



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 18, 2026 – 06:13 PM UTC

PDB ID : 4WDW / pdb_00004wdw
Title : 17beta-HSD5 in complex with 3,6-dihydropyridin-1(2H)-yl(5-methyl-1H-indol-2-yl)methanone
Authors : Amano, Y.; Yamaguchi, T.
Deposited on : 2014-09-09
Resolution : 1.94 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

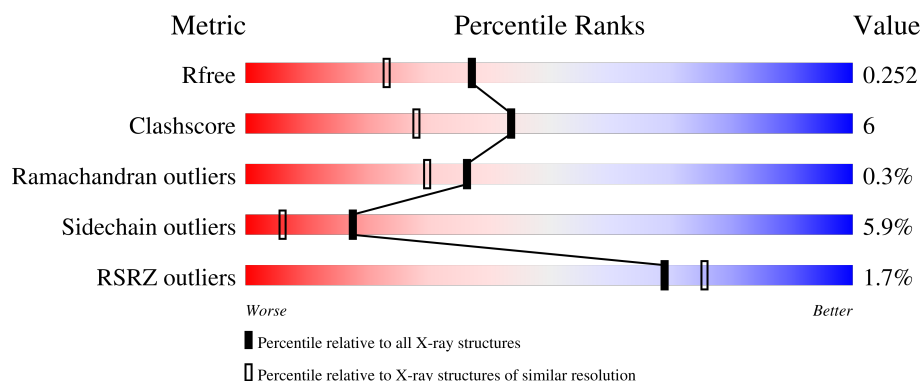
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.94 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}	180053	1452 (1.94-1.94)
Clashscore	190562	1494 (1.94-1.94)
Ramachandran outliers	187476	1479 (1.94-1.94)
Sidechain outliers	187428	1479 (1.94-1.94)
RSRZ outliers	180081	1453 (1.94-1.94)

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 ≥ 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	331	% 71% 16% .. 10%
1	B	331	2% 77% 12% . 9%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5069 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.

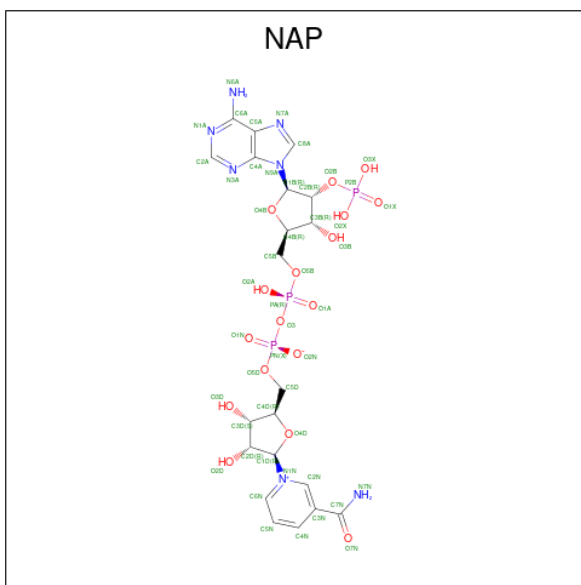
- Molecule 1 is a protein called Aldo-keto reductase family 1 member C3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	298	Total	C	N	O	S	0	0	0
			2380	1518	418	432	12			
1	B	301	Total	C	N	O	S	0	0	0
			2408	1536	423	437	12			

There are 18 discrepancies between the modelled and reference sequences:

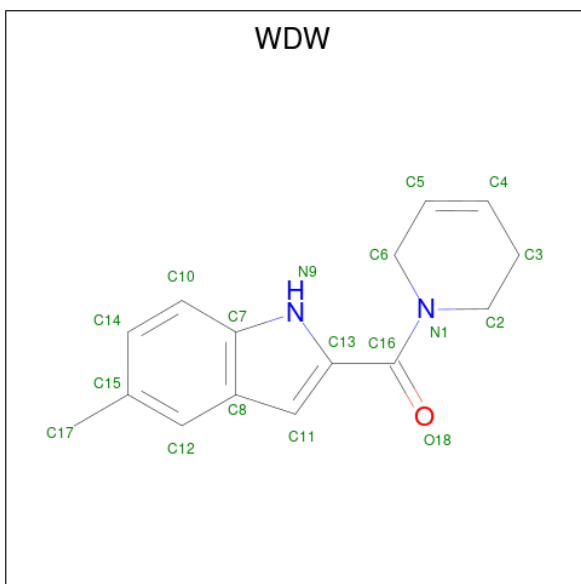
Chain	Residue	Modelled	Actual	Comment	Reference
A	5	GLN	HIS	variant	UNP P42330
A	324	LEU	-	expression tag	UNP P42330
A	325	GLU	-	expression tag	UNP P42330
A	326	HIS	-	expression tag	UNP P42330
A	327	HIS	-	expression tag	UNP P42330
A	328	HIS	-	expression tag	UNP P42330
A	329	HIS	-	expression tag	UNP P42330
A	330	HIS	-	expression tag	UNP P42330
A	331	HIS	-	expression tag	UNP P42330
B	5	GLN	HIS	variant	UNP P42330
B	324	LEU	-	expression tag	UNP P42330
B	325	GLU	-	expression tag	UNP P42330
B	326	HIS	-	expression tag	UNP P42330
B	327	HIS	-	expression tag	UNP P42330
B	328	HIS	-	expression tag	UNP P42330
B	329	HIS	-	expression tag	UNP P42330
B	330	HIS	-	expression tag	UNP P42330
B	331	HIS	-	expression tag	UNP P42330

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NAP) (formula: C₂₁H₂₈N₇O₁₇P₃).



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 3,6-dihydropyridin-1(2H)-yl(5-methyl-1H-indol-2-yl)methanone (CCD ID: WDW) (formula: C₁₅H₁₆N₂O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			18	15	2	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			18	15	2	1		

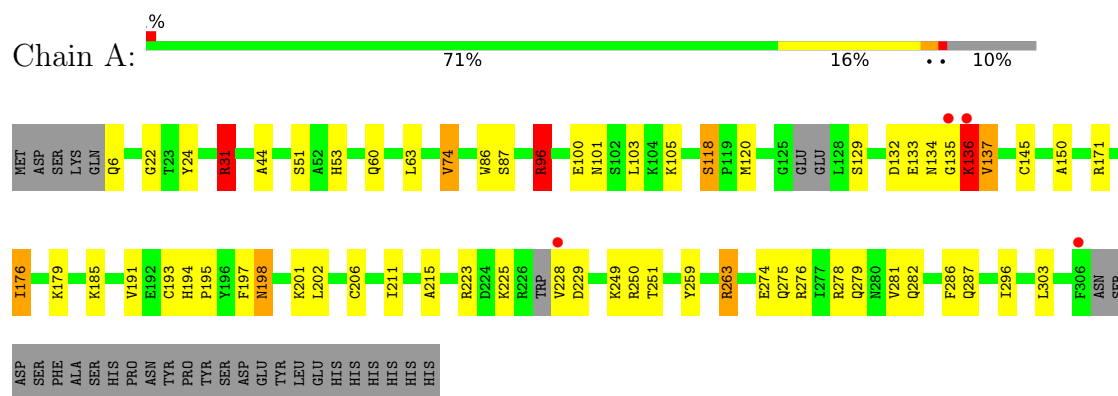
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	74	Total	O	0	0
			74	74		
4	B	75	Total	O	0	0
			75	75		

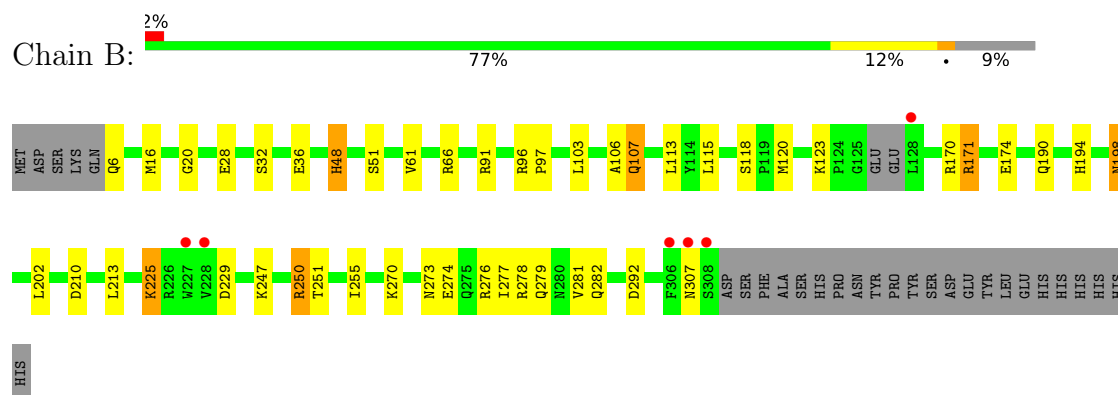
3 Residue-property plots

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: Aldo-keto reductase family 1 member C3



- Molecule 1: Aldo-keto reductase family 1 member C3



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	55.13Å 57.92Å 60.33Å 81.03° 69.72° 79.11°	Depositor
Resolution (Å)	14.60 – 1.94 14.60 – 1.94	Depositor EDS
% Data completeness (in resolution range)	93.5 (14.60-1.94) 93.5 (14.60-1.94)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.87 (at 1.94Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.199 , 0.253 0.198 , 0.252	Depositor DCC
R_{free} test set	2404 reflections (4.76%)	wwPDB-VP
Wilson B-factor (Å ²)	28.3	Xtriage
Anisotropy	0.080	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.45 , 38.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5069	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 15.39% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: WDW, NAP

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	1.26	3/2428 (0.1%)	1.28	14/3278 (0.4%)
1	B	1.34	6/2459 (0.2%)	1.30	17/3323 (0.5%)
All	All	1.30	9/4887 (0.2%)	1.29	31/6601 (0.5%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	307	ASN	CA-C	7.79	1.57	1.52
1	A	44	ALA	N-CA	6.03	1.54	1.46
1	B	48	HIS	C-O	-5.85	1.17	1.24
1	A	191	VAL	N-CA	5.74	1.52	1.46
1	A	51	SER	CA-C	5.73	1.59	1.53
1	B	255	ILE	CA-C	5.58	1.59	1.52
1	B	210	ASP	CA-C	5.13	1.59	1.53
1	B	51	SER	C-O	-5.05	1.19	1.24
1	B	16	MET	CA-C	5.04	1.58	1.52

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	96	ARG	NE-CZ-NH2	10.67	128.80	119.20
1	A	229	ASP	CA-C-N	-7.81	111.61	120.04
1	A	229	ASP	C-N-CA	-7.81	111.61	120.04
1	B	91	ARG	CA-C-N	7.13	127.45	119.32
1	B	91	ARG	C-N-CA	7.13	127.45	119.32
1	B	307	ASN	N-CA-C	7.07	120.15	108.48
1	A	96	ARG	NE-CZ-NH1	-6.91	114.59	121.50
1	B	250	ARG	NE-CZ-NH2	6.69	125.22	119.20
1	B	61	VAL	N-CA-C	-6.50	104.15	110.72
1	A	176	ILE	CB-CA-C	-6.46	103.58	112.04

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	74	VAL	CB-CA-C	-6.32	99.62	110.30
1	B	123	LYS	CA-C-N	-6.14	113.95	120.03
1	B	123	LYS	C-N-CA	-6.14	113.95	120.03
1	B	229	ASP	CA-C-N	6.10	125.82	119.05
1	B	229	ASP	C-N-CA	6.10	125.82	119.05
1	A	185	LYS	CA-C-N	-6.03	113.73	119.76
1	A	185	LYS	C-N-CA	-6.03	113.73	119.76
1	B	255	ILE	N-CA-C	-5.70	105.18	110.53
1	B	274	GLU	N-CA-C	5.58	117.80	111.11
1	B	247	LYS	N-CA-C	5.50	117.27	111.28
1	B	292	ASP	N-CA-C	-5.47	105.22	111.07
1	B	118	SER	CA-C-N	-5.36	114.25	120.04
1	B	118	SER	C-N-CA	-5.36	114.25	120.04
1	A	137	VAL	N-CA-C	5.20	120.16	109.34
1	A	251	THR	CA-C-N	5.16	124.33	118.97
1	A	251	THR	C-N-CA	5.16	124.33	118.97
1	A	53	HIS	N-CA-C	-5.14	105.11	111.33
1	B	194	HIS	CA-C-N	-5.14	114.37	119.56
1	B	194	HIS	C-N-CA	-5.14	114.37	119.56
1	A	31	ARG	NE-CZ-NH2	5.02	123.72	119.20
1	A	150	ALA	N-CA-C	-5.01	106.00	111.82

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	2380	0	2418	30	0
1	B	2408	0	2440	27	0
2	A	48	0	25	3	0
2	B	48	0	25	4	0
3	A	18	0	16	1	0
3	B	18	0	16	3	0
4	A	74	0	0	0	0
4	B	75	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5069	0	4940	60	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 6.

All (60) 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:B:171:ARG:NH1	1:B:174:GLU:HG3	1.90	0.85
1:A:135:GLY:HA3	1:A:136:LYS:HB2	1.60	0.83
3:B:402:WDW:C11	3:B:402:WDW:H12	2.10	0.79
1:B:198:ASN:HD22	1:B:198:ASN:C	1.90	0.79
3:B:402:WDW:H12	3:B:402:WDW:H4	1.64	0.78
1:A:279:GLN:NE2	2:A:401:NAP:H62A	1.82	0.77
1:A:250:ARG:HH11	1:A:282:GLN:HE21	1.35	0.74
1:A:132:ASP:OD1	1:A:136:LYS:HB3	1.88	0.74
1:A:96:ARG:HD2	1:A:100:GLU:OE2	1.88	0.73
1:B:171:ARG:NH1	1:B:174:GLU:OE1	2.22	0.73
1:A:135:GLY:CA	1:A:136:LYS:HB2	2.19	0.71
1:B:171:ARG:HH11	1:B:174:GLU:HG3	1.53	0.70
1:A:259:TYR:O	1:A:263:ARG:HG3	1.93	0.69
1:A:101:ASN:HD21	1:A:105:LYS:HE3	1.60	0.67
1:A:250:ARG:HH11	1:A:282:GLN:NE2	1.95	0.64
1:B:279:GLN:NE2	2:B:401:NAP:H62A	1.95	0.64
1:B:278:ARG:HG2	1:B:278:ARG:HH21	1.62	0.63
1:A:198:ASN:C	1:A:198:ASN:HD22	2.07	0.63
1:B:171:ARG:NH1	1:B:174:GLU:CG	2.60	0.61
1:A:24:TYR:CD2	3:A:402:WDW:H8	2.39	0.57
1:B:225:LYS:H	1:B:225:LYS:HD2	1.70	0.57
1:B:279:GLN:O	1:B:282:GLN:HB2	2.05	0.56
1:B:270:LYS:HB2	2:B:401:NAP:H52N	1.88	0.56
1:A:101:ASN:ND2	1:A:105:LYS:HE3	2.22	0.54
1:B:66:ARG:CZ	1:B:107:GLN:HG3	2.38	0.54
1:A:274:GLU:O	1:A:278:ARG:HG3	2.09	0.53
1:B:171:ARG:HH11	1:B:174:GLU:CG	2.19	0.53
1:B:32:SER:O	1:B:36:GLU:HG3	2.10	0.52
1:B:278:ARG:O	1:B:281:VAL:HG22	2.11	0.51
1:B:20:GLY:HA2	1:B:48:HIS:HB3	1.93	0.51
1:B:96:ARG:HB3	1:B:97:PRO:HD3	1.92	0.51
1:B:28:GLU:H	1:B:28:GLU:CD	2.18	0.50
1:B:66:ARG:NH1	1:B:107:GLN:HG3	2.27	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:278:ARG:HG2	1:B:278:ARG:NH2	2.25	0.49
1:B:106:ALA:C	1:B:107:GLN:HG2	2.34	0.49
1:B:170:ARG:O	1:B:174:GLU:HG2	2.13	0.48
3:B:402:WDW:C11	3:B:402:WDW:C2	2.89	0.47
1:A:259:TYR:HB2	1:A:296:ILE:HD13	1.97	0.47
1:B:171:ARG:NH1	1:B:174:GLU:CD	2.72	0.46
1:A:145:CYS:HB3	1:A:179:LYS:HD3	1.97	0.45
1:B:276:ARG:HD2	2:B:401:NAP:C5A	2.47	0.45
1:A:22:GLY:HA3	2:A:401:NAP:H4D	1.99	0.45
1:A:31:ARG:N	1:A:31:ARG:HD2	2.33	0.44
1:A:171:ARG:O	1:A:171:ARG:HD3	2.18	0.43
1:A:194:HIS:HB2	1:A:195:PRO:CD	2.48	0.43
1:A:145:CYS:HB3	1:A:179:LYS:CD	2.48	0.43
1:A:60:GLN:NE2	1:A:60:GLN:H	2.17	0.42
1:A:276:ARG:HD2	2:A:401:NAP:C5A	2.49	0.42
1:B:190:GLN:OE1	2:B:401:NAP:H2N	2.19	0.42
1:A:118:SER:OG	1:A:120:MET:HG2	2.19	0.41
1:A:250:ARG:HG3	1:A:286:PHE:CE2	2.55	0.41
1:B:113:LEU:HD21	1:B:115:LEU:HD21	2.02	0.41
1:A:86:TRP:CG	1:A:87:SER:H	2.38	0.41
1:A:197:PHE:HB2	1:A:303:LEU:O	2.20	0.41
1:A:223:ARG:HA	1:A:228:VAL:HG11	2.01	0.41
1:B:251:THR:OG1	1:B:279:GLN:NE2	2.53	0.41
1:A:86:TRP:CG	1:A:87:SER:N	2.88	0.41
1:A:193:CYS:HB3	1:A:215:ALA:CB	2.51	0.41
1:B:273:ASN:O	1:B:277:ILE:HG13	2.20	0.41
1:A:206:CYS:HB3	1:A:211:ILE:O	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	292/331 (88%)	281 (96%)	9 (3%)	2 (1%)	18	9
1	B	297/331 (90%)	284 (96%)	13 (4%)	0	100	100
All	All	589/662 (89%)	565 (96%)	22 (4%)	2 (0%)	36	30

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	136	LYS
1	A	137	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	263/295 (89%)	242 (92%)	21 (8%)	11	2
1	B	266/295 (90%)	256 (96%)	10 (4%)	29	15
All	All	529/590 (90%)	498 (94%)	31 (6%)	18	6

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	GLN
1	A	31	ARG
1	A	63	LEU
1	A	74	VAL
1	A	96	ARG
1	A	103	LEU
1	A	118	SER
1	A	129	SER
1	A	133	GLU
1	A	134	ASN
1	A	136	LYS
1	A	176	ILE
1	A	198	ASN
1	A	201	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	202	LEU
1	A	225	LYS
1	A	249	LYS
1	A	263	ARG
1	A	275	GLN
1	A	281	VAL
1	A	287	GLN
1	B	6	GLN
1	B	103	LEU
1	B	107	GLN
1	B	120	MET
1	B	171	ARG
1	B	198	ASN
1	B	202	LEU
1	B	213	LEU
1	B	225	LYS
1	B	250	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	56	ASN
1	A	60	GLN
1	A	101	ASN
1	A	198	ASN
1	A	279	GLN
1	A	282	GLN
1	B	6	GLN
1	B	56	ASN
1	B	60	GLN
1	B	198	ASN
1	B	279	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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
2	NAP	A	401	-	50,52,52	1.14	4 (8%)	71,80,80	1.20	8 (11%)
3	WDW	A	402	-	19,20,20	0.94	1 (5%)	23,28,28	2.08	9 (39%)
2	NAP	B	401	-	50,52,52	1.16	6 (12%)	71,80,80	1.20	6 (8%)
3	WDW	B	402	-	19,20,20	0.57	0	23,28,28	2.14	11 (47%)

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	NAP	A	401	-	-	2/35/67/67	0/5/5/5
3	WDW	A	402	-	-	2/8/16/16	0/3/3/3
2	NAP	B	401	-	-	4/35/67/67	0/5/5/5
3	WDW	B	402	-	-	6/8/16/16	0/3/3/3

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	NAP	P2B-O2B	3.80	1.66	1.59
2	B	401	NAP	P2B-O2B	3.48	1.65	1.59
2	A	401	NAP	C6A-N6A	2.87	1.41	1.34
2	B	401	NAP	C6A-N6A	2.77	1.41	1.34
2	A	401	NAP	C3N-C7N	-2.56	1.46	1.50
3	A	402	WDW	C16-N1	2.42	1.38	1.34

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	NAP	C7N-N7N	2.40	1.37	1.33
2	A	401	NAP	C7N-N7N	2.30	1.37	1.33
2	B	401	NAP	C3N-C7N	-2.23	1.47	1.50
2	B	401	NAP	PN-O3	2.15	1.61	1.59
2	B	401	NAP	O4D-C4D	-2.13	1.40	1.45

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	402	WDW	C11-C13-N9	-4.88	104.31	109.15
3	B	402	WDW	C7-N9-C13	3.74	113.03	109.01
3	A	402	WDW	C11-C13-N9	-3.68	105.50	109.15
3	A	402	WDW	C7-N9-C13	3.60	112.87	109.01
3	B	402	WDW	C8-C12-C15	-3.57	117.77	122.64
3	A	402	WDW	C8-C12-C15	-3.55	117.81	122.64
3	A	402	WDW	C3-C2-N1	3.53	116.78	110.74
2	B	401	NAP	C2N-C3N-C4N	3.43	122.25	118.26
3	A	402	WDW	C10-C7-C8	3.19	125.02	122.13
3	B	402	WDW	C17-C15-C12	-2.95	116.93	120.92
3	B	402	WDW	C8-C11-C13	2.90	110.01	107.41
2	B	401	NAP	O4D-C4D-C3D	-2.85	99.50	105.15
2	B	401	NAP	C4B-O4B-C1B	-2.77	103.34	109.47
3	A	402	WDW	C14-C15-C12	2.77	122.04	117.96
3	A	402	WDW	C13-C16-N1	2.76	123.16	119.76
2	B	401	NAP	O3B-C3B-C4B	-2.59	103.64	111.08
2	B	401	NAP	O2D-C2D-C3D	-2.56	103.61	111.82
2	A	401	NAP	O2D-C2D-C3D	-2.42	104.07	111.82
3	A	402	WDW	C14-C10-C7	-2.40	114.93	119.57
3	B	402	WDW	C14-C10-C7	-2.30	115.14	119.57
3	B	402	WDW	C14-C15-C12	2.30	121.35	117.96
2	A	401	NAP	P2B-O2B-C2B	-2.30	117.30	123.43
2	A	401	NAP	O3X-P2B-O1X	2.29	119.75	110.83
2	A	401	NAP	O5D-C5D-C4D	2.24	116.62	108.99
2	B	401	NAP	C6N-C5N-C4N	-2.24	116.23	119.45
2	A	401	NAP	O2B-P2B-O1X	-2.23	101.40	109.33
3	B	402	WDW	O18-C16-C13	2.22	123.40	119.25
3	B	402	WDW	C13-C16-N1	-2.17	117.09	119.76
2	A	401	NAP	N9A-C8A-N7A	-2.16	110.87	113.94
3	A	402	WDW	O18-C16-C13	-2.15	115.25	119.25
2	A	401	NAP	O3X-P2B-O2X	2.11	115.72	107.80
2	A	401	NAP	O2A-PA-O1A	2.11	122.26	112.44
3	B	402	WDW	C8-C7-N9	-2.05	105.52	107.65

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	402	WDW	O18-C16-N1	-2.03	119.47	122.67

There are no chirality outliers.

All (14) torsion outliers are listed below:

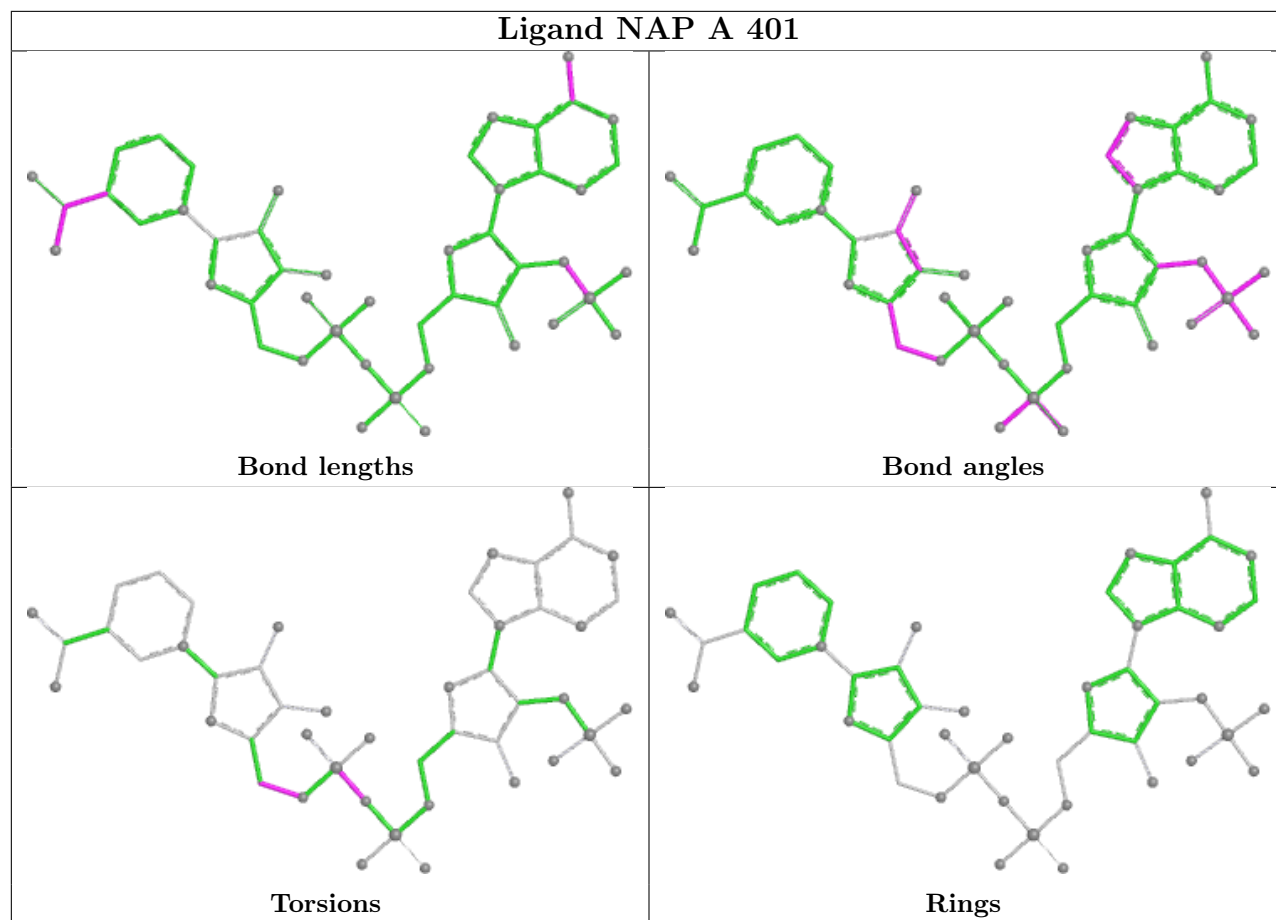
Mol	Chain	Res	Type	Atoms
3	B	402	WDW	N9-C13-C16-N1
3	B	402	WDW	N9-C13-C16-O18
2	B	401	NAP	O4D-C4D-C5D-O5D
3	B	402	WDW	C13-C16-N1-C2
3	B	402	WDW	O18-C16-N1-C2
2	A	401	NAP	PA-O3-PN-O5D
2	B	401	NAP	PA-O3-PN-O5D
3	A	402	WDW	N9-C13-C16-O18
3	A	402	WDW	N9-C13-C16-N1
2	A	401	NAP	C4D-C5D-O5D-PN
2	B	401	NAP	O4B-C4B-C5B-O5B
2	B	401	NAP	PA-O3-PN-O2N
3	B	402	WDW	C11-C13-C16-O18
3	B	402	WDW	C11-C13-C16-N1

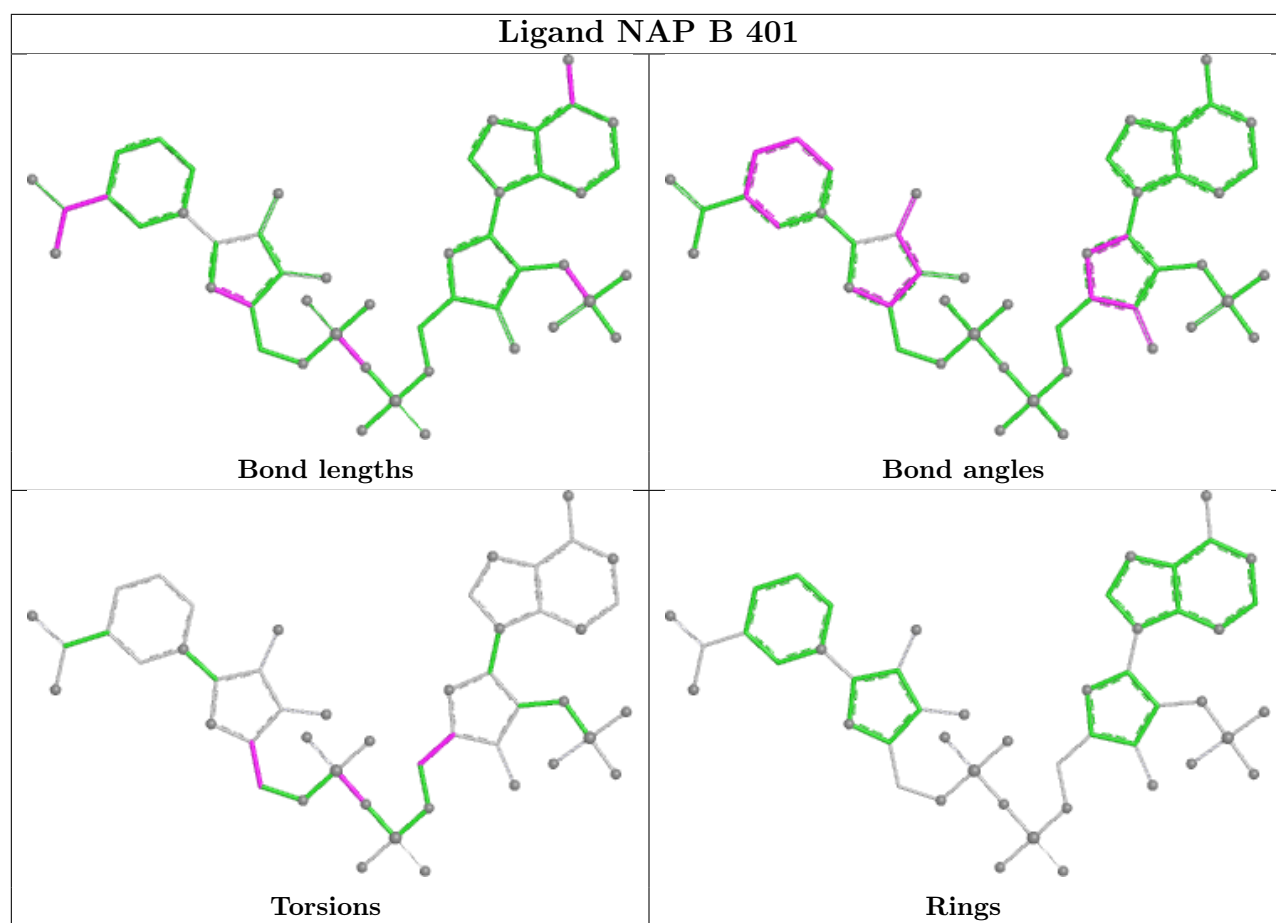
There are no ring outliers.

4 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	NAP	3	0
3	A	402	WDW	1	0
2	B	401	NAP	4	0
3	B	402	WDW	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 [i](#)

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

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th 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 ²)	Q<0.9
1	A	298/331 (90%)	-0.16	4 (1%) 75 80	17, 28, 51, 74	0
1	B	301/331 (90%)	-0.24	6 (1%) 65 72	17, 26, 51, 113	0
All	All	599/662 (90%)	-0.20	10 (1%) 69 75	17, 27, 51, 113	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	227	TRP	4.8
1	A	136	LYS	3.5
1	A	306	PHE	3.2
1	A	135	GLY	3.0
1	B	308	SER	2.8
1	A	228	VAL	2.6
1	B	307	ASN	2.5
1	B	306	PHE	2.4
1	B	228	VAL	2.4
1	B	128	LEU	2.1

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](#)

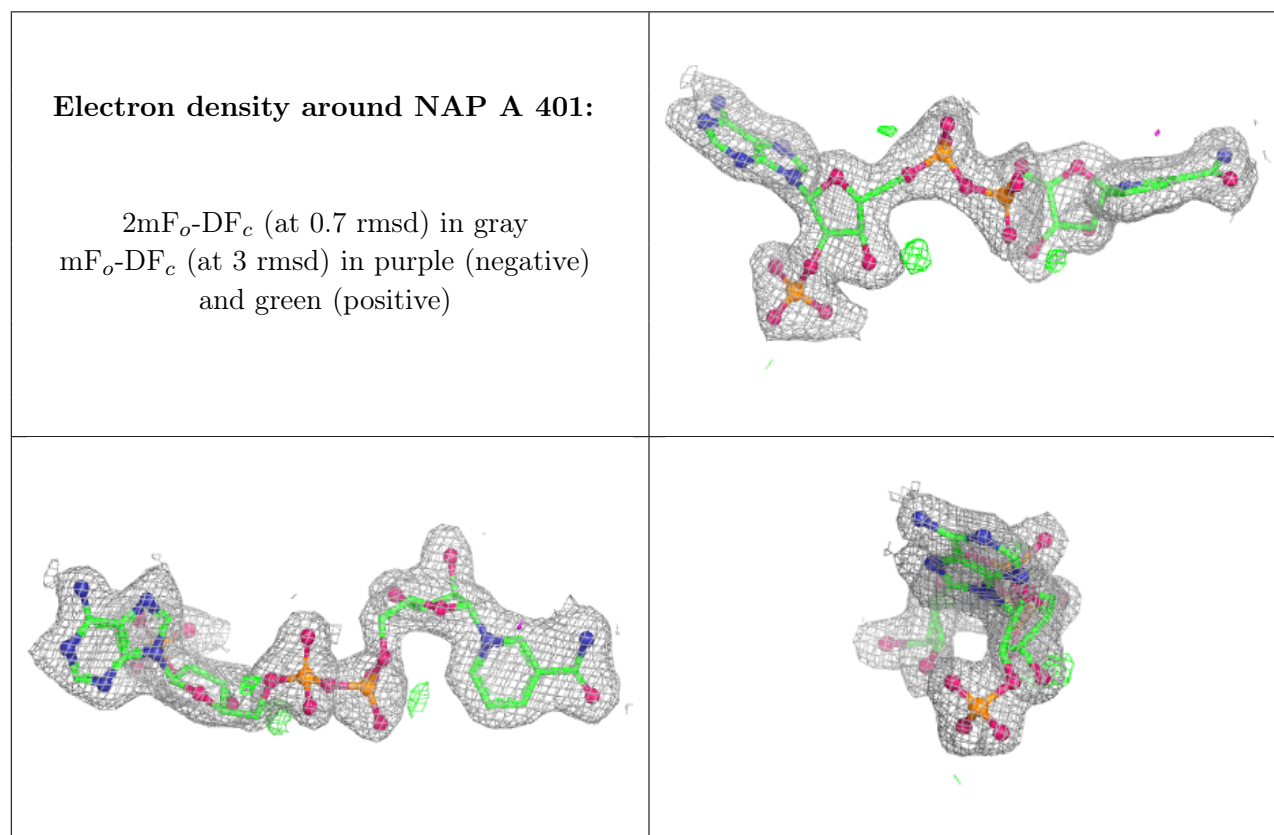
There are no oligosaccharides in this entry.

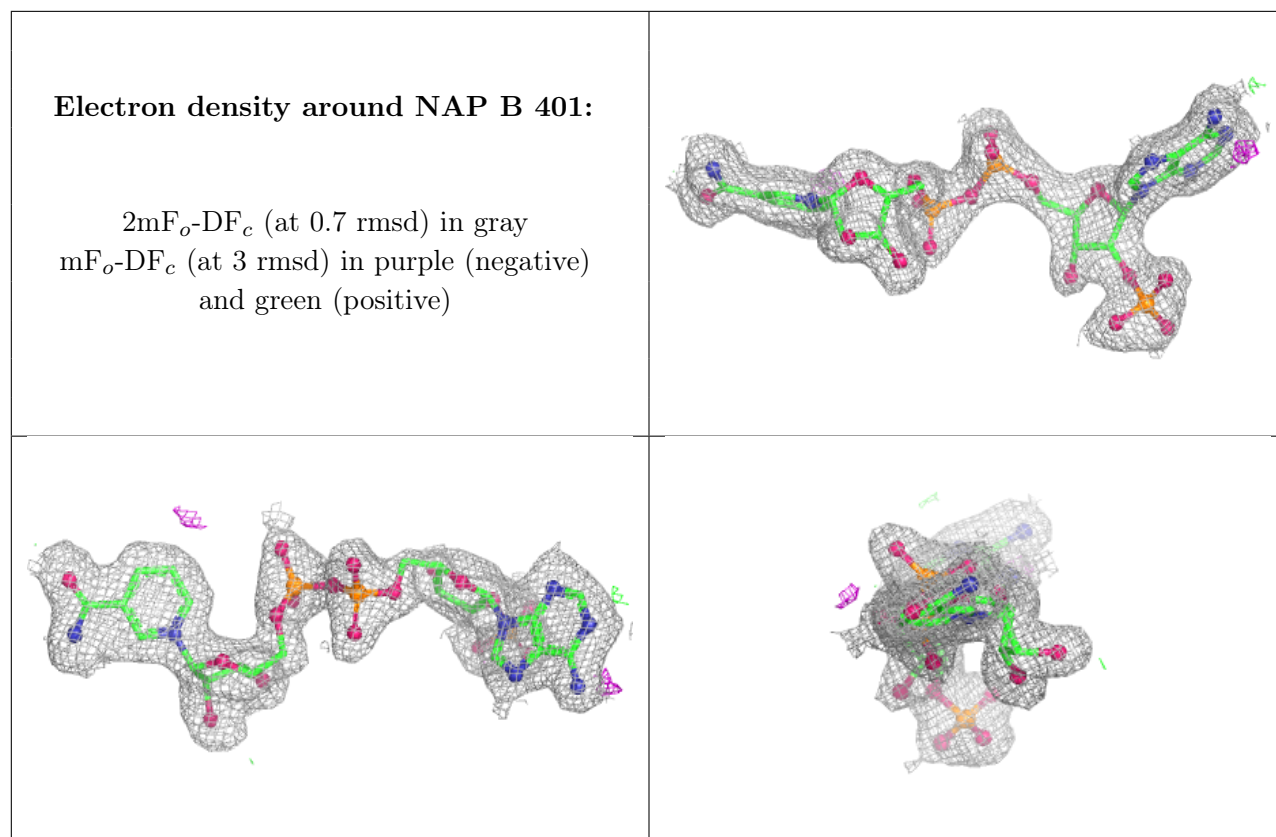
6.4 Ligands [i](#)

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. The B-factors column lists the minimum, median, 95th 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
3	WDW	A	402	18/18	0.75	0.12	38,60,65,66	0
3	WDW	B	402	18/18	0.82	0.12	30,46,65,68	0
2	NAP	A	401	48/48	0.97	0.06	23,28,33,37	0
2	NAP	B	401	48/48	0.98	0.05	18,24,31,40	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.





6.5 Other polymers [i](#)

There are no such residues in this entry.