



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 03:35 pm BST

PDB ID : 5YJL
Title : Crystal structure of Arabidopsis glutamyl-tRNA reductase in complex with NADPH and GBP
Authors : Zhao, A.; Han, F.
Deposited on : 2017-10-11
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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

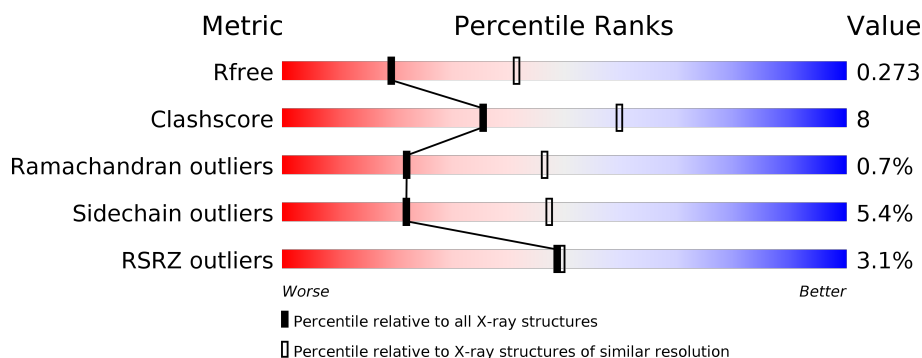
1 Overall quality at a glance

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 ≥ 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	472	<div> <div>4%</div> <div> <div></div> <div>67%</div> <div>18%</div> <div>•</div> <div>13%</div> </div> </div>
1	B	472	<div> <div>2%</div> <div> <div></div> <div>71%</div> <div>16%</div> <div>•</div> <div>12%</div> </div> </div>
2	C	310	<div> <div>2%</div> <div> <div></div> <div>67%</div> <div>13%</div> <div>•</div> <div>19%</div> </div> </div>
2	D	310	<div> <div>2%</div> <div> <div></div> <div>64%</div> <div>17%</div> <div>•</div> <div>18%</div> </div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 10577 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 Glutamyl-tRNA reductase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	411	Total	C	N	O	S	0	0	0
			3115	1951	558	583	23			
1	B	415	Total	C	N	O	S	0	0	0
			3131	1965	553	589	24			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	72	SER	-	expression tag	UNP P42804
B	72	SER	-	expression tag	UNP P42804

- Molecule 2 is a protein called Glutamyl-tRNA reductase-binding protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	251	Total	C	N	O	S	0	0	0
			1942	1227	327	375	13			
2	D	253	Total	C	N	O	S	0	0	0
			1965	1243	333	376	13			

There are 68 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	8	MET	-	expression tag	UNP Q9LU39
C	9	GLY	-	expression tag	UNP Q9LU39
C	10	SER	-	expression tag	UNP Q9LU39
C	11	SER	-	expression tag	UNP Q9LU39
C	12	HIS	-	expression tag	UNP Q9LU39
C	13	HIS	-	expression tag	UNP Q9LU39
C	14	HIS	-	expression tag	UNP Q9LU39
C	15	HIS	-	expression tag	UNP Q9LU39
C	16	HIS	-	expression tag	UNP Q9LU39
C	17	HIS	-	expression tag	UNP Q9LU39

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Chain	Residue	Modelled	Actual	Comment	Reference
C	18	SER	-	expression tag	UNP Q9LU39
C	19	SER	-	expression tag	UNP Q9LU39
C	20	GLY	-	expression tag	UNP Q9LU39
C	21	LEU	-	expression tag	UNP Q9LU39
C	22	VAL	-	expression tag	UNP Q9LU39
C	23	PRO	-	expression tag	UNP Q9LU39
C	24	ARG	-	expression tag	UNP Q9LU39
C	25	GLY	-	expression tag	UNP Q9LU39
C	26	SER	-	expression tag	UNP Q9LU39
C	27	HIS	-	expression tag	UNP Q9LU39
C	28	MET	-	expression tag	UNP Q9LU39
C	29	ALA	-	expression tag	UNP Q9LU39
C	30	SER	-	expression tag	UNP Q9LU39
C	31	MET	-	expression tag	UNP Q9LU39
C	32	THR	-	expression tag	UNP Q9LU39
C	33	GLY	-	expression tag	UNP Q9LU39
C	34	GLY	-	expression tag	UNP Q9LU39
C	35	GLN	-	expression tag	UNP Q9LU39
C	36	GLN	-	expression tag	UNP Q9LU39
C	37	MET	-	expression tag	UNP Q9LU39
C	38	GLY	-	expression tag	UNP Q9LU39
C	39	ARG	-	expression tag	UNP Q9LU39
C	40	GLY	-	expression tag	UNP Q9LU39
C	41	SER	-	expression tag	UNP Q9LU39
D	8	MET	-	expression tag	UNP Q9LU39
D	9	GLY	-	expression tag	UNP Q9LU39
D	10	SER	-	expression tag	UNP Q9LU39
D	11	SER	-	expression tag	UNP Q9LU39
D	12	HIS	-	expression tag	UNP Q9LU39
D	13	HIS	-	expression tag	UNP Q9LU39
D	14	HIS	-	expression tag	UNP Q9LU39
D	15	HIS	-	expression tag	UNP Q9LU39
D	16	HIS	-	expression tag	UNP Q9LU39
D	17	HIS	-	expression tag	UNP Q9LU39
D	18	SER	-	expression tag	UNP Q9LU39
D	19	SER	-	expression tag	UNP Q9LU39
D	20	GLY	-	expression tag	UNP Q9LU39
D	21	LEU	-	expression tag	UNP Q9LU39
D	22	VAL	-	expression tag	UNP Q9LU39
D	23	PRO	-	expression tag	UNP Q9LU39
D	24	ARG	-	expression tag	UNP Q9LU39
D	25	GLY	-	expression tag	UNP Q9LU39

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Chain	Residue	Modelled	Actual	Comment	Reference
D	26	SER	-	expression tag	UNP Q9LU39
D	27	HIS	-	expression tag	UNP Q9LU39
D	28	MET	-	expression tag	UNP Q9LU39
D	29	ALA	-	expression tag	UNP Q9LU39
D	30	SER	-	expression tag	UNP Q9LU39
D	31	MET	-	expression tag	UNP Q9LU39
D	32	THR	-	expression tag	UNP Q9LU39
D	33	GLY	-	expression tag	UNP Q9LU39
D	34	GLY	-	expression tag	UNP Q9LU39
D	35	GLN	-	expression tag	UNP Q9LU39
D	36	GLN	-	expression tag	UNP Q9LU39
D	37	MET	-	expression tag	UNP Q9LU39
D	38	GLY	-	expression tag	UNP Q9LU39
D	39	ARG	-	expression tag	UNP Q9LU39
D	40	GLY	-	expression tag	UNP Q9LU39
D	41	SER	-	expression tag	UNP Q9LU39

- # NAP
-
- The chemical structure of Naproxen (NAP) is shown, featuring a naphthalene ring system. The structure includes a carboxylic acid group (-COOH) at the 2-position, a chiral center at the 1-position, and a 6-methoxy group (-OCH₃). The stereochemistry is indicated by wedged and dashed bonds. The structure is labeled with various atoms and groups, including N, O, C, H, and S, and is associated with the chemical formula C₁₅H₁₁NO₄.



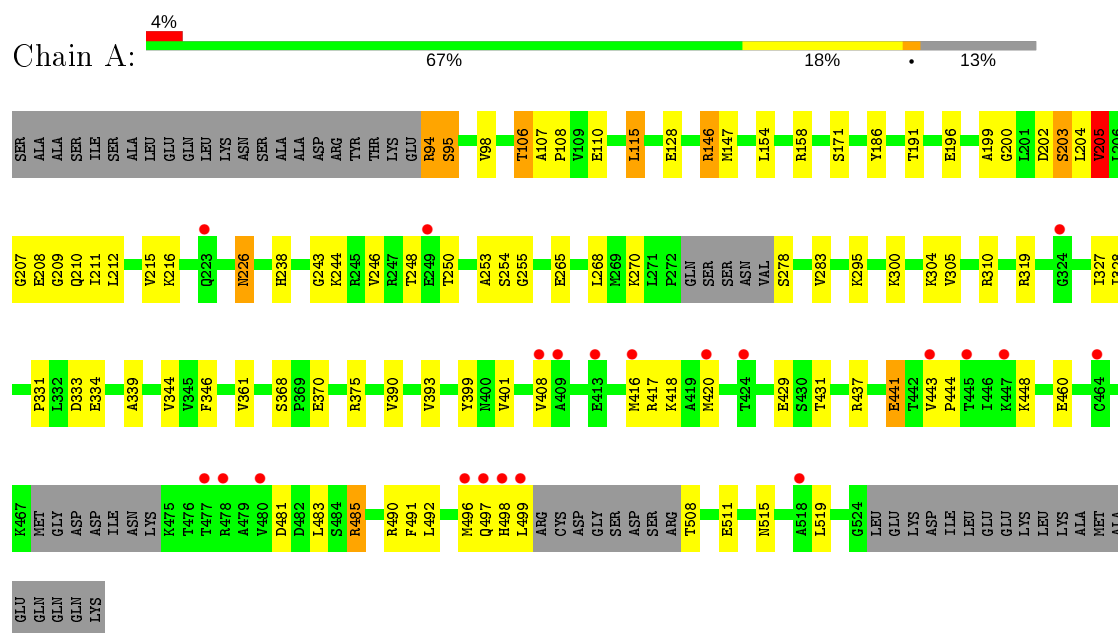
WORLD WIDE
PDB
PROTEIN DATA BANK

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	87	Total 87	O 87	0	0
4	C	70	Total 70	O 70	0	0
4	B	109	Total 109	O 109	0	0
4	D	62	Total 62	O 62	0	0

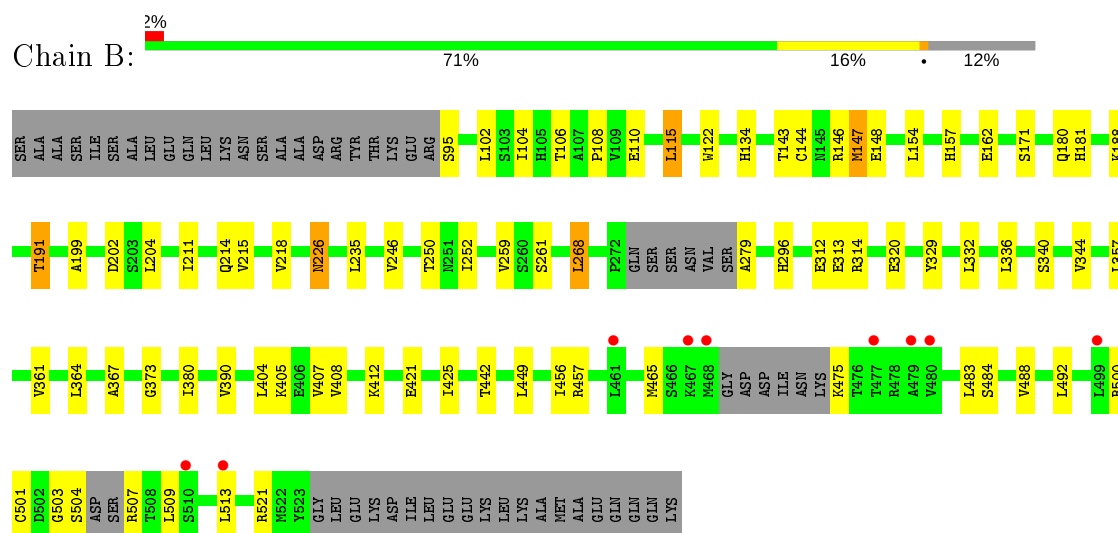
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Glutamyl-tRNA reductase 1



• Molecule 1: Glutamyl-tRNA reductase 1



• Molecule 2: Glutamyl-tRNA reductase-binding protein

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	60.34Å 83.76Å 344.58Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.96 – 2.70 32.96 – 2.70	Depositor EDS
% Data completeness (in resolution range)	98.5 (32.96-2.70) 98.5 (32.96-2.70)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.88 (at 2.68Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.213 , 0.274 0.214 , 0.273	Depositor DCC
R_{free} test set	2459 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	56.3	Xtriage
Anisotropy	0.186	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 45.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.39$, $\langle L^2 \rangle = 0.21$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	10577	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.59% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.42	0/3157	0.56	1/4264 (0.0%)
1	B	0.45	0/3173	0.57	0/4290
2	C	0.44	0/1985	0.54	0/2700
2	D	0.46	0/2008	0.56	0/2729
All	All	0.44	0/10323	0.56	1/13983 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	115	LEU	CA-CB-CG	5.59	128.16	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	3115	0	3138	65	0
1	B	3131	0	3157	53	0
2	C	1942	0	1855	22	0
2	D	1965	0	1901	31	0
3	A	48	0	25	3	0
3	B	48	0	25	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	87	0	0	13	0
4	B	109	0	0	14	0
4	C	70	0	0	8	0
4	D	62	0	0	3	0
All	All	10577	0	10101	165	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 (165) 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:128:GLU:OE2	4:A:701:HOH:O	1.85	0.94
1:B:340:SER:HB3	1:B:364:LEU:HD22	1.57	0.85
1:B:501:CYS:SG	4:B:789:HOH:O	2.29	0.83
2:C:120:GLN:HG2	2:C:130:GLN:HG2	1.65	0.78
1:A:361:VAL:HG21	1:A:390:VAL:HG13	1.67	0.77
3:A:601:NAP:O3X	4:A:702:HOH:O	2.05	0.75
1:A:115:LEU:HD13	1:A:171:SER:HB3	1.72	0.72
2:C:167:TYR:OH	4:C:401:HOH:O	2.06	0.72
1:B:115:LEU:HD13	1:B:171:SER:HB3	1.72	0.71
1:A:94:ARG:N	4:A:708:HOH:O	2.24	0.71
1:A:208:GLU:HB2	1:A:210:GLN:HG2	1.74	0.70
1:A:146:ARG:NH1	1:A:202:ASP:OD2	2.24	0.69
1:B:503:GLY:O	4:B:701:HOH:O	2.11	0.69
1:B:226:ASN:OD1	1:B:226:ASN:N	2.20	0.69
2:C:140:PRO:O	4:C:402:HOH:O	2.11	0.68
1:A:196:GLU:OE1	2:C:271:LYS:NZ	2.27	0.68
1:B:199:ALA:HB1	1:B:246:VAL:HG11	1.74	0.67
1:A:499:LEU:HD21	1:A:519:LEU:HD12	1.77	0.67
1:B:134:HIS:ND1	1:B:162:GLU:OE2	2.28	0.67
1:B:313:GLU:OE1	4:B:702:HOH:O	2.13	0.66
1:A:278:SER:N	4:A:710:HOH:O	2.28	0.66
1:B:475:LYS:N	4:B:710:HOH:O	2.27	0.66
1:A:361:VAL:HG23	1:A:393:VAL:HG21	1.77	0.66
1:A:205:VAL:O	4:A:703:HOH:O	2.15	0.64
1:A:209:GLY:HA3	1:A:254:SER:HA	1.80	0.64
1:B:504:SER:O	1:B:507:ARG:N	2.31	0.63
1:A:498:HIS:HB3	1:A:515:ASN:ND2	2.14	0.62
2:D:145:VAL:HG12	2:D:148:ARG:HD3	1.81	0.62
1:A:319:ARG:HA	1:A:327:ILE:HD12	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:101:PRO:HG2	2:D:169:VAL:HB	1.82	0.61
1:A:460:GLU:HB3	1:B:483:LEU:HD12	1.83	0.61
2:C:173:ARG:NE	4:C:408:HOH:O	2.29	0.60
1:A:203:SER:O	4:A:704:HOH:O	2.16	0.60
1:A:158:ARG:NE	4:A:707:HOH:O	2.23	0.60
1:B:361:VAL:HG21	1:B:390:VAL:HG13	1.83	0.60
1:A:497:GLN:N	4:A:711:HOH:O	2.34	0.59
1:A:209:GLY:N	1:A:253:ALA:O	2.35	0.59
1:A:250:THR:O	1:A:418:LYS:NZ	2.30	0.58
1:B:421:GLU:O	1:B:425:ILE:HG13	2.03	0.58
1:B:509:LEU:HA	4:B:789:HOH:O	2.04	0.58
1:B:204:LEU:O	4:B:703:HOH:O	2.17	0.57
1:B:521:ARG:NH1	4:B:716:HOH:O	2.37	0.57
1:B:115:LEU:HB3	1:B:147:MET:HG3	1.87	0.57
1:A:210:GLN:HA	1:A:255:GLY:H	1.71	0.56
1:A:238:HIS:NE2	1:A:429:GLU:OE1	2.38	0.55
1:B:314:ARG:NH2	4:B:718:HOH:O	2.39	0.55
2:D:120:GLN:HG2	2:D:130:GLN:HG2	1.89	0.54
2:C:173:ARG:HG3	2:C:186:TRP:CZ3	2.43	0.54
1:A:200:GLY:HA2	1:A:210:GLN:HG3	1.90	0.53
1:A:226:ASN:N	1:A:226:ASN:OD1	2.41	0.53
2:C:221:ARG:NH1	4:C:411:HOH:O	2.32	0.53
1:B:380:ILE:O	3:B:601:NAP:H6N	2.07	0.53
1:A:331:PRO:HG2	1:A:334:GLU:HG3	1.89	0.53
1:B:250:THR:OG1	1:B:252:ILE:HG13	2.09	0.53
1:B:500:ARG:NH2	4:B:721:HOH:O	2.43	0.53
2:D:208:VAL:HA	2:D:238:MET:CE	2.39	0.53
1:A:209:GLY:N	1:A:210:GLN:HG2	2.25	0.52
2:C:101:PRO:HG2	2:C:169:VAL:HB	1.91	0.52
1:A:94:ARG:HB2	1:A:94:ARG:HH11	1.73	0.52
1:A:199:ALA:HB1	1:A:246:VAL:HG11	1.91	0.52
1:B:106:THR:OG1	1:B:181:HIS:ND1	2.38	0.52
2:C:80:LEU:HD11	2:D:80:LEU:HD11	1.92	0.51
1:B:202:ASP:OD1	2:D:271:LYS:NZ	2.39	0.51
1:A:481:ASP:OD1	1:A:485:ARG:NH1	2.44	0.51
1:A:204:LEU:O	1:A:205:VAL:HB	2.11	0.51
1:B:211:ILE:O	1:B:215:VAL:HG23	2.11	0.51
1:A:216:LYS:NZ	4:A:718:HOH:O	2.44	0.51
2:D:211:ILE:HB	2:D:238:MET:HE1	1.93	0.50
1:B:180:GLN:OE1	4:B:704:HOH:O	2.19	0.50
1:A:448:LYS:NZ	4:A:719:HOH:O	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:104:ILE:HD13	1:B:405:LYS:HG3	1.93	0.50
1:A:295:LYS:NZ	4:A:720:HOH:O	2.44	0.50
2:D:173:ARG:HG3	2:D:186:TRP:CZ3	2.46	0.50
2:D:106:ASN:O	2:D:108:SER:N	2.42	0.49
1:A:443:VAL:HB	1:A:444:PRO:HD3	1.93	0.49
1:B:332:LEU:HD21	3:B:601:NAP:H2A	1.94	0.49
2:C:285:TRP:NE1	2:C:289:LYS:HE2	2.26	0.49
1:B:191:THR:HB	1:B:235:LEU:HD11	1.95	0.49
1:B:457:ARG:HG3	1:B:484:SER:HB2	1.93	0.49
1:B:500:ARG:NH2	4:B:723:HOH:O	2.44	0.49
1:A:492:LEU:O	1:A:496:MET:HG2	2.13	0.49
2:C:270:GLU:OE2	4:C:403:HOH:O	2.19	0.48
1:A:211:ILE:O	1:A:215:VAL:HG23	2.13	0.48
1:B:122:TRP:CZ3	1:B:218:VAL:HA	2.48	0.48
2:D:204:ALA:O	2:D:207:ILE:HG22	2.15	0.47
1:A:483:LEU:HD23	1:B:483:LEU:HD23	1.96	0.47
1:A:416:MET:O	1:A:420:MET:N	2.46	0.47
1:B:259:VAL:HG11	3:B:601:NAP:H5N	1.96	0.47
2:D:223:CYS:O	2:D:227:VAL:HG13	2.14	0.47
1:B:144:CYS:SG	3:B:601:NAP:C6N	3.03	0.47
2:C:267:VAL:HG11	2:C:273:ALA:HB2	1.96	0.47
1:B:157:HIS:HB3	2:D:285:TRP:CE3	2.50	0.47
1:A:490:ARG:HB3	1:B:456:ILE:HD13	1.97	0.47
2:D:208:VAL:HA	2:D:238:MET:HE2	1.96	0.46
2:D:172:ASP:O	2:D:189:SER:HB3	2.15	0.46
1:A:98:VAL:HG22	1:A:186:TYR:HD1	1.80	0.46
1:A:106:THR:HG23	1:A:107:ALA:H	1.81	0.46
1:A:270:LYS:HE3	1:A:399:TYR:CE1	2.50	0.46
2:D:142:ASP:OD1	2:D:144:THR:HG22	2.16	0.46
1:A:368:SER:OG	1:A:370:GLU:OE1	2.33	0.46
1:A:95:SER:O	1:A:437:ARG:NH2	2.42	0.46
2:C:135:GLY:HA3	2:C:170:ALA:O	2.16	0.46
2:D:242:ASP:OD1	2:D:260:ARG:NH2	2.40	0.46
1:A:210:GLN:HB3	1:A:255:GLY:HA3	1.98	0.45
1:A:108:PRO:HD3	4:A:706:HOH:O	2.15	0.45
2:D:162:LYS:HD2	2:D:162:LYS:HA	1.69	0.45
2:D:276:SER:O	2:D:280:MET:HG3	2.17	0.45
2:D:105:LEU:HA	2:D:105:LEU:HD23	1.78	0.45
2:C:206:ASP:OD2	4:C:404:HOH:O	2.21	0.45
2:D:66:ARG:NH2	4:D:417:HOH:O	2.50	0.45
1:A:205:VAL:HG12	1:A:208:GLU:CD	2.37	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:108:PRO:HB2	1:B:110:GLU:CD	2.37	0.45
1:A:508:THR:HG23	1:A:511:GLU:H	1.82	0.45
1:B:279:ALA:N	4:B:728:HOH:O	2.49	0.45
2:C:243:ARG:HG3	2:C:244:LEU:HG	1.99	0.45
2:C:229:LEU:HA	2:C:229:LEU:HD12	1.83	0.44
1:A:265:GLU:OE2	4:A:705:HOH:O	2.21	0.44
2:D:157:PHE:HB3	2:D:159:GLU:HG2	1.99	0.44
2:D:221:ARG:HD3	2:D:285:TRP:HA	1.99	0.44
1:B:312:GLU:OE1	4:B:705:HOH:O	2.21	0.44
2:D:150:SER:OG	2:D:154:ARG:NH2	2.51	0.44
2:D:95:VAL:HG22	4:D:425:HOH:O	2.17	0.44
1:A:498:HIS:HB3	1:A:515:ASN:HD22	1.83	0.44
2:D:179:ASP:OD1	2:D:180:PHE:N	2.49	0.44
1:A:508:THR:O	1:A:511:GLU:HG2	2.18	0.43
1:B:457:ARG:HB2	1:B:488:VAL:HG21	2.00	0.43
1:A:200:GLY:CA	1:A:210:GLN:HG3	2.48	0.43
2:C:114:ARG:NH1	4:C:414:HOH:O	2.38	0.43
1:A:339:ALA:O	1:A:375:ARG:NE	2.52	0.43
2:D:71:LEU:HD23	2:D:71:LEU:HA	1.89	0.43
2:D:242:ASP:CG	2:D:260:ARG:HH22	2.20	0.43
3:A:601:NAP:H2D	3:A:601:NAP:H2N	1.79	0.42
2:C:66:ARG:HD3	2:C:192:TYR:CE1	2.54	0.42
1:B:312:GLU:HG3	1:B:329:TYR:CD2	2.54	0.42
1:A:283:VAL:HG22	1:A:346:PHE:HB2	2.01	0.42
1:A:310:ARG:HB3	3:A:601:NAP:O1X	2.20	0.42
2:C:276:SER:O	2:C:280:MET:HG3	2.19	0.42
2:D:249:ARG:HG2	2:D:251:TRP:CH2	2.55	0.42
1:A:108:PRO:HB2	1:A:110:GLU:OE2	2.20	0.42
1:B:404:LEU:O	1:B:408:VAL:HG23	2.20	0.42
2:D:207:ILE:HD11	2:D:274:LYS:HG2	2.01	0.42
1:A:250:THR:O	1:A:418:LYS:HG2	2.20	0.42
1:A:212:LEU:HD13	1:A:243:GLY:HA3	2.02	0.42
1:A:300:LYS:HD3	1:A:300:LYS:HA	1.81	0.42
1:A:208:GLU:HB2	1:A:210:GLN:CG	2.48	0.41
1:A:209:GLY:HA3	1:A:210:GLN:HA	1.71	0.41
1:A:304:LYS:HE3	1:A:328:ILE:CD1	2.50	0.41
1:B:143:THR:HG22	1:B:214:GLN:HG2	2.02	0.41
2:C:284:ALA:HA	2:C:287:VAL:HG22	2.00	0.41
1:A:441:GLU:C	1:A:444:PRO:HD2	2.40	0.41
1:B:146:ARG:NH1	1:B:148:GLU:OE2	2.54	0.41
1:B:336:LEU:HD23	1:B:336:LEU:HA	1.61	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:264:PRO:HG2	4:C:443:HOH:O	2.20	0.41
1:B:211:ILE:O	1:B:211:ILE:HG22	2.21	0.41
2:D:139:ARG:HD2	4:D:413:HOH:O	2.19	0.41
1:B:405:LYS:HE3	1:B:405:LYS:HB3	1.85	0.41
2:D:204:ALA:O	2:D:208:VAL:HG23	2.21	0.41
1:B:268:LEU:HA	1:B:268:LEU:HD12	1.82	0.41
1:B:261:SER:HB2	1:B:296:HIS:NE2	2.36	0.41
1:B:367:ALA:O	1:B:373:GLY:HA2	2.21	0.41
1:B:188:LYS:HA	1:B:191:THR:HG23	2.03	0.40
1:B:95:SER:N	4:B:734:HOH:O	2.53	0.40
1:A:491:PHE:HE1	1:B:492:LEU:HD21	1.87	0.40
1:A:244:LYS:O	1:A:248:THR:HG23	2.22	0.40
2:C:140:PRO:HB3	2:C:145:VAL:HG23	2.04	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	403/472 (85%)	376 (93%)	22 (6%)	5 (1%)	13	32
1	B	407/472 (86%)	396 (97%)	11 (3%)	0	100	100
2	C	249/310 (80%)	236 (95%)	11 (4%)	2 (1%)	19	43
2	D	251/310 (81%)	242 (96%)	7 (3%)	2 (1%)	19	43
All	All	1310/1564 (84%)	1250 (95%)	51 (4%)	9 (1%)	22	46

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	205	VAL
1	A	408	VAL

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Mol	Chain	Res	Type
1	A	417	ARG
2	C	108	SER
1	A	203	SER
2	C	110	SER
2	D	55	SER
2	D	107	ARG
1	A	207	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	332/400 (83%)	315 (95%)	17 (5%)	24	50
1	B	336/400 (84%)	320 (95%)	16 (5%)	25	53
2	C	212/269 (79%)	200 (94%)	12 (6%)	20	44
2	D	216/269 (80%)	202 (94%)	14 (6%)	17	38
All	All	1096/1338 (82%)	1037 (95%)	59 (5%)	22	47

All (59) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	94	ARG
1	A	95	SER
1	A	106	THR
1	A	146	ARG
1	A	147	MET
1	A	154	LEU
1	A	191	THR
1	A	205	VAL
1	A	226	ASN
1	A	268	LEU
1	A	305	VAL
1	A	333	ASP
1	A	344	VAL
1	A	401	VAL

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Mol	Chain	Res	Type
1	A	431	THR
1	A	441	GLU
1	A	485	ARG
2	C	74	VAL
2	C	105	LEU
2	C	142	ASP
2	C	144	THR
2	C	152	THR
2	C	155	GLU
2	C	160	GLU
2	C	220	PHE
2	C	227	VAL
2	C	229	LEU
2	C	271	LYS
2	C	302	LEU
1	B	102	LEU
1	B	115	LEU
1	B	147	MET
1	B	154	LEU
1	B	191	THR
1	B	226	ASN
1	B	268	LEU
1	B	320	GLU
1	B	344	VAL
1	B	357	LEU
1	B	407	VAL
1	B	412	LYS
1	B	442	THR
1	B	449	LEU
1	B	465	MET
1	B	513	LEU
2	D	80	LEU
2	D	82	HIS
2	D	89	VAL
2	D	142	ASP
2	D	143	ASP
2	D	144	THR
2	D	146	LEU
2	D	160	GLU
2	D	161	VAL
2	D	220	PHE
2	D	224	ASN

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Mol	Chain	Res	Type
2	D	227	VAL
2	D	305	VAL
2	D	306	VAL

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 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 ⓘ

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	NAP	A	601	-	45,52,52	1.67	3 (6%)	56,80,80	1.27	3 (5%)
3	NAP	B	601	-	45,52,52	1.71	5 (11%)	56,80,80	1.17	4 (7%)

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	NAP	A	601	-	-	11/31/67/67	0/5/5/5
3	NAP	B	601	-	-	12/31/67/67	0/5/5/5

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	601	NAP	O7N-C7N	8.59	1.40	1.24
3	B	601	NAP	O7N-C7N	8.44	1.40	1.24
3	B	601	NAP	C2A-N3A	4.20	1.38	1.32
3	A	601	NAP	C2A-N3A	3.89	1.38	1.32
3	B	601	NAP	C2A-N1A	2.84	1.39	1.33
3	A	601	NAP	C2A-N1A	2.35	1.38	1.33
3	B	601	NAP	C2N-N1N	2.18	1.37	1.35
3	B	601	NAP	O4D-C4D	-2.01	1.40	1.45

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	601	NAP	N3A-C2A-N1A	-5.77	119.65	128.68
3	B	601	NAP	N3A-C2A-N1A	-5.27	120.44	128.68
3	A	601	NAP	C6N-N1N-C2N	-3.64	118.66	121.97
3	B	601	NAP	C2N-C3N-C4N	2.90	121.55	118.26
3	B	601	NAP	C6N-N1N-C2N	-2.57	119.63	121.97
3	A	601	NAP	C3N-C7N-N7N	2.25	120.45	117.75
3	B	601	NAP	C5N-C4N-C3N	-2.10	117.85	120.34

There are no chirality outliers.

All (23) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	601	NAP	C5B-O5B-PA-O3
3	A	601	NAP	O4D-C1D-N1N-C2N
3	A	601	NAP	O4D-C1D-N1N-C6N
3	A	601	NAP	C2D-C1D-N1N-C2N
3	A	601	NAP	C2D-C1D-N1N-C6N
3	B	601	NAP	C5B-O5B-PA-O3
3	B	601	NAP	C2B-O2B-P2B-O2X
3	B	601	NAP	O4D-C1D-N1N-C2N
3	B	601	NAP	O4D-C1D-N1N-C6N
3	B	601	NAP	C2D-C1D-N1N-C2N
3	B	601	NAP	C2D-C1D-N1N-C6N
3	A	601	NAP	O4B-C4B-C5B-O5B

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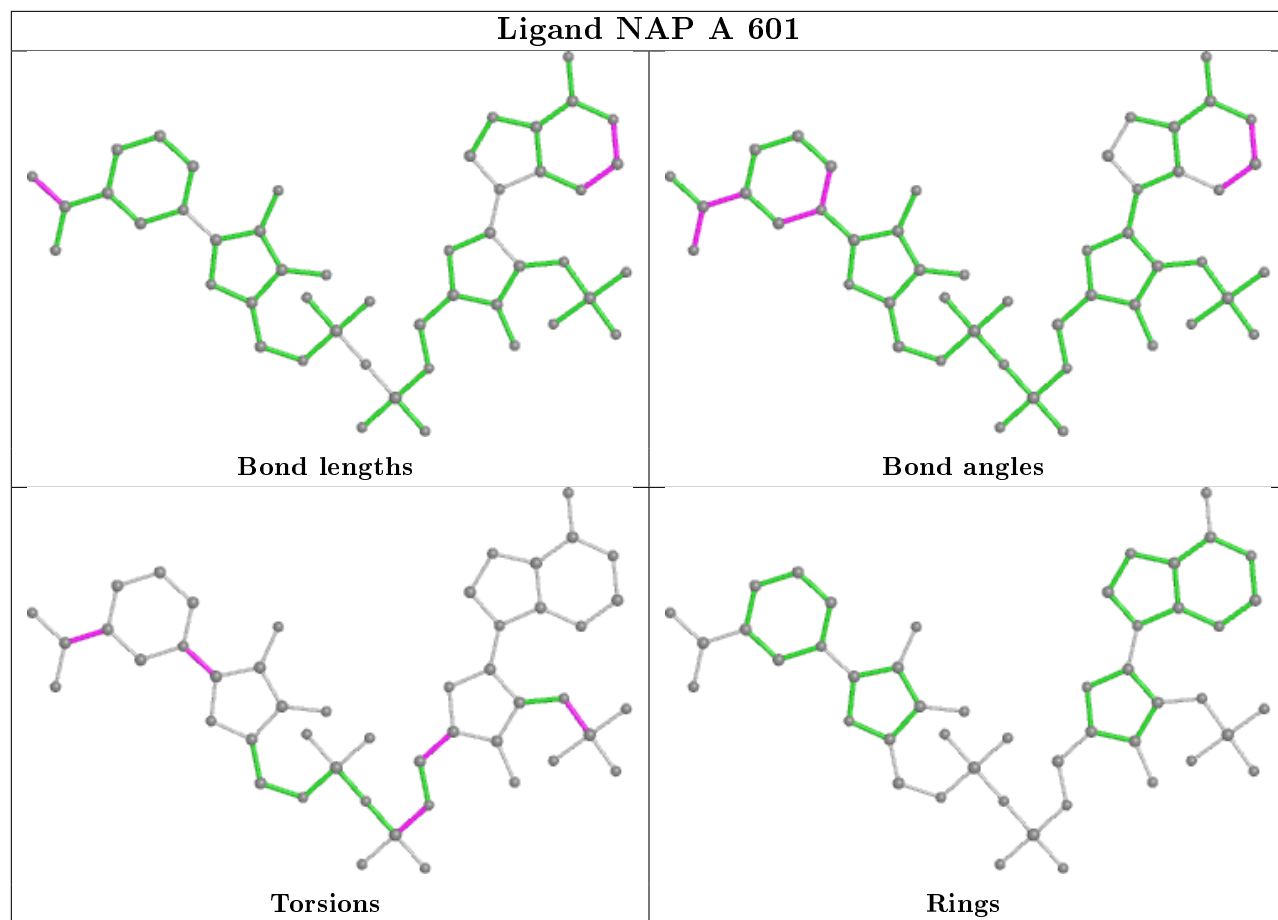
Mol	Chain	Res	Type	Atoms
3	B	601	NAP	C3B-C2B-O2B-P2B
3	B	601	NAP	C1B-C2B-O2B-P2B
3	A	601	NAP	C2B-O2B-P2B-O2X
3	A	601	NAP	C5B-O5B-PA-O1A
3	A	601	NAP	C5B-O5B-PA-O2A
3	A	601	NAP	C4N-C3N-C7N-O7N
3	A	601	NAP	C4N-C3N-C7N-N7N
3	B	601	NAP	O4B-C4B-C5B-O5B
3	B	601	NAP	C4N-C3N-C7N-O7N
3	B	601	NAP	PN-O3-PA-O2A
3	B	601	NAP	C5B-O5B-PA-O2A

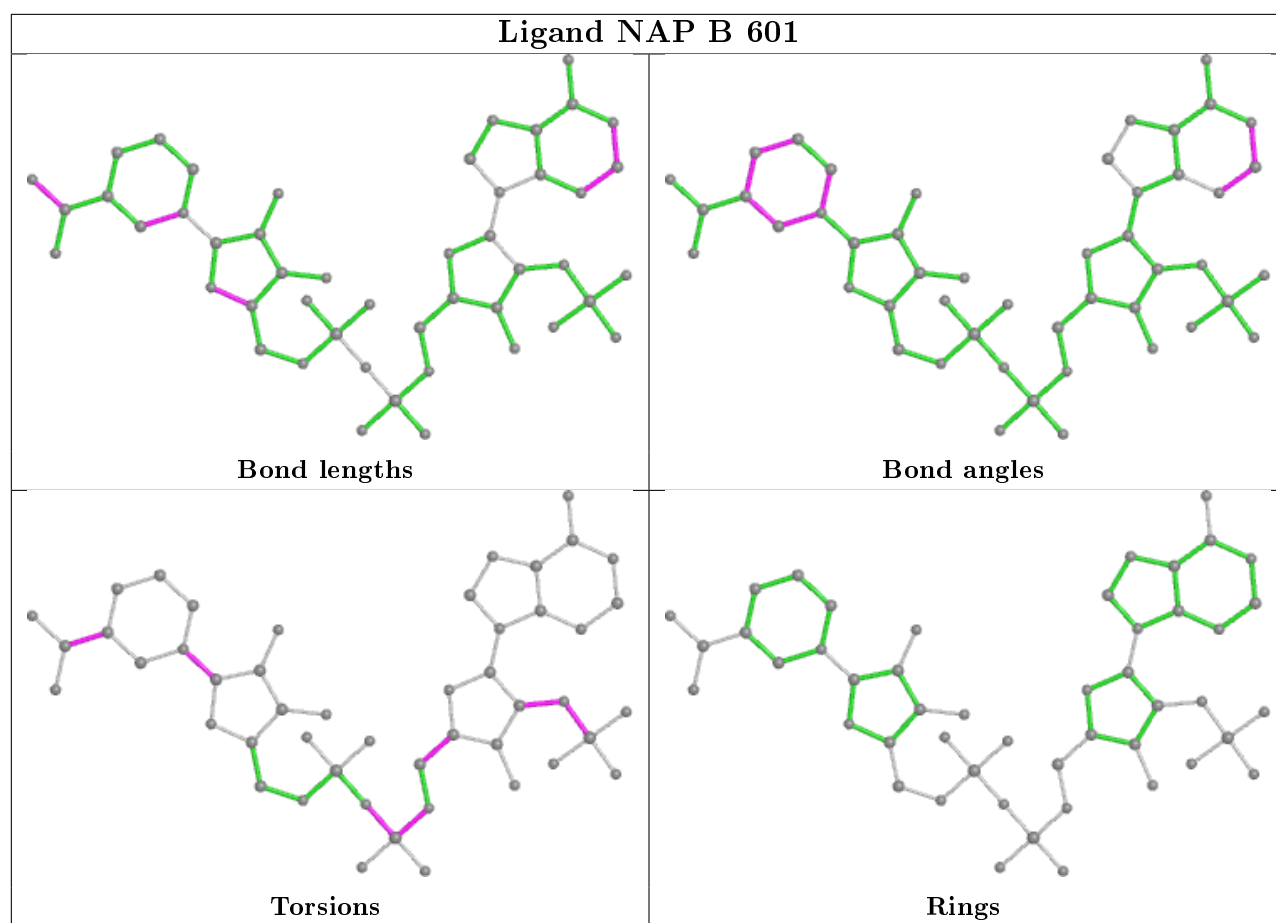
There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	601	NAP	3	0
3	B	601	NAP	4	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, 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(Å²)	Q<0.9
1	A	411/472 (87%)	0.05	21 (5%)	28	26	42, 59, 90, 110	1 (0%)
1	B	415/472 (87%)	-0.21	9 (2%)	62	63	37, 53, 75, 85	3 (0%)
2	C	251/310 (80%)	-0.11	5 (1%)	65	67	41, 54, 83, 98	0
2	D	253/310 (81%)	0.01	6 (2%)	59	60	37, 52, 86, 104	0
All	All	1330/1564 (85%)	-0.07	41 (3%)	49	49	37, 55, 85, 110	4 (0%)

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	54	ALA	5.1
1	A	499	LEU	4.9
2	C	161	VAL	4.5
1	B	513	LEU	4.3
2	C	233	VAL	3.9
1	A	497	GLN	3.9
1	A	416	MET	3.9
1	A	249	GLU	3.8
1	B	499	LEU	3.8
1	A	477	THR	3.6
1	A	518	ALA	3.6
1	A	443	VAL	3.6
2	C	141	GLY	3.5
2	D	142	ASP	3.5
1	A	498	HIS	3.4
1	B	477	THR	3.4
1	B	479	ALA	3.2
2	C	80	LEU	3.0
2	D	111	PRO	2.8
1	A	478	ARG	2.7
1	A	480	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	413	GLU	2.7
1	A	424	THR	2.7
1	B	468	MET	2.5
1	B	480	VAL	2.4
1	A	223	GLN	2.4
1	A	447	LYS	2.4
1	A	409	ALA	2.3
2	D	55	SER	2.3
1	A	324	GLY	2.3
1	B	467	LYS	2.3
1	A	420	MET	2.3
1	A	496	MET	2.3
1	A	445	THR	2.3
2	C	232	VAL	2.3
2	D	161	VAL	2.3
1	A	408	VAL	2.2
1	B	510	SER	2.2
1	B	461	LEU	2.1
2	D	110	SER	2.1
1	A	464	CYS	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 carbohydrates in this entry.

6.4 Ligands [i](#)

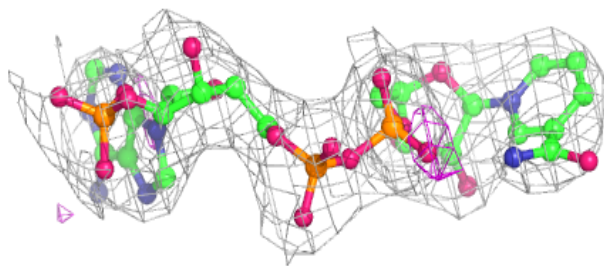
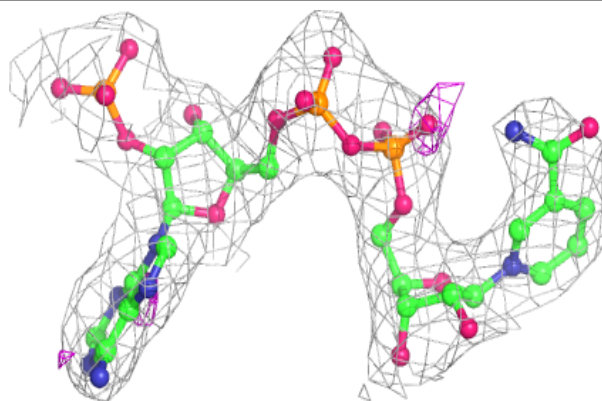
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

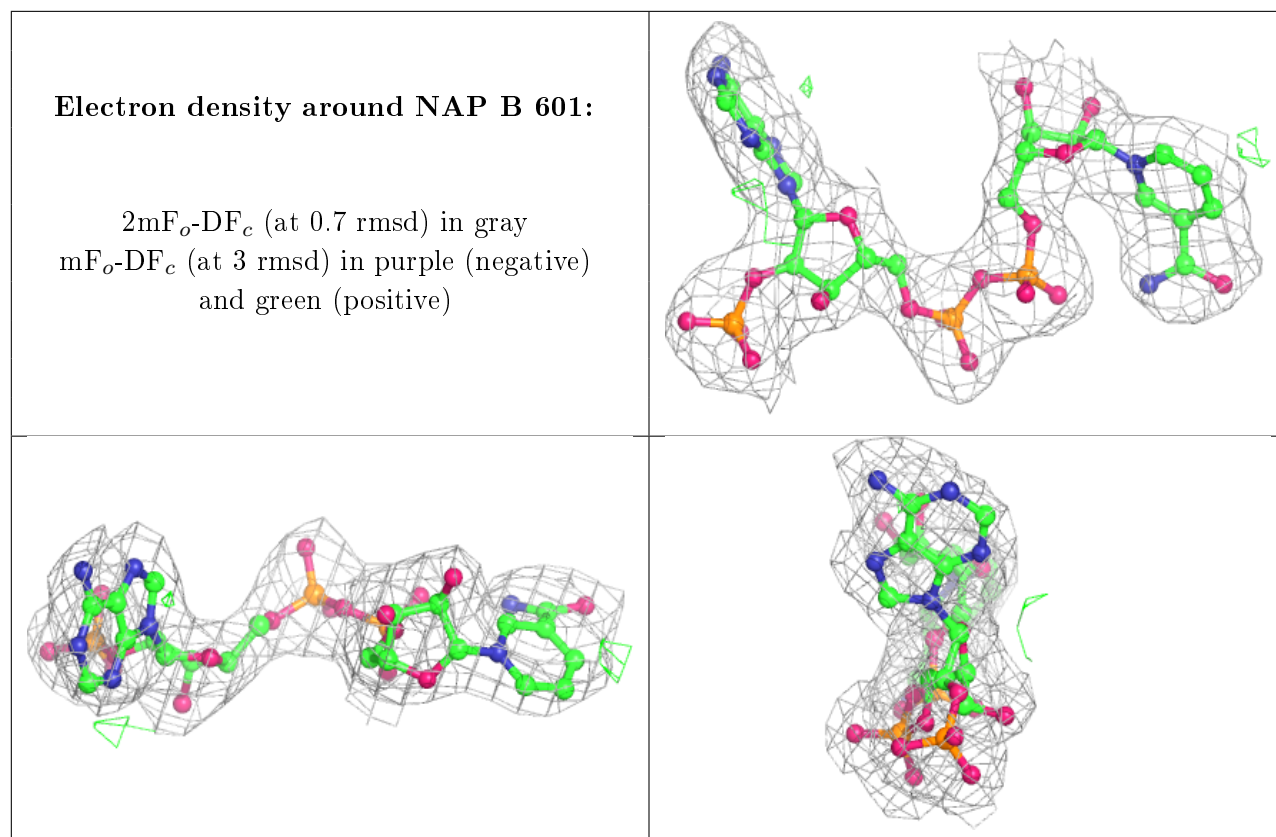
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	NAP	A	601	48/48	0.96	0.12	50,59,65,69	0
3	NAP	B	601	48/48	0.96	0.13	39,49,57,58	0

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 NAP A 601:

$2mF_o-DF_c$ (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.