

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: C<sub>21</sub>H<sub>28</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	B	1	Total 48	C 21	N 7	O 17	P 3	0	0

- Molecule 3 is URIDINE-DIPHOSPHATE-N-ACETYLGLUCOSAMINE (three-letter code: UD1) (formula:  $C_{17}H_{27}N_3O_{17}P_2$ ).



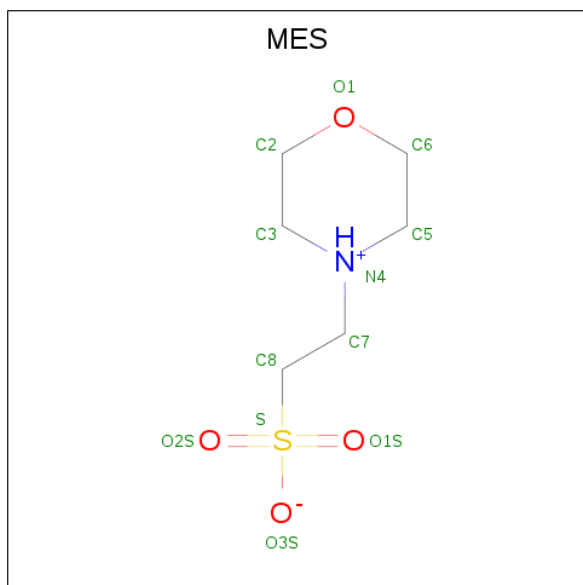
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	14	0
			39	17	3	17	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	P	14	0
			39	17	3	17	2		

- Molecule 4 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C<sub>6</sub>H<sub>13</sub>NO<sub>4</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

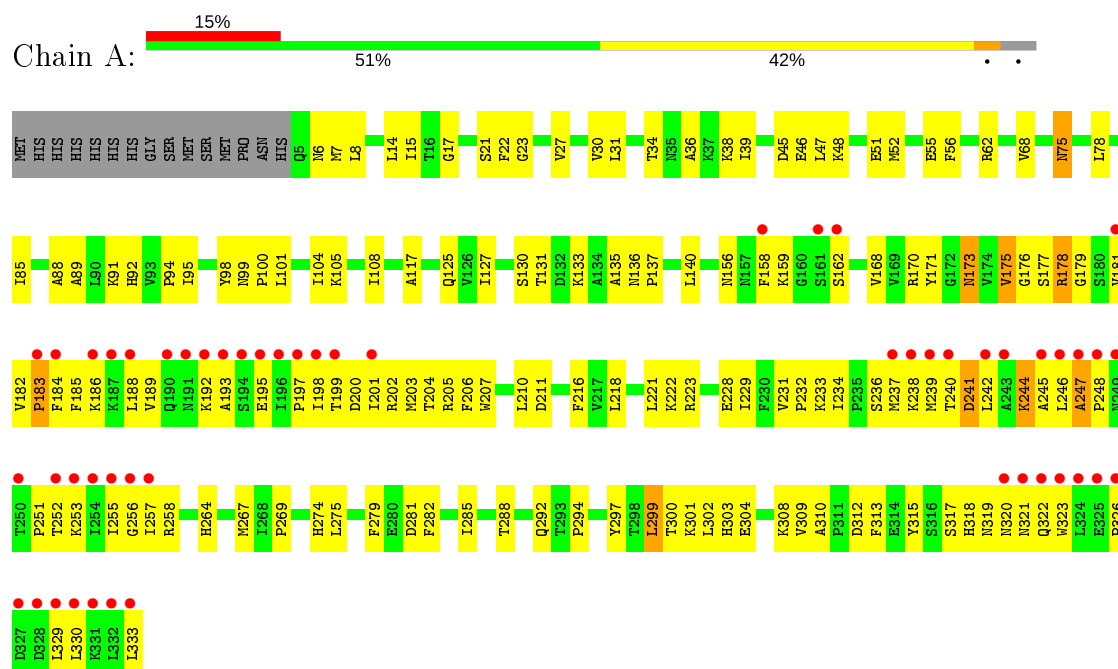
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	77	Total	O	0	0
			77	77		
5	B	91	Total	O	0	0
			91	91		

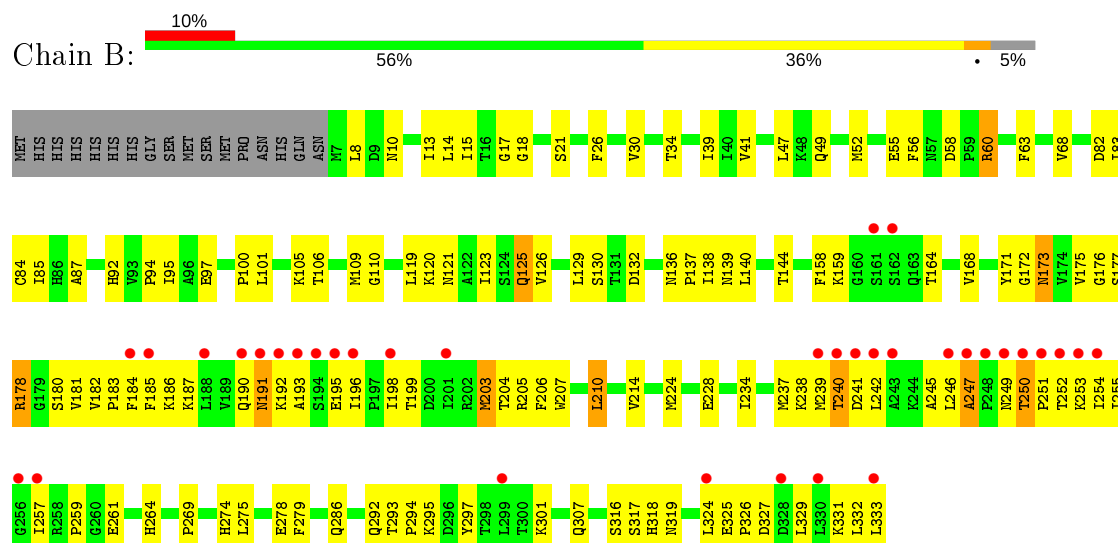
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: UDP-GlcNAc C6 dehydratase



#### • Molecule 1: UDP-GlcNAc C6 dehydratase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	109.85Å 109.85Å 107.98Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.70 48.95 – 2.70	Depositor EDS
% Data completeness (in resolution range)	97.6 (50.00-2.70) 97.7 (48.95-2.70)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.43 (at 2.69Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.204 , 0.269 0.196 , 0.259	Depositor DCC
$R_{free}$ test set	2005 reflections (9.86%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	22.0	Xtriage
Anisotropy	0.125	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 56.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.045 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	5517	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.07% 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: NAP, UD1, MES

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	0/2641	0.62	0/3568
1	B	0.36	0/2624	0.63	0/3545
All	All	0.36	0/5265	0.62	0/7113

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	2590	0	2641	165	0
1	B	2573	0	2627	134	0
2	A	48	0	25	5	0
2	B	48	0	25	3	0
3	A	39	0	25	1	0
3	B	39	0	25	0	0
4	B	12	0	13	0	0
5	A	77	0	0	4	0
5	B	91	0	0	0	0
All	All	5517	0	5381	299	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 28.

All (299) 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:198:ILE:HG22	1:A:199:THR:H	1.31	0.92
1:A:223:ARG:HA	1:A:301:LYS:HB2	1.56	0.88
1:A:176:GLY:HA2	1:A:183:PRO:HD3	1.54	0.87
1:B:8:LEU:HD22	1:B:13:ILE:HD11	1.56	0.86
1:A:186:LYS:HG2	1:A:246:LEU:HD22	1.58	0.84
1:A:173:ASN:H	1:A:173:ASN:HD22	1.22	0.84
1:A:233:LYS:HD2	1:A:281:ASP:HA	1.60	0.84
1:A:247:ALA:H	1:A:248:PRO:HD3	1.43	0.83
1:A:309:VAL:HG12	1:A:310:ALA:H	1.43	0.82
1:A:55:GLU:HG3	1:A:56:PHE:CD1	2.14	0.82
1:A:182:VAL:HB	1:A:183:PRO:HD3	1.62	0.80
1:B:176:GLY:HA2	1:B:183:PRO:HD3	1.64	0.80
1:B:136:ASN:HD21	1:B:269:PRO:HB3	1.46	0.79
1:B:195:GLU:HA	1:B:251:PRO:HG2	1.68	0.76
1:B:55:GLU:HG3	1:B:56:PHE:CD1	2.20	0.75
1:A:198:ILE:HG22	1:A:199:THR:N	2.01	0.75
1:A:8:LEU:HD12	1:A:34:THR:HG21	1.67	0.75
1:B:173:ASN:HD22	1:B:173:ASN:H	1.33	0.75
1:A:223:ARG:HB2	1:A:300:THR:HB	1.69	0.74
1:A:241:ASP:HA	1:A:244:LYS:HD3	1.66	0.74
1:B:100:PRO:HA	1:B:140:LEU:CD2	2.18	0.74
1:A:92:HIS:CE1	1:A:94:PRO:HG2	2.23	0.74
1:B:182:VAL:HG13	1:B:246:LEU:HD11	1.69	0.73
1:B:175:VAL:HG21	1:B:332:LEU:HD13	1.68	0.73
1:B:182:VAL:HG22	1:B:242:LEU:HD11	1.69	0.72
1:B:58:ASP:OD1	1:B:60:ARG:HG2	1.89	0.72
1:A:55:GLU:HG3	1:A:56:PHE:HD1	1.54	0.71
1:B:92:HIS:CD2	1:B:94:PRO:HG2	2.25	0.71
1:A:199:THR:HB	1:A:256:GLY:O	1.91	0.71
1:A:136:ASN:HD21	1:A:269:PRO:HB3	1.56	0.70
1:A:45:ASP:HB3	1:A:48:LYS:HE3	1.75	0.69
1:B:8:LEU:HD23	1:B:83:ILE:HD12	1.74	0.68
1:A:173:ASN:H	1:A:173:ASN:ND2	1.92	0.68
1:A:309:VAL:HG12	1:A:310:ALA:N	2.10	0.67
1:A:68:VAL:HG22	2:A:334:NAP:N1A	2.10	0.67
1:A:176:GLY:HA2	1:A:183:PRO:CD	2.24	0.66
1:B:186:LYS:HZ3	1:B:333:LEU:HD23	1.60	0.66
1:A:244:LYS:HA	1:A:248:PRO:HG3	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:333:LEU:HD12	1:B:333:LEU:H	1.59	0.66
1:B:186:LYS:NZ	1:B:333:LEU:HD23	2.11	0.66
1:A:198:ILE:HG12	1:A:252:THR:HB	1.78	0.66
1:B:204:THR:HG22	1:B:317:SER:HB2	1.75	0.65
1:A:189:VAL:HG21	1:A:247:ALA:HB2	1.78	0.65
1:B:239:MET:HE1	1:B:242:LEU:HD23	1.78	0.64
1:A:181:VAL:HG13	1:A:182:VAL:H	1.62	0.64
1:A:17:GLY:HA2	2:A:334:NAP:H1B	1.80	0.63
1:B:181:VAL:HG13	1:B:182:VAL:N	2.14	0.63
1:A:99:ASN:N	1:A:100:PRO:HD3	2.15	0.62
1:A:313:PHE:CZ	1:A:315:TYR:HB2	2.35	0.61
1:A:238:LYS:HD3	1:A:240:THR:OG1	2.00	0.61
1:B:159:LYS:HZ1	1:B:293:THR:N	1.99	0.61
1:A:238:LYS:HE2	1:A:240:THR:HG23	1.83	0.61
1:B:140:LEU:O	1:B:144:THR:HG23	2.01	0.60
1:A:177:SER:O	1:A:179:GLY:N	2.34	0.60
1:A:246:LEU:HD21	1:A:333:LEU:HD11	1.82	0.60
1:B:181:VAL:HG13	1:B:182:VAL:H	1.66	0.60
1:B:49:GLN:HG2	1:B:63:PHE:CD1	2.37	0.60
1:A:186:LYS:HG3	1:A:246:LEU:HD13	1.83	0.60
1:A:247:ALA:N	1:A:248:PRO:HD3	2.15	0.60
1:B:327:ASP:O	1:B:331:LYS:HG3	2.01	0.60
1:A:198:ILE:CG2	1:A:199:THR:H	2.11	0.60
1:A:239:MET:SD	1:A:242:LEU:HD23	2.42	0.60
1:A:246:LEU:O	1:A:247:ALA:HB2	2.01	0.59
1:A:186:LYS:HZ3	1:A:333:LEU:HD21	1.67	0.59
1:A:189:VAL:HG21	1:A:246:LEU:O	2.03	0.59
1:A:201:ILE:HG22	1:A:201:ILE:O	2.02	0.59
1:B:136:ASN:ND2	1:B:269:PRO:HB3	2.17	0.59
1:A:231:VAL:CG1	1:A:267:MET:HG2	2.34	0.58
1:B:293:THR:HG23	1:B:293:THR:O	2.04	0.58
1:A:75:ASN:ND2	1:A:117:ALA:HA	2.18	0.58
1:B:198:ILE:HG22	1:B:199:THR:N	2.19	0.58
1:A:100:PRO:HA	1:A:140:LEU:CD2	2.34	0.58
1:A:199:THR:HA	1:A:256:GLY:H	1.69	0.58
1:A:38:LYS:HD2	1:A:62:ARG:HG3	1.86	0.57
1:B:187:LYS:O	1:B:191:ASN:HB2	2.04	0.57
1:B:325:GLU:OE1	1:B:325:GLU:N	2.36	0.57
1:B:130:SER:HB2	1:B:168:VAL:CG1	2.33	0.57
1:B:292:GLN:O	1:B:294:PRO:HD3	2.04	0.57
1:A:15:ILE:HA	1:A:85:ILE:O	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:158:PHE:CG	1:A:159:LYS:N	2.73	0.57
1:B:190:GLN:C	1:B:192:LYS:H	2.07	0.57
1:B:119:LEU:HD22	1:B:158:PHE:CD2	2.40	0.56
1:B:329:LEU:HD12	1:B:332:LEU:HD12	1.86	0.56
1:B:49:GLN:OE1	1:B:63:PHE:HB3	2.05	0.56
1:B:119:LEU:HD22	1:B:158:PHE:HD2	1.70	0.56
1:B:159:LYS:NZ	1:B:293:THR:HB	2.20	0.56
1:A:318:HIS:NE2	1:A:319:ASN:ND2	2.54	0.56
1:B:184:PHE:C	1:B:186:LYS:H	2.09	0.56
1:A:181:VAL:HG13	1:A:182:VAL:N	2.20	0.56
1:A:98:TYR:C	1:A:100:PRO:HD3	2.26	0.56
1:B:203:MET:HB3	1:B:239:MET:HB3	1.87	0.56
1:A:299:LEU:CD2	1:A:303:HIS:HA	2.36	0.55
1:A:228:GLU:HG3	1:A:297:TYR:CE2	2.42	0.55
1:A:188:LEU:C	1:A:193:ALA:HB2	2.26	0.55
1:A:206:PHE:CE1	1:A:317:SER:HB3	2.41	0.55
1:A:186:LYS:HE2	1:A:333:LEU:HD11	1.87	0.55
1:B:182:VAL:HG13	1:B:246:LEU:CD1	2.36	0.55
1:B:293:THR:O	1:B:295:LYS:HE3	2.07	0.55
1:A:244:LYS:O	1:A:326:PRO:HB2	2.07	0.55
1:B:206:PHE:HB3	1:B:234:ILE:CD1	2.37	0.54
1:B:171:TYR:O	2:B:334:NAP:H5N	2.07	0.54
1:A:201:ILE:O	1:A:238:LYS:HE3	2.07	0.54
1:A:47:LEU:O	1:A:51:GLU:HG2	2.07	0.54
1:B:173:ASN:HD21	1:B:205:ARG:HD2	1.72	0.54
1:A:257:ILE:HG22	1:A:258:ARG:N	2.22	0.54
1:A:229:ILE:HB	1:A:285:ILE:HB	1.90	0.54
1:A:198:ILE:CG1	1:A:252:THR:HB	2.37	0.53
1:A:244:LYS:HG3	1:A:326:PRO:HG3	1.90	0.53
1:A:330:LEU:O	1:A:330:LEU:HD23	2.08	0.53
1:B:224:MET:O	1:B:301:LYS:HE2	2.07	0.53
1:B:159:LYS:HZ3	1:B:293:THR:HB	1.73	0.53
1:A:236:SER:O	1:A:323:TRP:HA	2.09	0.53
1:B:249:ASN:O	1:B:250:THR:HB	2.09	0.53
1:A:135:ALA:HA	5:A:393:HOH:O	2.09	0.53
1:A:195:GLU:HG2	1:A:253:LYS:H	1.73	0.53
1:B:138:ILE:HG13	1:B:139:ASN:N	2.23	0.53
1:A:186:LYS:NZ	1:A:333:LEU:HD21	2.23	0.52
1:B:184:PHE:HA	1:B:187:LYS:HE2	1.91	0.52
1:A:238:LYS:HZ1	1:A:240:THR:HG21	1.74	0.52
1:B:333:LEU:HD12	1:B:333:LEU:N	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:333:LEU:H	1:B:333:LEU:CD1	2.22	0.52
1:A:14:LEU:HD13	1:A:78:LEU:HD23	1.92	0.52
1:B:105:LYS:O	1:B:109:MET:HB2	2.10	0.52
1:B:100:PRO:HB3	1:B:140:LEU:HD22	1.92	0.52
1:B:278:GLU:HG3	1:B:279:PHE:N	2.24	0.52
1:A:75:ASN:HD21	1:A:117:ALA:HA	1.74	0.52
1:B:204:THR:HG22	1:B:317:SER:CB	2.40	0.52
1:A:264:HIS:CG	1:A:318:HIS:HB3	2.45	0.52
1:A:173:ASN:HD21	1:A:205:ARG:HD2	1.75	0.51
1:B:136:ASN:N	1:B:137:PRO:CD	2.74	0.51
1:A:242:LEU:HD13	1:A:329:LEU:HD21	1.91	0.51
1:A:274:HIS:H	1:A:274:HIS:CD2	2.29	0.51
1:A:309:VAL:HG11	1:A:313:PHE:CD2	2.46	0.51
1:A:330:LEU:HA	1:A:333:LEU:HB2	1.93	0.51
1:B:228:GLU:HG3	1:B:297:TYR:CE1	2.46	0.51
1:B:257:ILE:HG23	1:B:261:GLU:HB2	1.93	0.51
1:B:83:ILE:HG12	1:B:125:GLN:HG3	1.93	0.51
1:A:137:PRO:HA	5:A:351:HOH:O	2.11	0.51
1:B:316:SER:HB2	1:B:318:HIS:CE1	2.46	0.51
1:B:100:PRO:CB	1:B:140:LEU:HD22	2.41	0.50
1:B:245:ALA:HB2	1:B:326:PRO:CB	2.42	0.50
1:B:8:LEU:HD13	1:B:34:THR:HG21	1.93	0.50
1:A:173:ASN:ND2	1:A:205:ARG:HD2	2.26	0.50
1:A:231:VAL:HG13	1:A:267:MET:HG2	1.94	0.50
1:B:173:ASN:H	1:B:173:ASN:ND2	2.08	0.50
1:A:203:MET:HG2	3:A:335:UD1:O2'	2.12	0.50
1:B:247:ALA:HB1	1:B:250:THR:CG2	2.42	0.50
1:A:101:LEU:HG	1:A:105:LYS:HE3	1.95	0.49
1:B:237:MET:HE2	1:B:324:LEU:O	2.13	0.49
1:B:84:CYS:HB3	1:B:126:VAL:HG22	1.93	0.49
1:B:92:HIS:HD2	1:B:95:ILE:H	1.60	0.49
1:B:132:ASP:OD1	1:B:172:GLY:HA2	2.12	0.49
1:B:177:SER:OG	1:B:180:SER:HB3	2.13	0.49
1:A:185:PHE:HB3	1:A:246:LEU:HB2	1.95	0.49
1:A:197:PRO:O	1:A:198:ILE:HD13	2.14	0.48
1:A:200:ASP:OD2	1:A:202:ARG:HB2	2.12	0.48
1:B:52:MET:HA	1:B:55:GLU:HG2	1.95	0.48
1:B:68:VAL:HG22	2:B:334:NAP:N1A	2.28	0.48
1:B:195:GLU:O	1:B:195:GLU:HG3	2.13	0.48
1:B:245:ALA:HB2	1:B:326:PRO:HB3	1.94	0.48
1:B:182:VAL:N	1:B:183:PRO:HD2	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:8:LEU:HD22	1:B:13:ILE:CD1	2.37	0.48
1:A:242:LEU:HD13	1:A:329:LEU:CD2	2.44	0.48
1:B:239:MET:CE	1:B:242:LEU:HD23	2.44	0.48
1:B:18:GLY:HA3	1:B:41:VAL:HG13	1.96	0.47
1:B:238:LYS:NZ	1:B:240:THR:HG21	2.29	0.47
1:B:319:ASN:CG	1:B:319:ASN:O	2.52	0.47
1:B:8:LEU:CD2	1:B:83:ILE:HD12	2.44	0.47
1:A:319:ASN:OD1	1:A:319:ASN:O	2.32	0.47
1:B:173:ASN:HD22	1:B:173:ASN:N	2.09	0.47
1:A:186:LYS:HE2	1:A:246:LEU:HD21	1.96	0.47
1:A:275:LEU:CD1	1:A:288:THR:HG22	2.45	0.47
1:A:62:ARG:HH11	1:A:62:ARG:HG2	1.79	0.47
1:A:88:ALA:O	1:A:89:ALA:HB2	2.15	0.47
1:B:49:GLN:HG2	1:B:63:PHE:HD1	1.79	0.47
1:B:238:LYS:HE2	1:B:240:THR:HB	1.95	0.47
1:B:316:SER:HB2	1:B:318:HIS:ND1	2.30	0.47
1:A:189:VAL:CG2	1:A:247:ALA:HB2	2.43	0.47
1:B:203:MET:HB3	1:B:239:MET:CB	2.44	0.47
1:B:101:LEU:HG	1:B:105:LYS:HE3	1.97	0.47
1:B:159:LYS:HE3	1:B:292:GLN:HB2	1.97	0.47
1:B:198:ILE:CG2	1:B:199:THR:N	2.77	0.47
1:B:17:GLY:HA2	2:B:334:NAP:H1B	1.97	0.46
1:A:184:PHE:C	1:A:186:LYS:H	2.19	0.46
1:A:239:MET:CE	1:A:242:LEU:HD23	2.45	0.46
1:A:104:ILE:HG23	1:A:108:ILE:HD12	1.97	0.46
1:A:91:LYS:HE2	2:A:334:NAP:O2N	2.15	0.46
1:A:257:ILE:CG2	1:A:258:ARG:N	2.78	0.46
1:A:173:ASN:OD1	1:A:205:ARG:HD2	2.15	0.46
1:A:202:ARG:O	1:A:204:THR:HG23	2.15	0.46
1:B:318:HIS:CG	1:B:319:ASN:N	2.84	0.46
1:A:197:PRO:HB3	1:A:255:ILE:CD1	2.46	0.46
1:B:240:THR:HG22	1:B:241:ASP:OD1	2.15	0.46
1:A:133:LYS:O	1:A:137:PRO:HB3	2.16	0.46
1:A:173:ASN:N	1:A:173:ASN:ND2	2.60	0.46
1:A:182:VAL:C	1:A:184:PHE:H	2.19	0.46
1:A:195:GLU:OE2	1:A:251:PRO:HB2	2.16	0.46
1:A:156:ASN:C	1:A:158:PHE:H	2.20	0.46
1:B:210:LEU:O	1:B:214:VAL:HG23	2.15	0.46
1:A:192:LYS:HG3	1:A:192:LYS:O	2.16	0.45
1:A:186:LYS:HG2	1:A:246:LEU:CD2	2.39	0.45
1:B:15:ILE:HA	1:B:85:ILE:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:92:HIS:NE2	1:B:94:PRO:HG2	2.31	0.45
1:A:321:ASN:HB2	1:A:322:GLN:NE2	2.31	0.45
1:A:21:SER:OG	1:A:178:ARG:HB2	2.17	0.45
1:A:238:LYS:NZ	1:A:240:THR:HG21	2.31	0.45
1:B:123:ILE:O	1:B:164:THR:HG23	2.16	0.45
1:B:21:SER:OG	1:B:178:ARG:HB2	2.16	0.45
1:B:159:LYS:CE	1:B:292:GLN:HB2	2.46	0.45
1:A:222:LYS:HB3	1:A:302:LEU:HD11	1.99	0.45
1:B:207:TRP:CD1	1:B:237:MET:HB3	2.51	0.45
1:B:286:GLN:HE21	1:B:297:TYR:HD2	1.63	0.45
1:A:207:TRP:O	1:A:234:ILE:HB	2.17	0.45
1:B:247:ALA:HB1	1:B:250:THR:HG21	1.97	0.45
1:B:159:LYS:NZ	1:B:292:GLN:HB2	2.32	0.45
1:A:185:PHE:CD1	1:A:185:PHE:N	2.84	0.45
1:B:199:THR:OG1	1:B:203:MET:HE2	2.17	0.45
1:A:92:HIS:HE1	1:A:94:PRO:HG2	1.80	0.45
1:B:100:PRO:HA	1:B:140:LEU:HD22	1.95	0.44
1:B:120:LYS:HD3	1:B:121:ASN:CG	2.38	0.44
1:B:190:GLN:C	1:B:192:LYS:N	2.70	0.44
1:B:191:ASN:HD22	1:B:193:ALA:HB2	1.81	0.44
1:B:246:LEU:O	1:B:247:ALA:HB2	2.17	0.44
1:A:182:VAL:CB	1:A:183:PRO:HD3	2.40	0.44
1:A:92:HIS:HB3	1:A:95:ILE:HB	1.99	0.44
1:B:87:ALA:CB	1:B:129:LEU:HD12	2.47	0.44
1:A:279:PHE:HB2	1:A:282:PHE:O	2.18	0.44
1:A:185:PHE:HD1	1:A:185:PHE:N	2.16	0.44
1:A:223:ARG:NH1	1:A:304:GLU:OE2	2.51	0.44
1:A:30:VAL:HG12	1:A:39:ILE:HD11	2.00	0.44
1:B:14:LEU:HD23	1:B:15:ILE:N	2.33	0.44
1:B:184:PHE:HA	1:B:187:LYS:CE	2.47	0.44
1:A:195:GLU:OE1	1:A:253:LYS:HB2	2.18	0.44
1:A:55:GLU:HG3	1:A:56:PHE:CE1	2.53	0.44
1:B:100:PRO:CA	1:B:140:LEU:CD2	2.94	0.44
1:A:182:VAL:HG13	1:A:246:LEU:HD11	2.00	0.43
1:A:181:VAL:HG11	1:A:242:LEU:HD21	2.00	0.43
1:B:196:ILE:O	1:B:252:THR:HA	2.17	0.43
1:A:135:ALA:HB1	1:A:269:PRO:HG3	2.00	0.43
1:A:48:LYS:HZ1	2:A:334:NAP:P2B	2.40	0.43
1:B:253:LYS:HD2	1:B:255:ILE:HG23	1.99	0.43
1:B:82:ASP:O	1:B:123:ILE:HG23	2.18	0.43
1:A:292:GLN:O	1:A:294:PRO:HD3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:47:LEU:HD13	1:B:47:LEU:C	2.39	0.43
1:B:55:GLU:HG3	1:B:56:PHE:HD1	1.77	0.43
1:A:171:TYR:O	2:A:334:NAP:H5N	2.17	0.43
1:B:191:ASN:C	1:B:193:ALA:N	2.71	0.43
1:B:204:THR:HB	1:B:264:HIS:ND1	2.34	0.43
1:B:181:VAL:CG1	1:B:182:VAL:N	2.82	0.43
1:A:176:GLY:HA2	1:A:183:PRO:CG	2.48	0.43
1:A:199:THR:HA	1:A:256:GLY:N	2.33	0.43
1:A:247:ALA:H	1:A:248:PRO:CD	2.21	0.43
1:B:87:ALA:HB2	1:B:129:LEU:HD12	2.00	0.43
1:B:55:GLU:HG3	1:B:56:PHE:CE1	2.54	0.43
1:A:186:LYS:HZ1	1:A:333:LEU:HG	1.83	0.42
1:A:242:LEU:CD1	1:A:329:LEU:HD21	2.48	0.42
1:B:293:THR:HG23	1:B:295:LYS:HE3	2.00	0.42
1:A:223:ARG:HD2	1:A:304:GLU:OE1	2.19	0.42
1:A:175:VAL:HG22	1:A:207:TRP:CE3	2.55	0.42
1:B:100:PRO:CA	1:B:140:LEU:HD22	2.49	0.42
1:A:231:VAL:HG11	1:A:267:MET:HG2	2.01	0.42
1:A:195:GLU:HG3	1:A:251:PRO:O	2.19	0.42
1:A:8:LEU:O	1:A:36:ALA:HA	2.19	0.42
1:A:23:GLY:O	1:A:27:VAL:HG23	2.20	0.42
1:B:274:HIS:CE1	1:B:275:LEU:HG	2.54	0.42
1:B:26:PHE:O	1:B:30:VAL:HG23	2.20	0.42
1:A:310:ALA:O	1:A:312:ASP:N	2.53	0.42
1:A:241:ASP:O	1:A:326:PRO:HB3	2.20	0.42
1:A:198:ILE:CG2	1:A:199:THR:N	2.73	0.42
1:A:318:HIS:CE1	1:A:319:ASN:ND2	2.87	0.42
1:A:186:LYS:HE3	1:A:246:LEU:HD11	2.02	0.42
1:A:244:LYS:CA	1:A:248:PRO:HG3	2.48	0.42
1:A:31:LEU:CD2	1:A:39:ILE:HD12	2.50	0.42
1:A:173:ASN:ND2	5:A:349:HOH:O	2.54	0.41
1:A:246:LEU:O	1:A:247:ALA:CB	2.66	0.41
1:B:106:THR:O	1:B:110:GLY:HA3	2.20	0.41
1:B:30:VAL:HG12	1:B:39:ILE:HD11	2.01	0.41
1:A:236:SER:N	1:A:320:ASN:HD21	2.17	0.41
1:A:46:GLU:HG2	5:A:408:HOH:O	2.20	0.41
1:A:7:MET:CE	1:A:125:GLN:HE22	2.33	0.41
1:A:216:PHE:CE2	1:A:232:PRO:HD3	2.56	0.41
1:A:130:SER:HB2	1:A:168:VAL:CG1	2.50	0.41
1:A:45:ASP:OD1	1:A:48:LYS:HE2	2.19	0.41
1:A:309:VAL:HG11	1:A:313:PHE:CG	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:130:SER:HB3	1:A:170:ARG:HB2	2.02	0.41
1:A:205:ARG:HG2	1:A:205:ARG:HH11	1.85	0.41
1:B:238:LYS:C	1:B:240:THR:H	2.22	0.41
1:A:206:PHE:CD1	1:A:317:SER:HB3	2.56	0.41
1:A:22:PHE:HA	1:A:210:LEU:HD11	2.02	0.41
1:A:182:VAL:HG12	1:A:186:LYS:HE3	2.03	0.41
1:B:257:ILE:CG2	1:B:261:GLU:HB2	2.51	0.41
1:B:26:PHE:HD1	1:B:214:VAL:HG13	1.85	0.41
1:A:188:LEU:O	1:A:193:ALA:HB2	2.21	0.41
1:A:207:TRP:CD1	1:A:237:MET:HB3	2.55	0.41
1:A:52:MET:HA	1:A:55:GLU:HG2	2.03	0.41
1:B:237:MET:HE3	1:B:329:LEU:HB2	2.03	0.40
1:B:242:LEU:HD12	1:B:329:LEU:HD21	2.02	0.40
1:A:127:ILE:CD1	1:A:221:LEU:HD23	2.52	0.40
1:B:94:PRO:O	1:B:97:GLU:HB2	2.21	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	327/344 (95%)	283 (86%)	36 (11%)	8 (2%)	6	15
1	B	325/344 (94%)	298 (92%)	20 (6%)	7 (2%)	6	17
All	All	652/688 (95%)	581 (89%)	56 (9%)	15 (2%)	6	16

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	162	SER
1	A	178	ARG
1	A	247	ALA

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Mol	Chain	Res	Type
1	A	308	LYS
1	B	254	ILE
1	A	6	ASN
1	A	245	ALA
1	B	178	ARG
1	B	185	PHE
1	B	191	ASN
1	B	250	THR
1	A	183	PRO
1	B	247	ALA
1	B	259	PRO
1	A	175	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	290/304 (95%)	282 (97%)	8 (3%)	43	73
1	B	288/304 (95%)	280 (97%)	8 (3%)	43	73
All	All	578/608 (95%)	562 (97%)	16 (3%)	43	73

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	75	ASN
1	A	131	THR
1	A	173	ASN
1	A	211	ASP
1	A	218	LEU
1	A	241	ASP
1	A	244	LYS
1	A	299	LEU
1	B	10	ASN
1	B	60	ARG
1	B	125	GLN

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Mol	Chain	Res	Type
1	B	173	ASN
1	B	203	MET
1	B	210	LEU
1	B	240	THR
1	B	307	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	ASN
1	A	75	ASN
1	A	125	GLN
1	A	136	ASN
1	A	157	ASN
1	A	173	ASN
1	A	274	HIS
1	A	292	GLN
1	A	319	ASN
1	A	321	ASN
1	A	322	GLN
1	B	10	ASN
1	B	35	ASN
1	B	75	ASN
1	B	92	HIS
1	B	136	ASN
1	B	165	GLN
1	B	173	ASN
1	B	191	ASN
1	B	274	HIS
1	B	286	GLN
1	B	320	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

5 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	UD1	A	335	-	34,41,41	1.30	3 (8%)	45,62,62	1.51	3 (6%)
3	UD1	B	335	-	34,41,41	1.36	3 (8%)	45,62,62	1.52	3 (6%)
4	MES	B	336	-	12,12,12	0.93	1 (8%)	14,16,16	1.03	0
2	NAP	A	334	-	45,52,52	1.70	12 (26%)	56,80,80	1.66	8 (14%)
2	NAP	B	334	-	45,52,52	1.74	11 (24%)	56,80,80	1.64	8 (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
3	UD1	A	335	-	-	11/24/63/63	0/3/3/3
3	UD1	B	335	-	-	9/24/63/63	0/3/3/3
4	MES	B	336	-	-	2/6/14/14	0/1/1/1
2	NAP	A	334	-	-	4/31/67/67	0/5/5/5
2	NAP	B	334	-	-	2/31/67/67	0/5/5/5

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	334	NAP	C2N-N1N	4.23	1.40	1.35
3	B	335	UD1	C4-N3	4.18	1.40	1.33
3	A	335	UD1	C4-N3	3.98	1.40	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	334	NAP	C2N-N1N	3.89	1.39	1.35
2	B	334	NAP	P2B-O1X	3.58	1.62	1.50
2	A	334	NAP	C2A-N1A	3.33	1.40	1.33
2	B	334	NAP	C2A-N1A	3.28	1.40	1.33
3	B	335	UD1	PB-O1B	3.22	1.62	1.50
3	B	335	UD1	PA-O1A	3.17	1.62	1.50
2	B	334	NAP	PA-O1A	3.16	1.62	1.50
2	A	334	NAP	PA-O1A	3.14	1.62	1.50
3	A	335	UD1	PB-O1B	3.08	1.61	1.50
2	A	334	NAP	P2B-O1X	3.07	1.60	1.50
3	A	335	UD1	PA-O1A	3.05	1.61	1.50
2	B	334	NAP	PN-O1N	3.01	1.61	1.50
2	A	334	NAP	C4N-C3N	2.73	1.44	1.39
2	A	334	NAP	PN-O1N	2.73	1.60	1.50
2	B	334	NAP	C4A-N3A	2.67	1.39	1.35
4	B	336	MES	C8-S	2.58	1.81	1.77
2	B	334	NAP	C2A-N3A	2.55	1.36	1.32
2	B	334	NAP	C4N-C3N	2.52	1.43	1.39
2	A	334	NAP	C2D-C1D	-2.52	1.49	1.53
2	A	334	NAP	C2A-N3A	2.47	1.36	1.32
2	B	334	NAP	C2N-C3N	2.37	1.42	1.39
2	B	334	NAP	C7N-N7N	2.37	1.37	1.33
2	A	334	NAP	C7N-N7N	2.34	1.37	1.33
2	B	334	NAP	C2D-C1D	-2.19	1.50	1.53
2	A	334	NAP	C2N-C3N	2.15	1.42	1.39
2	A	334	NAP	O4B-C1B	2.13	1.44	1.41
2	A	334	NAP	C5N-C4N	2.04	1.43	1.38

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	335	UD1	O5'-C1'-O1'	-6.69	102.61	111.36
3	A	335	UD1	O5'-C1'-O1'	-6.53	102.83	111.36
2	A	334	NAP	C6N-N1N-C2N	6.35	127.76	121.97
2	B	334	NAP	C6N-N1N-C2N	6.18	127.61	121.97
2	B	334	NAP	C3N-C2N-N1N	-4.93	115.61	120.43
2	A	334	NAP	C3N-C2N-N1N	-4.88	115.66	120.43
3	A	335	UD1	C5-C4-N3	-3.94	114.63	123.31
3	B	335	UD1	C5-C4-N3	-3.92	114.68	123.31
2	A	334	NAP	C3D-C2D-C1D	3.91	106.87	100.98
2	B	334	NAP	C3D-C2D-C1D	3.69	106.53	100.98
3	A	335	UD1	C3B-C2B-C1B	3.47	106.20	100.98

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	335	UD1	C3B-C2B-C1B	3.29	105.94	100.98
2	B	334	NAP	O7N-C7N-C3N	3.27	123.55	119.63
2	A	334	NAP	O7N-C7N-C3N	3.08	123.32	119.63
2	B	334	NAP	C3N-C7N-N7N	-2.84	114.34	117.75
2	A	334	NAP	C5N-C6N-N1N	-2.59	116.69	120.40
2	A	334	NAP	N6A-C6A-N1A	2.55	123.87	118.57
2	A	334	NAP	C3N-C7N-N7N	-2.54	114.70	117.75
2	B	334	NAP	N6A-C6A-N1A	2.49	123.74	118.57
2	A	334	NAP	C1B-N9A-C4A	-2.44	122.35	126.64
2	B	334	NAP	C5N-C6N-N1N	-2.44	116.90	120.40
2	B	334	NAP	C1B-N9A-C4A	-2.33	122.56	126.64

There are no chirality outliers.

All (28) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	335	UD1	C8'-C7'-N2'-C2'
3	A	335	UD1	O7'-C7'-N2'-C2'
3	A	335	UD1	C1'-O1'-PB-O3A
3	A	335	UD1	O4B-C4B-C5B-O5B
3	A	335	UD1	C5B-O5B-PA-O1A
3	A	335	UD1	C5B-O5B-PA-O3A
4	B	336	MES	C8-C7-N4-C5
3	B	335	UD1	C8'-C7'-N2'-C2'
3	B	335	UD1	O7'-C7'-N2'-C2'
3	B	335	UD1	C1'-O1'-PB-O3A
3	B	335	UD1	C2B-C1B-N1-C6
3	B	335	UD1	O4B-C1B-N1-C6
3	A	335	UD1	C3B-C4B-C5B-O5B
3	B	335	UD1	C4'-C5'-C6'-O6'
3	B	335	UD1	O5'-C5'-C6'-O6'
4	B	336	MES	C8-C7-N4-C3
2	A	334	NAP	C2B-O2B-P2B-O1X
3	A	335	UD1	C4'-C5'-C6'-O6'
2	A	334	NAP	C2B-O2B-P2B-O2X
3	A	335	UD1	C5B-O5B-PA-O2A
3	B	335	UD1	C1'-O1'-PB-O2B
3	B	335	UD1	PA-O3A-PB-O1B
2	A	334	NAP	O4D-C4D-C5D-O5D
2	B	334	NAP	O4D-C4D-C5D-O5D
3	A	335	UD1	O5'-C5'-C6'-O6'
2	B	334	NAP	O4B-C4B-C5B-O5B

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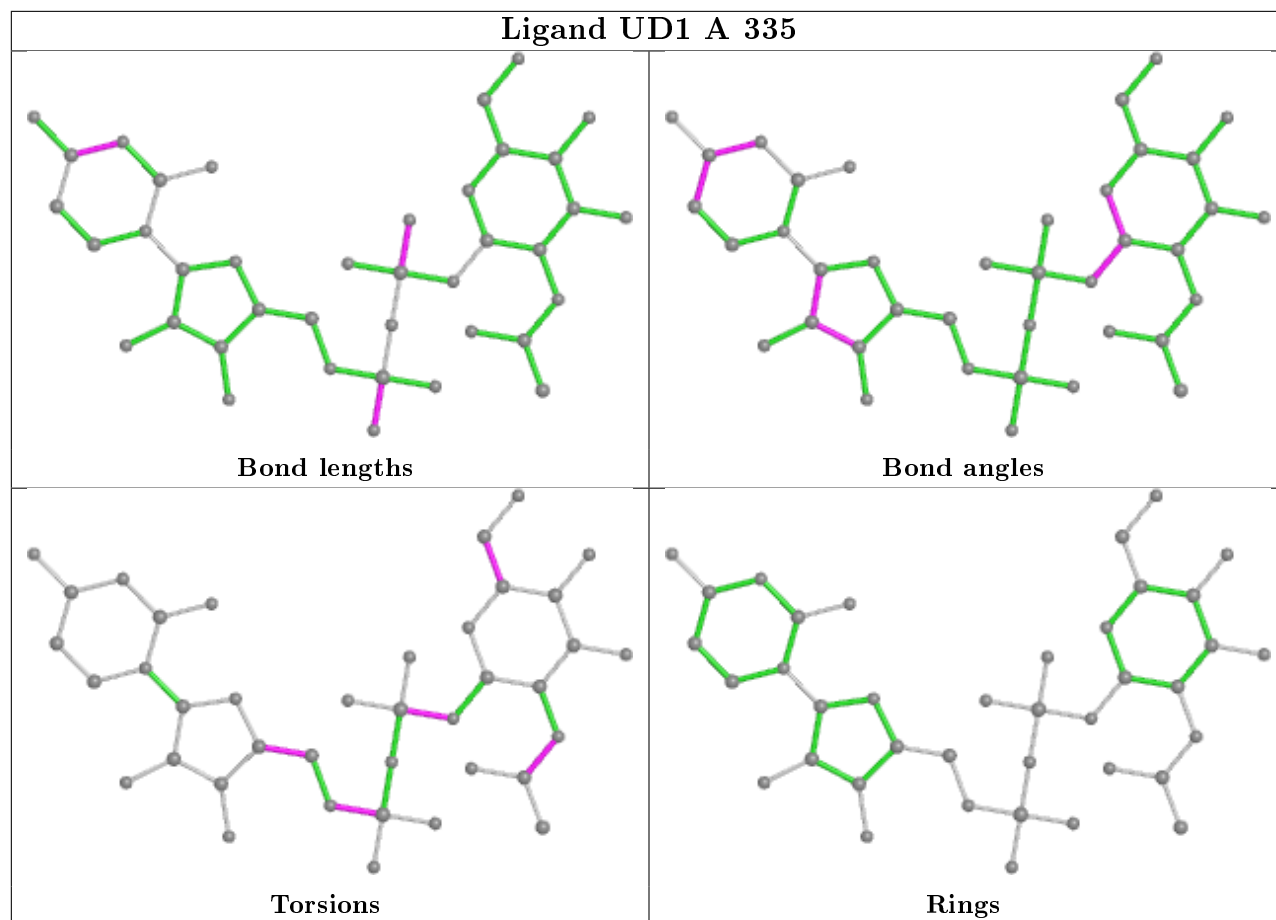
Mol	Chain	Res	Type	Atoms
3	A	335	UD1	C1'-O1'-PB-O1B
2	A	334	NAP	O4B-C4B-C5B-O5B

There are no ring outliers.

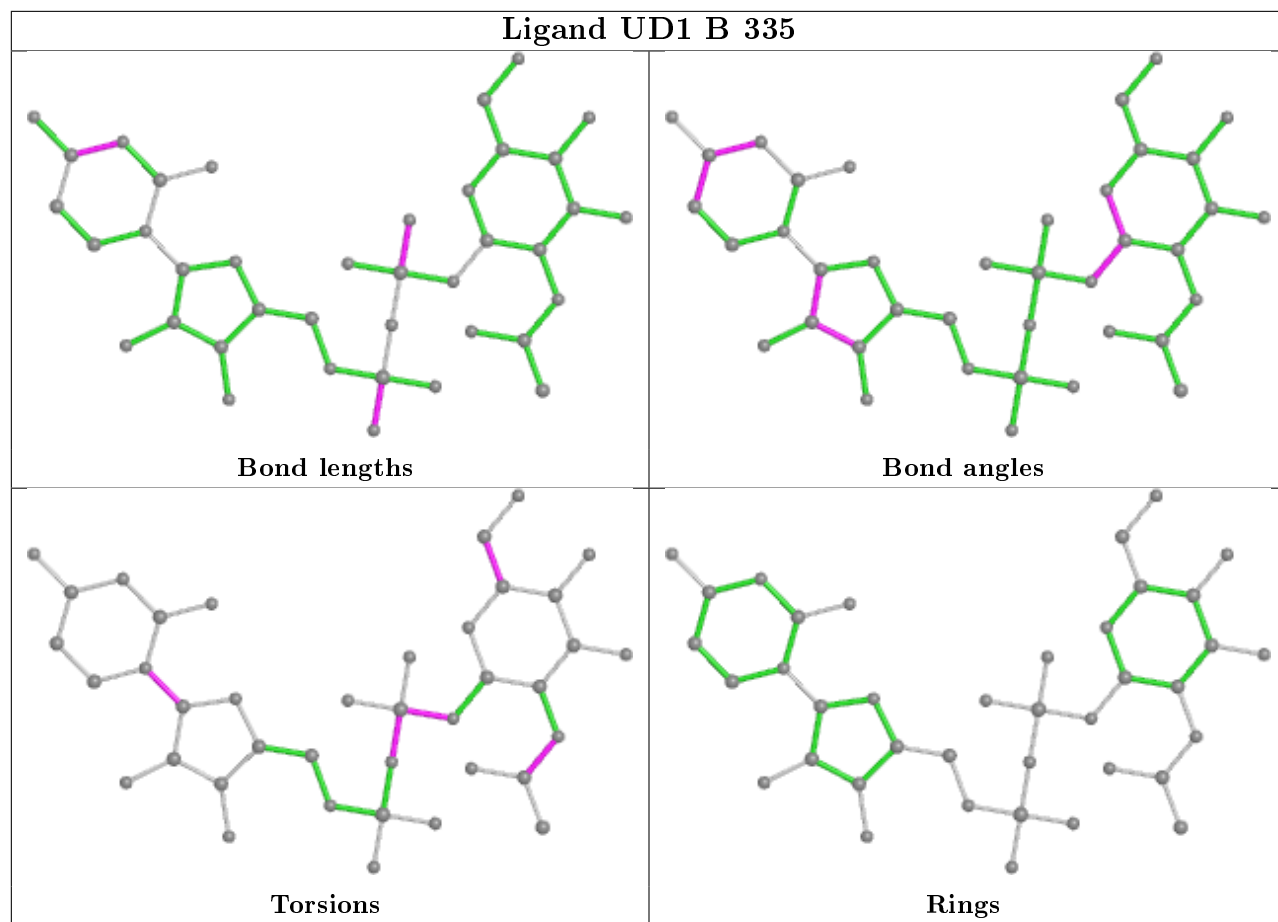
3 monomers are involved in 9 short contacts:

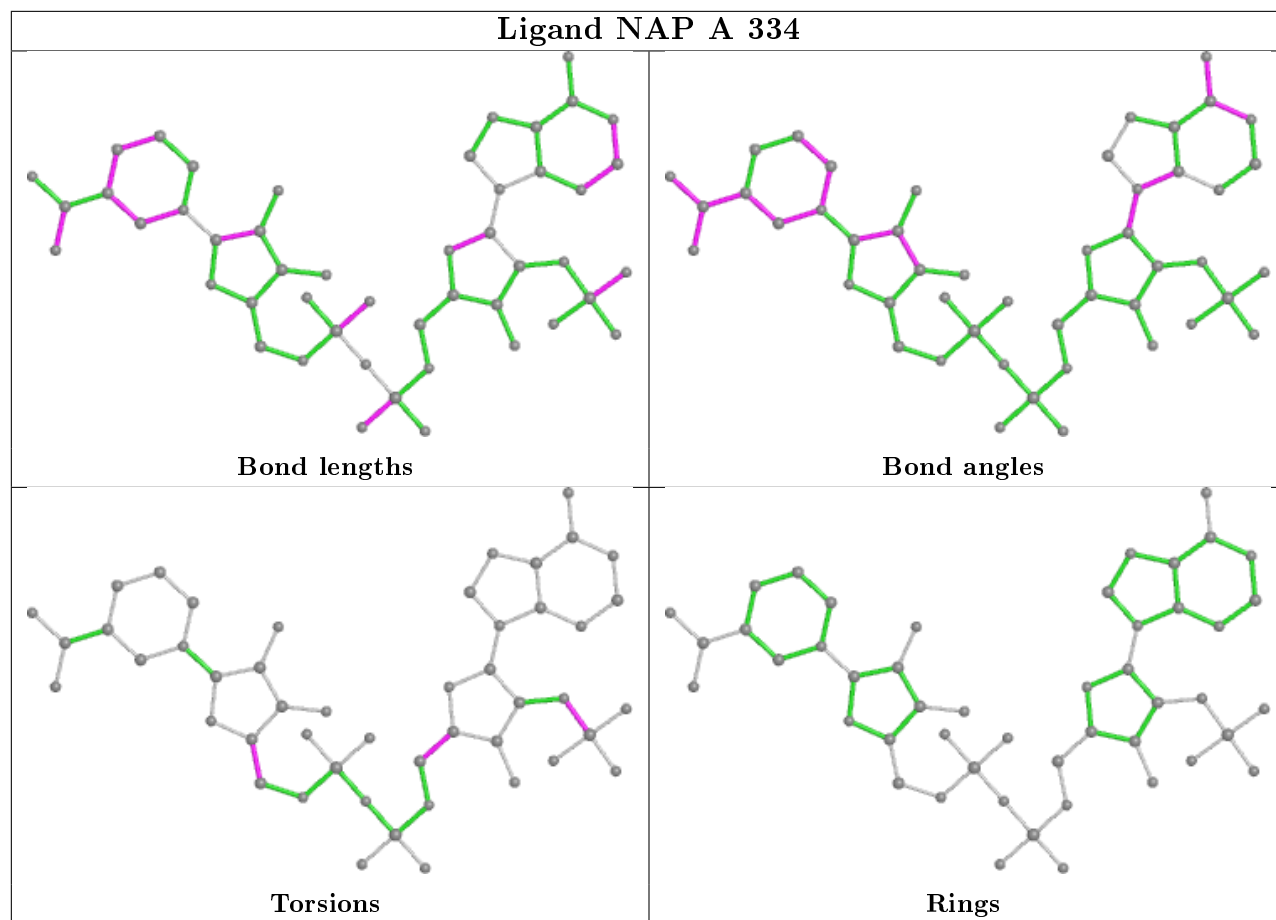
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	335	UD1	1	0
2	A	334	NAP	5	0
2	B	334	NAP	3	0

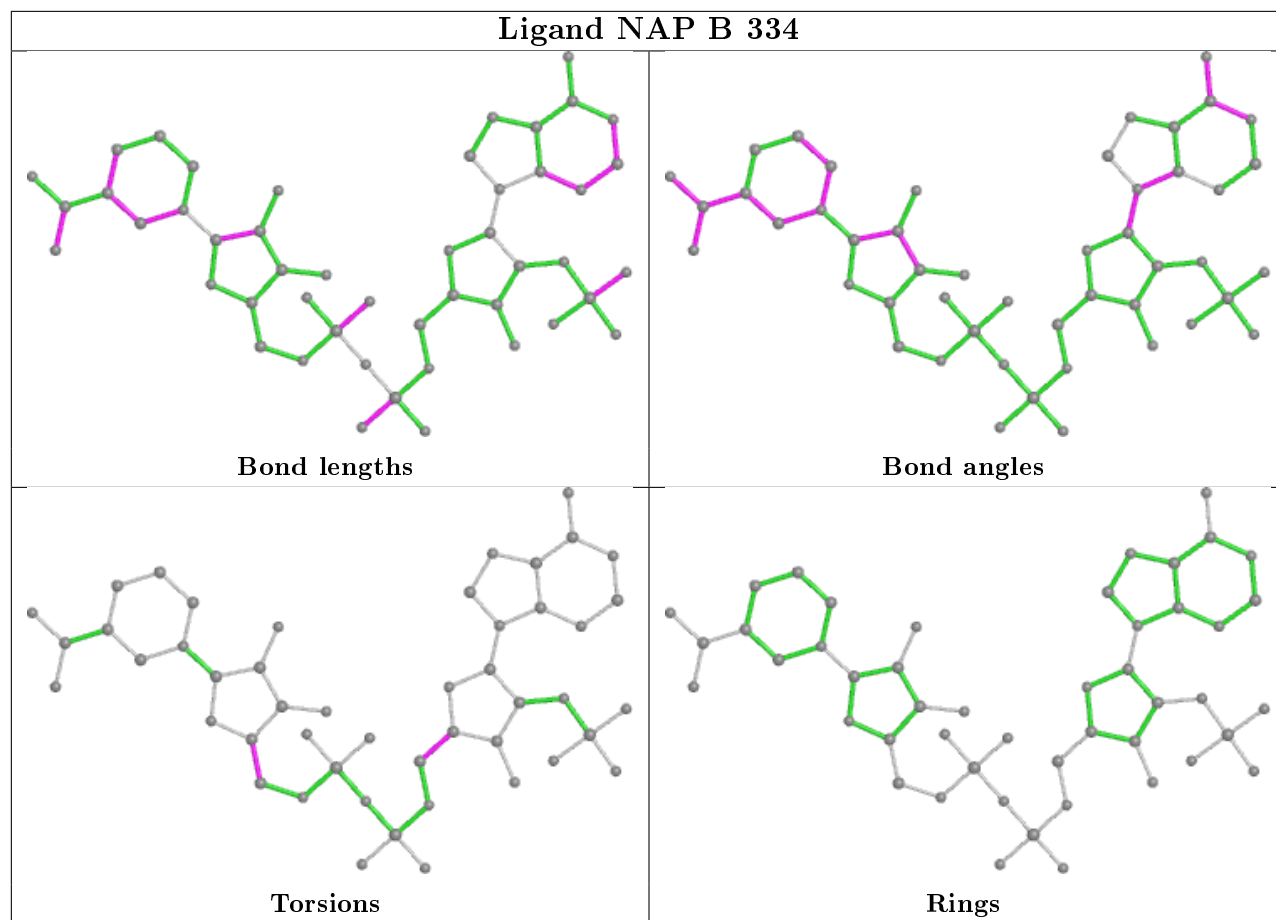
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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	329/344 (95%)	0.53	52 (15%) 2 1	5, 26, 80, 80	0
1	B	327/344 (95%)	0.23	35 (10%) 6 4	5, 22, 76, 80	0
All	All	656/688 (95%)	0.38	87 (13%) 3 2	5, 24, 80, 80	0

All (87) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	196	ILE	11.3
1	A	161	SER	8.2
1	A	247	ALA	8.1
1	A	243	ALA	8.0
1	A	248	PRO	7.9
1	A	330	LEU	6.7
1	A	246	LEU	6.6
1	A	326	PRO	6.5
1	B	196	ILE	6.3
1	B	161	SER	6.1
1	B	243	ALA	6.0
1	A	245	ALA	5.9
1	B	162	SER	5.7
1	A	249	ASN	5.5
1	A	191	ASN	5.1
1	A	186	LYS	5.1
1	A	188	LEU	5.0
1	A	183	PRO	4.8
1	A	192	LYS	4.8
1	A	237	MET	4.6
1	A	187	LYS	4.5
1	A	162	SER	4.4
1	B	193	ALA	4.3
1	A	239	MET	4.2

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Mol	Chain	Res	Type	RSRZ
1	A	240	THR	4.1
1	B	257	ILE	4.1
1	A	184	PHE	3.9
1	A	195	GLU	3.9
1	A	198	ILE	3.9
1	B	249	ASN	3.9
1	A	329	LEU	3.8
1	A	194	SER	3.8
1	A	332	LEU	3.7
1	A	190	GLN	3.7
1	B	195	GLU	3.7
1	B	242	LEU	3.7
1	B	194	SER	3.7
1	B	251	PRO	3.6
1	A	324	LEU	3.6
1	A	193	ALA	3.6
1	B	240	THR	3.6
1	B	253	LYS	3.6
1	A	333	LEU	3.6
1	B	324	LEU	3.6
1	A	181	VAL	3.4
1	A	320	ASN	3.3
1	B	191	ASN	3.3
1	A	250	THR	3.2
1	B	330	LEU	3.1
1	B	250	THR	3.0
1	A	197	PRO	3.0
1	A	323	TRP	3.0
1	B	192	LYS	2.9
1	A	257	ILE	2.9
1	B	239	MET	2.9
1	A	328	ASP	2.9
1	B	246	LEU	2.8
1	B	198	ILE	2.8
1	A	325	GLU	2.7
1	B	201	ILE	2.7
1	A	252	THR	2.7
1	A	199	THR	2.6
1	B	256	GLY	2.6
1	A	327	ASP	2.5
1	B	248	PRO	2.5
1	A	254	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	184	PHE	2.5
1	A	255	ILE	2.5
1	B	188	LEU	2.4
1	A	158	PHE	2.4
1	A	256	GLY	2.4
1	B	190	GLN	2.3
1	A	331	LYS	2.3
1	B	299	LEU	2.3
1	B	247	ALA	2.3
1	B	252	THR	2.3
1	A	201	ILE	2.3
1	A	253	LYS	2.3
1	B	328	ASP	2.3
1	B	333	LEU	2.2
1	B	241	ASP	2.2
1	A	321	ASN	2.2
1	A	242	LEU	2.2
1	B	185	PHE	2.1
1	A	238	LYS	2.1
1	A	322	GLN	2.0
1	B	254	ILE	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. 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( $\text{\AA}^2$ )	Q<0.9
4	MES	B	336	12/12	0.66	0.46	78,80,80,80	0
3	UD1	A	335	39/39	0.81	0.27	75,79,80,80	14

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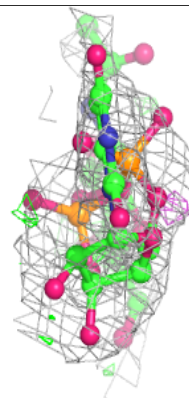
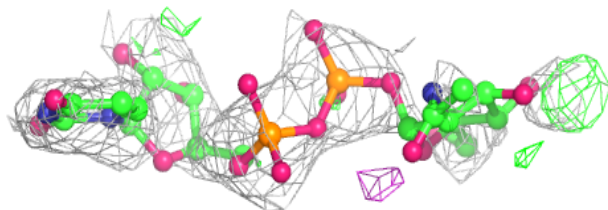
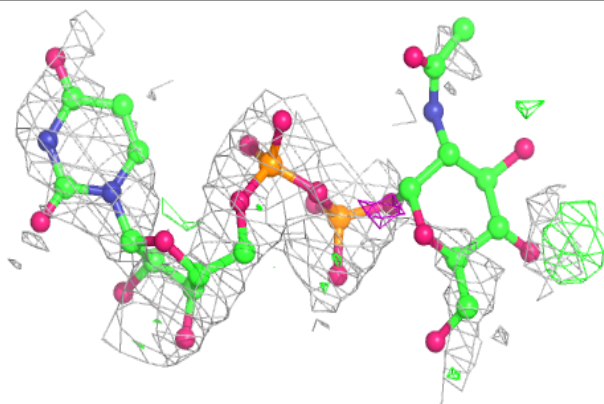
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	UD1	B	335	39/39	0.86	0.21	56,61,72,72	14
2	NAP	B	334	48/48	0.96	0.17	13,24,49,51	0
2	NAP	A	334	48/48	0.97	0.16	7,22,40,42	0

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.

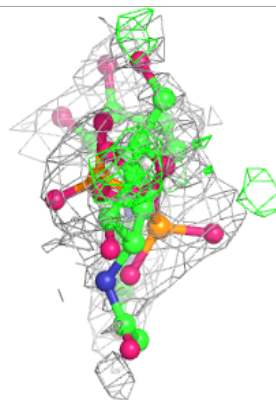
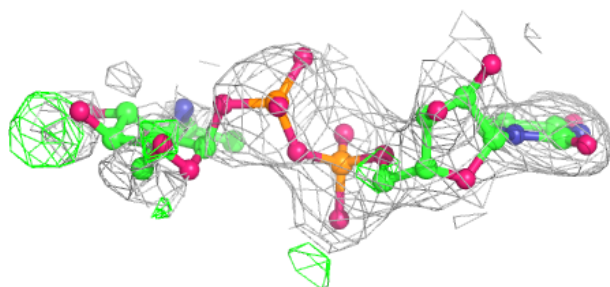
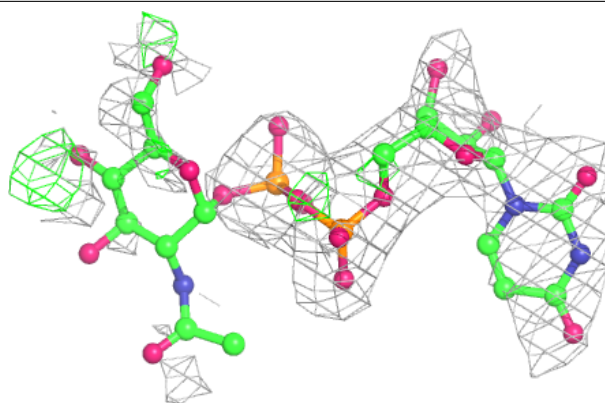
**Electron density around UD1 A 335:**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)

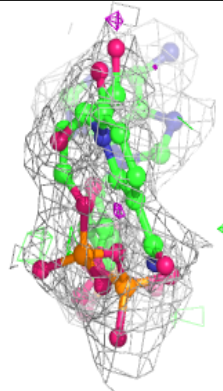
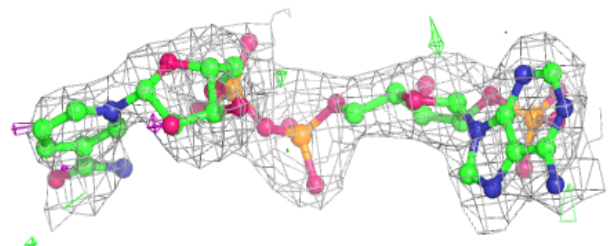
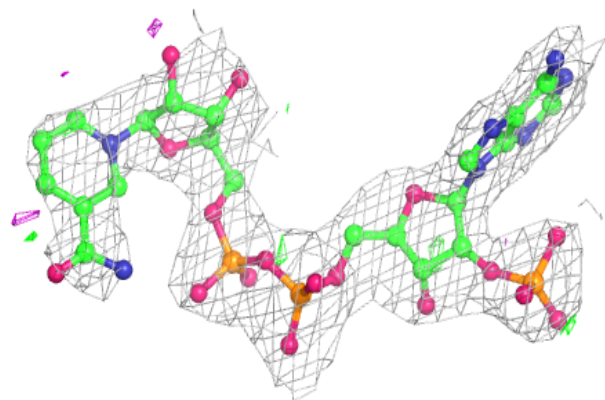


**Electron density around UD1 B 335:**

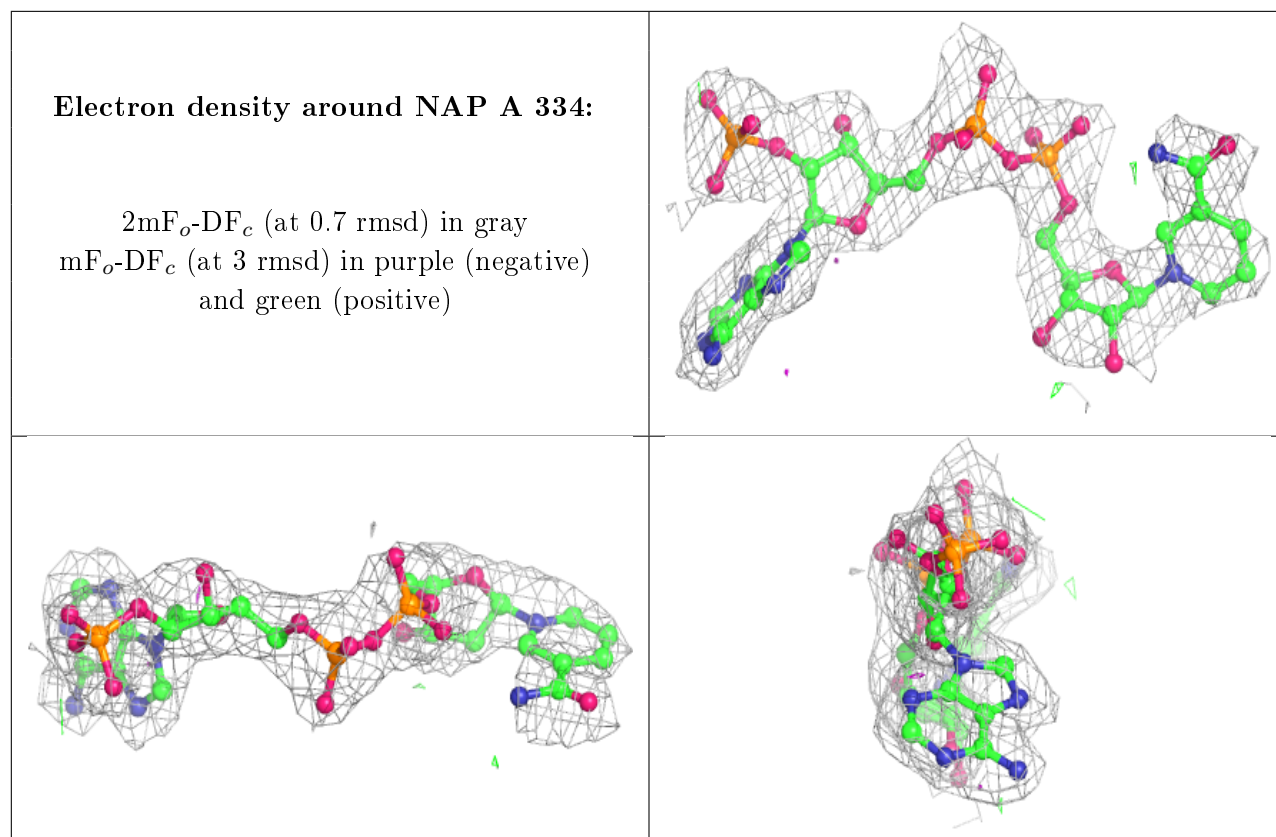
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around NAP B 334:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)







## 6.5 Other polymers [i](#)

There are no such residues in this entry.