



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 12:51 PM UTC

PDB ID : 1O9B / pdb_00001o9b
Title : QUINATE/SHIKIMATE DEHYDROGENASE YDIB COMPLEXED WITH NADH
Authors : Michel, G.; Cygler, M.
Deposited on : 2002-12-12
Resolution : 2.50 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

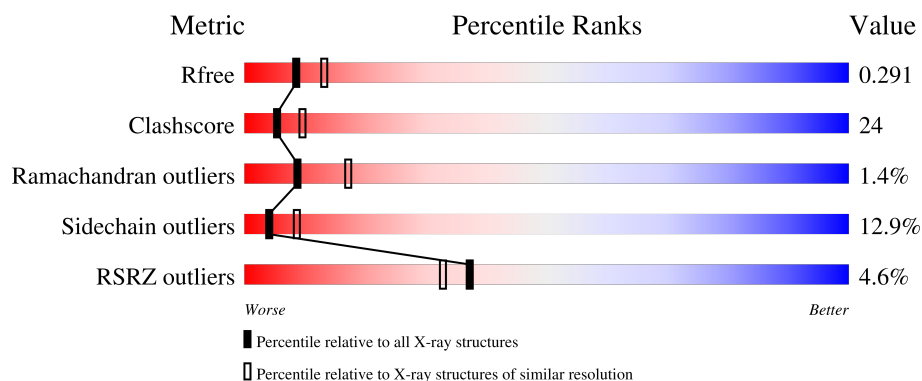
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	288	7% 56% 35% 6% ..
1	B	288	2% 54% 35% 9% .

2 Entry composition [i](#)

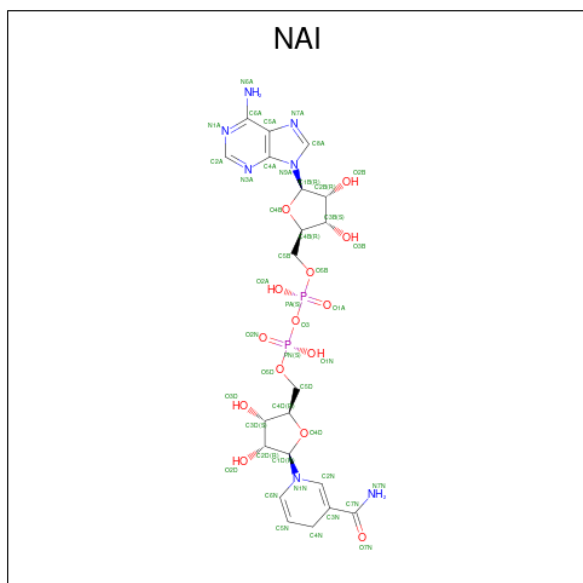
There are 4 unique types of molecules in this entry. The entry contains 4541 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 HYPOTHETICAL SHIKIMATE 5-DEHYDROGENASE-LIKE PROTEIN YDIB.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	281	Total	C	N	O	S	Se	58	0	1
			2137	1357	356	410	4	10			
1	B	281	Total	C	N	O	S	Se	16	0	1
			2137	1357	356	410	4	10			

- Molecule 2 is 1,4-DIHYDRONICOTINAMIDE ADENINE DINUCLEOTIDE (CCD ID: NAI) (formula: $C_{21}H_{29}N_7O_{14}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	B	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 3 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	P	0	0
			5	4	1		
3	A	1	Total	O	P	0	0
			5	4	1		
3	A	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		
3	B	1	Total	O	P	0	0
			5	4	1		

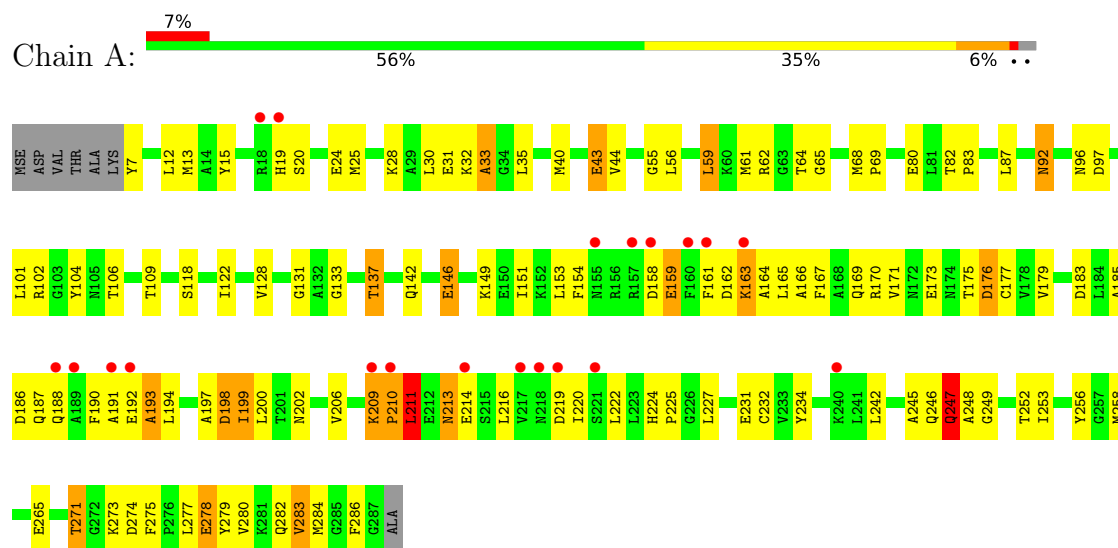
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	88	Total	O	0	0
			88	88		
4	B	66	Total	O	0	0
			66	66		

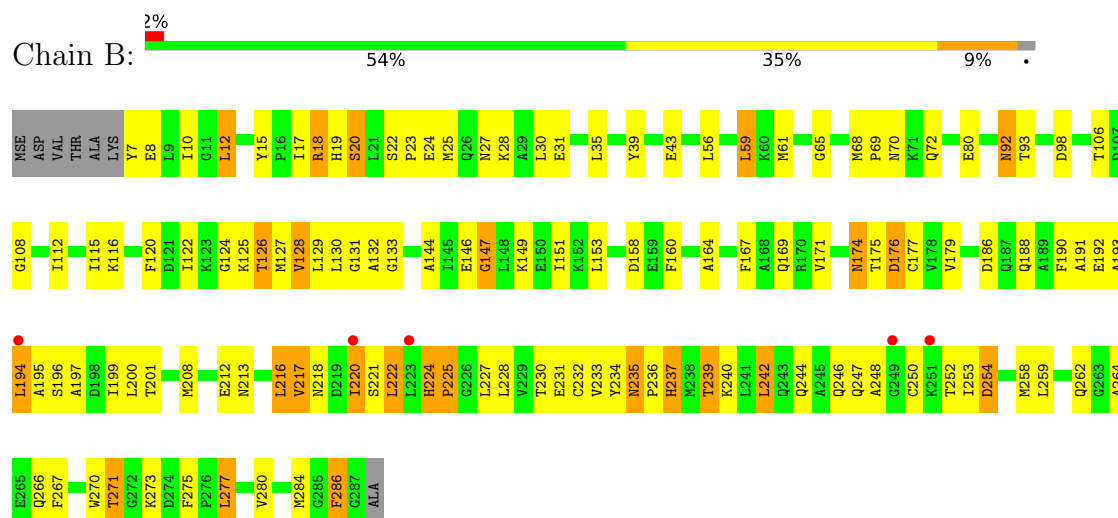
3 Residue-property plots [i](#)

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: HYPOTHETICAL SHIKIMATE 5-DEHYDROGENASE-LIKE PROTEIN YDIB



• Molecule 1: HYPOTHETICAL SHIKIMATE 5-DEHYDROGENASE-LIKE PROTEIN YDIB



4 Data and refinement statistics

Property	Value	Source
Space group	P 64	Depositor
Cell constants a, b, c, α , β , γ	157.87Å 157.87Å 40.01Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.80 – 2.50 19.80 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.9 (19.80-2.50) 99.7 (19.80-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.03 (at 2.50Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.226 , 0.294 0.219 , 0.291	Depositor DCC
R_{free} test set	973 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	44.6	Xtriage
Anisotropy	0.152	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 67.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.036 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4541	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.41% 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: PO4, NAI

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	0.68	4/2165 (0.2%)	1.19	16/2911 (0.5%)
1	B	0.62	1/2165 (0.0%)	1.04	11/2911 (0.4%)
All	All	0.65	5/4330 (0.1%)	1.12	27/5822 (0.5%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	211	LEU	C-N	-6.19	1.25	1.33
1	A	209	LYS	N-CA	6.00	1.54	1.46
1	B	286	PHE	C-N	-5.62	1.25	1.33
1	A	286	PHE	C-N	-5.48	1.25	1.33
1	A	209	LYS	CA-C	-5.40	1.46	1.52

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	209	LYS	O-C-N	-17.74	100.92	121.32
1	B	20	SER	N-CA-C	7.72	121.16	110.35
1	A	65	GLY	N-CA-C	-7.48	101.89	112.37
1	A	20	SER	N-CA-C	7.13	120.30	110.24
1	A	283	VAL	N-CA-C	6.74	118.31	110.62
1	B	147	GLY	N-CA-C	6.31	124.66	115.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	65	GLY	N-CA-C	-6.28	102.97	112.89
1	A	44	VAL	N-CA-C	6.27	117.12	107.78
1	A	209	LYS	CA-C-O	-6.24	111.62	120.16
1	B	220	ILE	N-CA-C	-6.18	104.60	113.07
1	A	185	ALA	N-CA-C	-6.00	105.26	113.30
1	A	198	ASP	N-CA-C	-5.91	106.20	113.41
1	A	220	ILE	N-CA-C	-5.91	104.70	113.39
1	A	197	ALA	N-CA-C	5.89	119.69	110.32
1	B	8	GLU	N-CA-C	5.83	119.17	110.14
1	B	70	ASN	N-CA-C	5.71	120.95	113.30
1	B	277	LEU	N-CA-C	5.59	117.82	111.11
1	A	176	ASP	N-CA-C	-5.55	106.51	113.28
1	A	193	ALA	N-CA-C	-5.44	105.26	111.14
1	A	163	LYS	N-CA-C	-5.32	105.65	111.82
1	B	196	SER	N-CA-C	-5.29	105.10	112.30
1	A	118	SER	N-CA-C	-5.27	106.63	113.16
1	A	101	LEU	N-CA-C	5.25	117.08	108.52
1	A	211	LEU	O-C-N	5.24	129.56	122.59
1	B	254	ASP	N-CA-C	5.08	116.66	110.41
1	B	199	ILE	N-CA-C	5.06	115.20	108.11
1	B	176	ASP	N-CA-C	-5.06	106.02	113.61

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	209	LYS	Mainchain

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	2137	0	2129	108	0
1	B	2137	0	2129	101	0
2	A	44	0	27	4	0
2	B	44	0	27	2	0
3	A	15	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	10	0	0	0	0
4	A	88	0	0	2	0
4	B	66	0	0	3	0
All	All	4541	0	4312	205	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 24.

All (205) 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:271:THR:HG22	1:B:273:LYS:H	1.15	1.06
1:B:175:THR:HG22	1:B:177:CYS:H	1.21	1.04
1:A:271:THR:HG22	1:A:273:LYS:H	1.27	0.98
1:B:191:ALA:HA	1:B:222:LEU:HD21	1.46	0.95
1:A:122:ILE:HD11	1:A:146:GLU:HB3	1.50	0.92
1:B:267:PHE:O	1:B:271:THR:HB	1.77	0.85
1:B:271:THR:CG2	1:B:273:LYS:H	1.87	0.85
1:B:231:GLU:HG2	1:B:239:THR:HG21	1.58	0.85
1:A:56:LEU:HA	1:A:61:MSE:HE3	1.60	0.81
1:B:112:ILE:HG21	1:B:146:GLU:OE1	1.80	0.81
1:A:153:LEU:HD12	1:A:154:PHE:N	1.97	0.80
1:A:151:ILE:HB	1:A:179:VAL:HG22	1.63	0.80
1:B:190:PHE:O	1:B:194:LEU:HB2	1.82	0.80
1:A:175:THR:HG22	1:A:176:ASP:H	1.47	0.79
1:A:92:ASN:HD21	1:A:106:THR:H	1.32	0.77
1:B:127:MSE:HE2	1:B:201:THR:OG1	1.84	0.77
1:B:131:GLY:O	1:B:153:LEU:HD11	1.86	0.76
1:B:116:LYS:HD2	4:B:2043:HOH:O	1.85	0.75
1:A:169:GLN:O	1:A:173:GLU:HG3	1.87	0.74
1:B:175:THR:HG22	1:B:176:ASP:N	2.04	0.72
1:B:129:LEU:O	1:B:153:LEU:HD12	1.90	0.71
1:B:175:THR:HG22	1:B:176:ASP:H	1.54	0.71
1:A:131:GLY:O	1:A:153:LEU:HD11	1.91	0.71
1:B:144:ALA:HB1	1:B:175:THR:HG21	1.71	0.71
1:A:61:MSE:HE1	1:B:59:LEU:HD21	1.74	0.69
1:A:153:LEU:HD12	1:A:154:PHE:H	1.58	0.68
1:A:232:CYS:SG	1:A:258:MSE:HE1	2.33	0.68
1:B:271:THR:HG22	1:B:273:LYS:N	1.99	0.68
1:B:242:LEU:HD21	1:B:252:THR:HB	1.73	0.68
1:B:212:GLU:HG2	1:B:213:ASN:N	2.07	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:217:VAL:HG22	1:B:244:GLN:OE1	1.92	0.68
1:A:167:PHE:O	1:A:171:VAL:HG23	1.94	0.67
1:B:240:LYS:O	1:B:244:GLN:HG3	1.95	0.66
1:B:128:VAL:HG12	1:B:200:LEU:HD12	1.76	0.66
1:A:56:LEU:CA	1:A:61:MSE:HE3	2.26	0.65
1:A:234:TYR:HB2	1:A:256:TYR:CE1	2.30	0.65
1:B:230:THR:HG22	1:B:253:ILE:HB	1.79	0.65
1:B:115:ILE:HA	1:B:253:ILE:CD1	2.27	0.65
1:B:175:THR:HG22	1:B:177:CYS:N	2.04	0.62
1:A:175:THR:HG22	1:A:176:ASP:N	2.14	0.62
1:A:211:LEU:C	1:A:213:ASN:H	2.07	0.61
1:A:35:LEU:HD21	1:A:273:LYS:HG3	1.82	0.61
1:A:232:CYS:HA	1:A:258:MSE:CE	2.31	0.60
1:A:206:VAL:HG21	1:A:216:LEU:HD11	1.83	0.60
1:A:188:GLN:HE21	1:A:188:GLN:HA	1.65	0.60
1:B:126:THR:HG22	1:B:197:ALA:HA	1.83	0.60
1:B:242:LEU:CD2	1:B:252:THR:HB	2.31	0.60
1:A:128:VAL:O	1:A:200:LEU:HD12	2.02	0.59
1:A:224:HIS:HB2	1:A:225:PRO:HD2	1.84	0.59
1:B:175:THR:CG2	1:B:176:ASP:H	2.15	0.59
1:B:128:VAL:HG12	1:B:200:LEU:CD1	2.31	0.59
1:B:259:LEU:O	1:B:262:GLN:HG3	2.02	0.59
1:A:188:GLN:HA	1:A:188:GLN:NE2	2.18	0.59
1:A:279:TYR:O	1:A:283:VAL:HG23	2.03	0.59
1:A:188:GLN:C	1:A:190:PHE:H	2.10	0.59
1:A:166:ALA:O	1:A:169:GLN:HB2	2.03	0.59
1:B:92:ASN:HD21	1:B:106:THR:H	1.49	0.59
1:A:55:GLY:O	1:A:59:LEU:HB2	2.03	0.59
1:A:82:THR:HB	1:A:83:PRO:HD2	1.85	0.59
1:A:161:PHE:O	1:A:164:ALA:HB3	2.03	0.58
1:B:191:ALA:CA	1:B:222:LEU:HD21	2.26	0.58
1:A:133:GLY:O	1:A:137:THR:OG1	2.22	0.58
1:A:234:TYR:HB2	1:A:256:TYR:CD1	2.38	0.58
1:A:199:ILE:HG13	1:A:200:LEU:N	2.19	0.57
1:A:92:ASN:HD22	1:A:92:ASN:H	1.50	0.57
1:A:59:LEU:HD23	1:A:61:MSE:HE2	1.86	0.57
1:A:188:GLN:C	1:A:190:PHE:N	2.62	0.57
1:B:115:ILE:HA	1:B:253:ILE:HD11	1.86	0.57
1:A:186:ASP:O	1:A:188:GLN:N	2.38	0.56
1:A:232:CYS:O	2:A:301:NAI:H2N	2.04	0.56
1:B:108:GLY:O	1:B:112:ILE:HG12	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:245:ALA:C	1:A:247:GLN:N	2.60	0.56
1:B:235:ASN:HA	1:B:236:PRO:C	2.28	0.56
1:A:97:ASP:OD2	1:A:102:ARG:NH1	2.39	0.56
1:A:15:TYR:HD1	1:A:43:GLU:HG2	1.70	0.56
1:B:174:ASN:HD22	1:B:174:ASN:N	2.04	0.56
1:B:24:GLU:O	1:B:28:LYS:HG2	2.06	0.55
1:A:232:CYS:CB	1:A:258:MSE:HE1	2.37	0.55
1:B:258:MSE:HE2	2:B:301:NAI:H4N	1.88	0.55
1:A:202:ASN:ND2	1:A:231:GLU:OE1	2.40	0.55
1:B:175:THR:CG2	1:B:176:ASP:N	2.70	0.54
1:A:275:PHE:O	1:A:277:LEU:N	2.39	0.54
1:A:206:VAL:HG11	1:A:216:LEU:CD1	2.38	0.54
1:B:224:HIS:CD2	1:B:227:LEU:HD13	2.43	0.54
1:B:225:PRO:HA	1:B:248:ALA:O	2.08	0.54
1:A:242:LEU:HD22	1:A:252:THR:HG23	1.89	0.53
1:B:127:MSE:HE2	1:B:201:THR:CB	2.38	0.53
1:A:210:PRO:HD2	1:A:211:LEU:H	1.73	0.53
1:A:232:CYS:HA	1:A:258:MSE:HE1	1.91	0.52
1:A:151:ILE:HG13	1:A:177:CYS:SG	2.49	0.52
1:A:271:THR:HG22	1:A:273:LYS:N	2.11	0.52
1:B:115:ILE:HG12	1:B:253:ILE:HD12	1.90	0.52
1:B:235:ASN:HB3	4:B:2056:HOH:O	2.09	0.52
1:A:191:ALA:HB1	1:A:222:LEU:CD2	2.40	0.52
1:A:206:VAL:HG12	1:A:214:GLU:O	2.09	0.52
1:B:231:GLU:HG2	1:B:239:THR:CG2	2.33	0.52
1:B:191:ALA:HA	1:B:222:LEU:CD2	2.30	0.52
1:A:161:PHE:C	1:A:161:PHE:CD1	2.88	0.52
1:B:217:VAL:CG2	1:B:217:VAL:O	2.58	0.52
1:A:278:GLU:HG3	4:A:2084:HOH:O	2.09	0.52
1:A:245:ALA:C	1:A:247:GLN:H	2.17	0.51
1:B:158:ASP:OD1	1:B:158:ASP:C	2.53	0.51
1:A:277:LEU:C	1:A:277:LEU:HD23	2.36	0.51
1:A:252:THR:CG2	1:A:253:ILE:N	2.74	0.51
1:B:151:ILE:HB	1:B:179:VAL:HG22	1.92	0.51
1:A:15:TYR:CD1	1:A:43:GLU:HG2	2.46	0.50
1:A:258:MSE:HE3	2:A:301:NAI:C7N	2.42	0.50
1:A:13:MSE:HE3	1:A:64:THR:HG21	1.94	0.50
1:A:165:LEU:O	1:A:169:GLN:N	2.40	0.50
1:B:188:GLN:NE2	1:B:188:GLN:HA	2.26	0.49
1:A:35:LEU:CD2	1:A:271:THR:HG23	2.42	0.49
1:B:128:VAL:HG12	1:B:128:VAL:O	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:ALA:CB	1:A:35:LEU:CD1	2.91	0.49
1:A:24:GLU:O	1:A:28:LYS:HG3	2.13	0.48
1:B:10:ILE:O	1:B:39:TYR:HA	2.13	0.48
1:A:194:LEU:HD21	1:A:200:LEU:HD22	1.95	0.48
1:B:174:ASN:N	1:B:174:ASN:ND2	2.62	0.48
1:B:264:ALA:HA	1:B:275:PHE:CG	2.48	0.48
1:A:190:PHE:O	1:A:193:ALA:N	2.46	0.48
1:A:198:ASP:O	1:A:227:LEU:HD12	2.14	0.48
1:A:59:LEU:HD21	1:B:61:MSE:HE1	1.95	0.47
1:A:211:LEU:C	1:A:213:ASN:N	2.70	0.47
1:A:159:GLU:CD	1:A:159:GLU:H	2.21	0.47
1:B:208:MSE:HB2	1:B:233:VAL:HG13	1.96	0.47
1:A:186:ASP:C	1:A:188:GLN:H	2.23	0.47
1:B:92:ASN:HD22	1:B:92:ASN:H	1.62	0.47
1:A:61:MSE:CE	1:B:59:LEU:HD21	2.42	0.47
1:A:191:ALA:HB1	1:A:222:LEU:HD22	1.94	0.47
1:B:158:ASP:OD1	1:B:160:PHE:N	2.37	0.47
1:B:149:LYS:HD3	4:B:2040:HOH:O	2.14	0.47
1:B:92:ASN:ND2	1:B:93:THR:OG1	2.47	0.47
1:A:87:LEU:HD22	1:A:170:ARG:HB3	1.97	0.47
1:A:87:LEU:CD2	1:A:170:ARG:HB3	2.45	0.47
1:A:28:LYS:CD	1:A:283:VAL:HG11	2.45	0.46
1:B:122:ILE:O	1:B:125:LYS:HB2	2.16	0.46
1:A:40:MSE:HE2	1:A:40:MSE:HB3	1.89	0.46
1:A:247:GLN:C	1:A:249:GLY:H	2.24	0.46
1:B:130:LEU:HD13	1:B:216:LEU:HD23	1.98	0.46
1:A:252:THR:HG22	1:A:253:ILE:N	2.31	0.45
1:A:133:GLY:N	2:A:301:NAI:O3B	2.49	0.45
1:A:32:LYS:HD2	1:A:279:TYR:CZ	2.50	0.45
1:B:126:THR:CG2	1:B:197:ALA:HA	2.46	0.45
1:B:25:MSE:HG3	1:B:284:MSE:HE2	1.98	0.45
1:B:224:HIS:HB2	1:B:225:PRO:CD	2.46	0.45
1:B:15:TYR:HE1	1:B:43:GLU:OE1	2.00	0.45
1:B:124:GLY:N	1:B:147:GLY:O	2.46	0.45
1:A:104:TYR:CD1	1:A:104:TYR:N	2.83	0.45
1:B:232:CYS:O	2:B:301:NAI:H2N	2.16	0.45
1:A:92:ASN:ND2	1:A:106:THR:H	2.09	0.45
1:B:234:TYR:O	1:B:235:ASN:HB2	2.16	0.44
1:B:235:ASN:CA	1:B:236:PRO:C	2.90	0.44
1:A:68:MSE:HA	1:A:69:PRO:HA	1.82	0.44
1:A:80:GLU:HB3	1:A:102:ARG:HG2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:92:ASN:ND2	1:B:92:ASN:C	2.76	0.44
1:B:120:PHE:CE2	1:B:125:LYS:HE2	2.52	0.44
1:A:31:GLU:C	1:A:33:ALA:H	2.25	0.44
1:B:186:ASP:C	1:B:188:GLN:N	2.74	0.44
1:A:188:GLN:O	1:A:190:PHE:N	2.51	0.44
1:B:18:ARG:O	1:B:18:ARG:HG2	2.15	0.44
1:A:188:GLN:HE21	1:A:188:GLN:CA	2.26	0.44
1:A:33:ALA:HB3	1:A:35:LEU:CD1	2.48	0.44
1:B:17:ILE:C	1:B:19:HIS:N	2.76	0.44
1:A:232:CYS:CA	1:A:258:MSE:HE1	2.48	0.43
1:B:225:PRO:O	1:B:250:CYS:HA	2.18	0.43
1:B:266:GLN:HB3	1:B:270:TRP:CZ3	2.53	0.43
1:A:92:ASN:HD22	1:A:92:ASN:N	2.12	0.43
1:B:18:ARG:HE	1:B:18:ARG:HB3	1.35	0.43
1:B:271:THR:CG2	1:B:273:LYS:N	2.70	0.43
1:B:271:THR:CG2	1:B:273:LYS:HB2	2.48	0.43
1:A:109:THR:HA	1:A:142:GLN:HG2	2.00	0.43
1:B:224:HIS:CB	1:B:225:PRO:CD	2.97	0.42
1:A:109:THR:HG22	1:A:142:GLN:NE2	2.34	0.42
1:B:27:ASN:O	1:B:31:GLU:HG3	2.19	0.42
1:A:56:LEU:N	1:A:61:MSE:HE3	2.35	0.42
1:B:228:LEU:HD12	1:B:228:LEU:HA	1.76	0.42
1:A:33:ALA:CB	1:A:35:LEU:HD12	2.49	0.42
1:A:59:LEU:HD21	1:B:61:MSE:CE	2.48	0.42
1:B:192:GLU:O	1:B:193:ALA:C	2.63	0.42
1:B:133:GLY:HA2	1:B:160:PHE:CE1	2.55	0.42
1:A:175:THR:CG2	1:A:176:ASP:H	2.27	0.42
1:B:112:ILE:HG23	1:B:122:ILE:HD13	2.02	0.42
1:B:240:LYS:HE3	1:B:240:LYS:HB3	1.78	0.42
1:B:195:ALA:HA	1:B:224:HIS:HE1	1.85	0.41
1:B:280:VAL:O	1:B:284:MSE:HG2	2.20	0.41
1:A:25:MSE:HG3	1:A:280:VAL:HG11	2.02	0.41
1:B:17:ILE:C	1:B:19:HIS:H	2.28	0.41
1:B:132:ALA:CB	1:B:164:ALA:HB2	2.51	0.41
1:B:237:HIS:ND1	1:B:237:HIS:C	2.79	0.41
1:A:33:ALA:HB1	1:A:35:LEU:CD1	2.50	0.41
1:B:271:THR:HG23	1:B:273:LYS:HG2	2.01	0.41
1:B:194:LEU:HD13	1:B:222:LEU:HD22	2.03	0.41
1:B:194:LEU:HD21	1:B:200:LEU:HD22	2.02	0.41
1:A:258:MSE:HE3	2:A:301:NAI:N7N	2.35	0.41
1:A:258:MSE:HB2	4:A:2049:HOH:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:277:LEU:HD23	1:A:277:LEU:O	2.20	0.41
1:A:62:ARG:NH1	1:A:96:ASN:O	2.54	0.41
1:A:25:MSE:HE3	1:A:25:MSE:HB2	1.98	0.41
1:A:163:LYS:HD2	1:A:163:LYS:HA	1.75	0.41
1:B:22:SER:N	1:B:23:PRO:CD	2.84	0.41
1:B:284:MSE:HB3	1:B:286:PHE:CZ	2.56	0.40
1:A:137:THR:HG22	1:A:167:PHE:CD2	2.56	0.40
1:B:12:LEU:HG	1:B:39:TYR:OH	2.21	0.40
1:B:167:PHE:O	1:B:171:VAL:HG23	2.21	0.40
1:A:24:GLU:HG2	1:A:284:MSE:SE	2.71	0.40
1:A:158:ASP:HB2	1:A:159:GLU:OE2	2.20	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	279/288 (97%)	252 (90%)	21 (8%)	6 (2%)	5	9
1	B	279/288 (97%)	252 (90%)	25 (9%)	2 (1%)	18	34
All	All	558/576 (97%)	504 (90%)	46 (8%)	8 (1%)	9	17

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	187	GLN
1	A	211	LEU
1	B	225	PRO
1	A	33	ALA
1	A	248	ALA
1	A	247	GLN
1	B	235	ASN

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Mol	Chain	Res	Type
1	A	210	PRO

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	224/218 (103%)	200 (89%)	24 (11%)	6	13
1	B	224/218 (103%)	190 (85%)	34 (15%)	3	5
All	All	448/436 (103%)	390 (87%)	58 (13%)	4	9

All (58) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	TYR
1	A	12	LEU
1	A	19	HIS
1	A	30	LEU
1	A	43	GLU
1	A	59	LEU
1	A	92	ASN
1	A	137	THR
1	A	146	GLU
1	A	149	LYS
1	A	159	GLU
1	A	162	ASP
1	A	183	ASP
1	A	192	GLU
1	A	199	ILE
1	A	213	ASN
1	A	219	ASP
1	A	246	GLN
1	A	247	GLN
1	A	265	GLU
1	A	271	THR
1	A	274	ASP

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Mol	Chain	Res	Type
1	A	278	GLU
1	A	282	GLN
1	B	7	TYR
1	B	12	LEU
1	B	18	ARG
1	B	20	SER
1	B	30	LEU
1	B	35	LEU
1	B	56	LEU
1	B	59	LEU
1	B	68	MSE
1	B	69	PRO
1	B	72	GLN
1	B	80	GLU
1	B	92	ASN
1	B	98	ASP
1	B	126	THR
1	B	128	VAL
1	B	169	GLN
1	B	174	ASN
1	B	194	LEU
1	B	216	LEU
1	B	217	VAL
1	B	218	ASN
1	B	220	ILE
1	B	221	SER
1	B	222	LEU
1	B	224	HIS
1	B	237	HIS
1	B	239	THR
1	B	242	LEU
1	B	246	GLN
1	B	247	GLN
1	B	254	ASP
1	B	271	THR
1	B	277	LEU

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	26	GLN
1	A	46	ASN

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Mol	Chain	Res	Type
1	A	92	ASN
1	A	155	ASN
1	A	188	GLN
1	A	246	GLN
1	A	262	GLN
1	B	92	ASN
1	B	174	ASN
1	B	187	GLN
1	B	188	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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](#)

7 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	NAI	B	301	-	47,48,48	1.35	9 (19%)	64,73,73	1.38	4 (6%)
3	PO4	A	303	-	4,4,4	0.94	0	6,6,6	0.56	0
3	PO4	A	302	-	4,4,4	1.38	1 (25%)	6,6,6	0.72	0
3	PO4	B	302	-	4,4,4	1.27	0	6,6,6	0.78	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAI	A	301	-	47,48,48	1.37	7 (14%)	64,73,73	1.39	4 (6%)
3	PO4	A	304	-	4,4,4	0.85	0	6,6,6	0.55	0
3	PO4	B	303	-	4,4,4	1.26	1 (25%)	6,6,6	0.59	0

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	NAI	B	301	-	-	5/29/72/72	0/5/5/5
2	NAI	A	301	-	-	6/29/72/72	0/5/5/5

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	301	NAI	C2A-N1A	3.27	1.39	1.33
2	B	301	NAI	C2A-N1A	3.16	1.39	1.33
2	A	301	NAI	PA-O3	-3.10	1.56	1.59
2	A	301	NAI	C6N-N1N	2.88	1.44	1.37
2	B	301	NAI	C6N-N1N	2.86	1.44	1.37
2	A	301	NAI	C7N-C3N	2.58	1.54	1.48
2	B	301	NAI	C4N-C5N	-2.53	1.42	1.49
2	A	301	NAI	C8A-N7A	2.51	1.36	1.31
2	B	301	NAI	PA-O3	-2.48	1.56	1.59
2	A	301	NAI	C4N-C5N	-2.38	1.42	1.49
2	B	301	NAI	PN-O3	2.27	1.61	1.59
3	B	303	PO4	P-O1	2.23	1.55	1.50
2	B	301	NAI	C7N-C3N	2.17	1.53	1.48
3	A	302	PO4	P-O1	2.15	1.55	1.50
2	B	301	NAI	C6N-C5N	2.15	1.39	1.33
2	B	301	NAI	C4A-N3A	2.11	1.38	1.34
2	B	301	NAI	C1D-N1N	2.05	1.52	1.46
2	A	301	NAI	C2N-C3N	2.03	1.40	1.35

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	NAI	C6N-N1N-C2N	6.38	126.15	119.32
2	B	301	NAI	C6N-N1N-C2N	6.09	125.84	119.32
2	B	301	NAI	C3N-C2N-N1N	-4.46	116.66	123.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	NAI	C1D-N1N-C2N	-4.38	113.93	121.14
2	A	301	NAI	C3N-C2N-N1N	-4.36	116.80	123.20
2	B	301	NAI	C1D-N1N-C2N	-3.98	114.59	121.14
2	B	301	NAI	O4B-C4B-C5B	-2.46	101.45	109.33
2	A	301	NAI	O5D-PN-O2N	2.14	117.42	108.94

There are no chirality outliers.

All (11) torsion outliers are listed below:

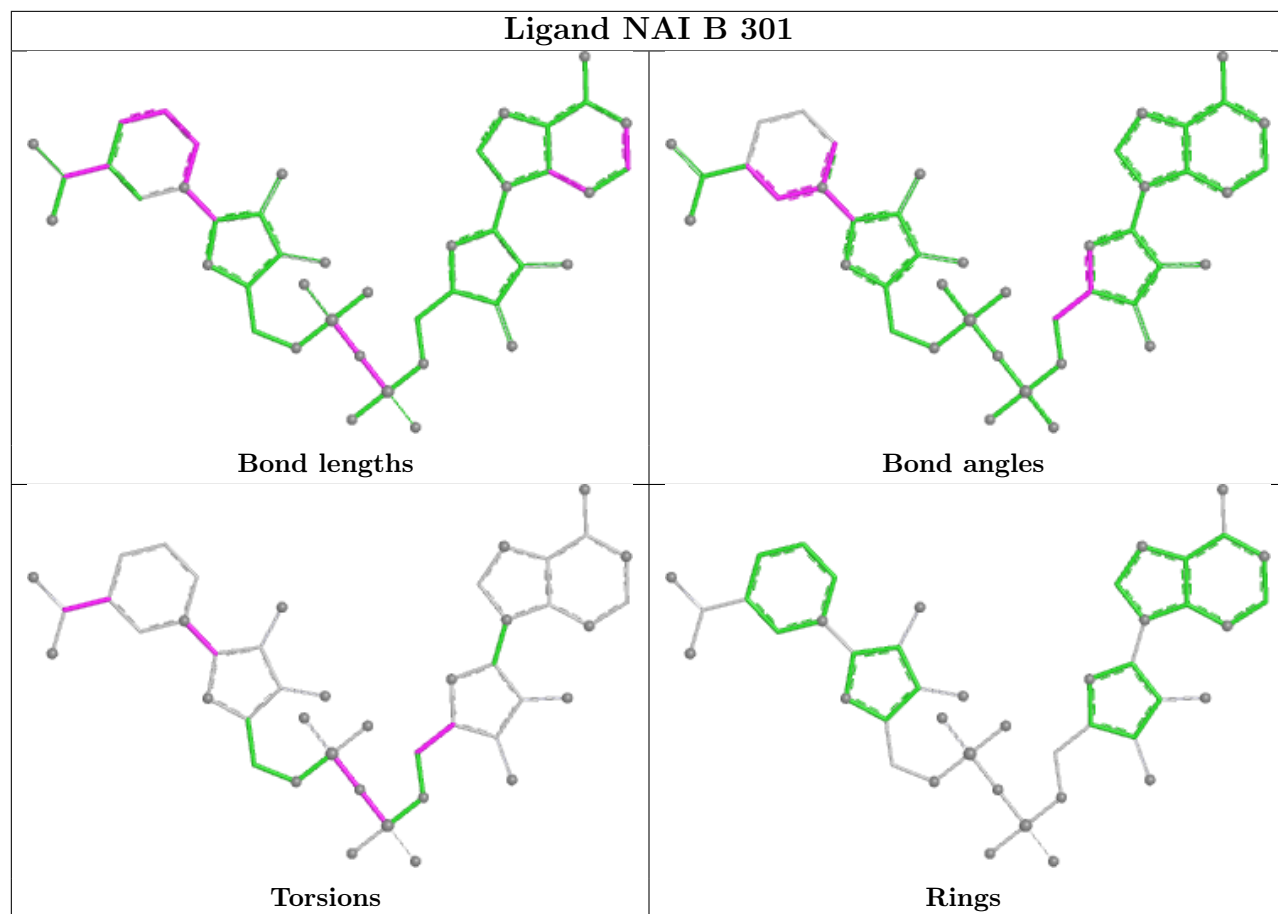
Mol	Chain	Res	Type	Atoms
2	A	301	NAI	PN-O3-PA-O5B
2	B	301	NAI	PN-O3-PA-O5B
2	A	301	NAI	PA-O3-PN-O2N
2	B	301	NAI	O4D-C1D-N1N-C2N
2	A	301	NAI	O4D-C1D-N1N-C2N
2	A	301	NAI	C2N-C3N-C7N-N7N
2	B	301	NAI	C2N-C3N-C7N-N7N
2	B	301	NAI	PA-O3-PN-O2N
2	A	301	NAI	PA-O3-PN-O1N
2	A	301	NAI	O4B-C4B-C5B-O5B
2	B	301	NAI	O4B-C4B-C5B-O5B

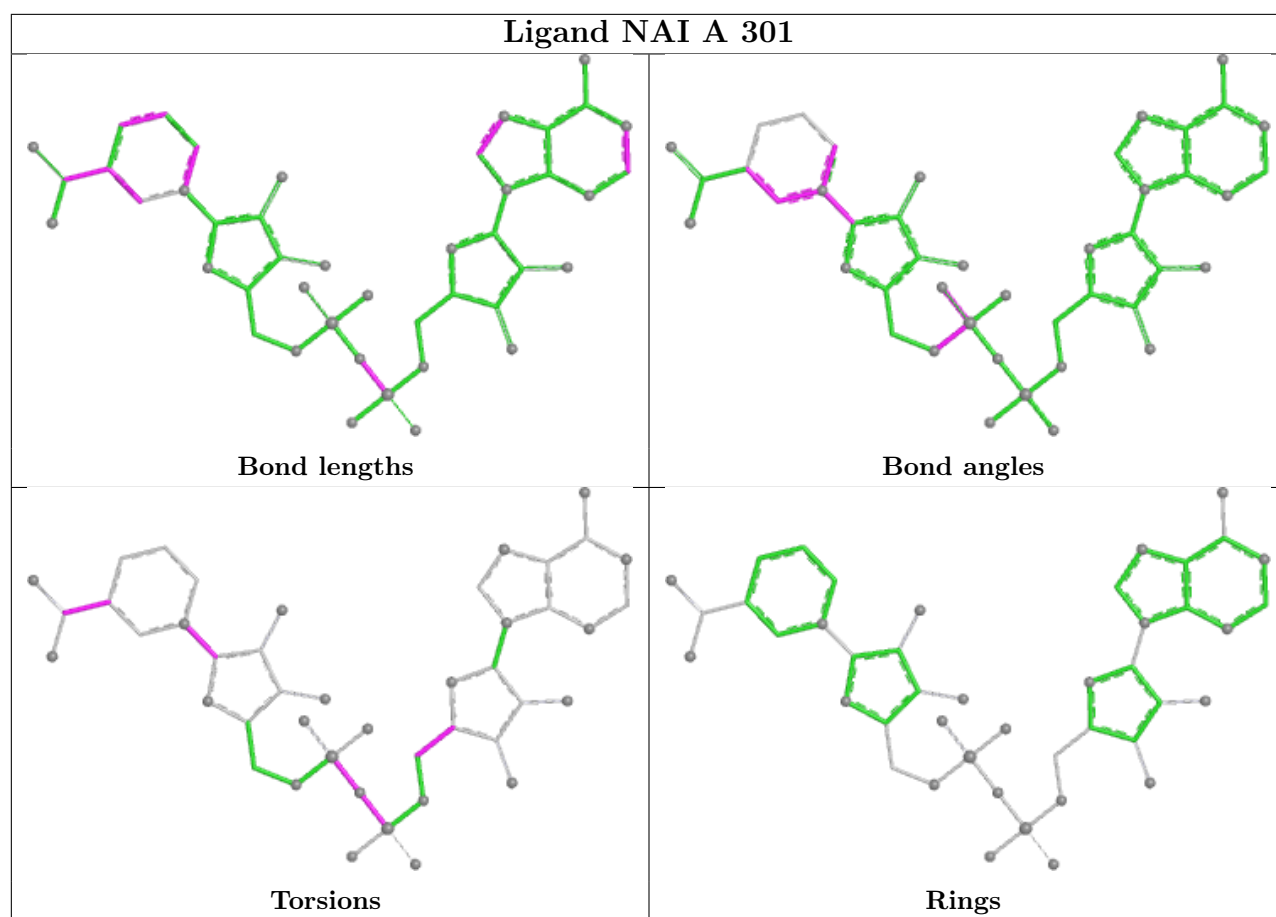
There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	301	NAI	2	0
2	A	301	NAI	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(Å ²)	Q<0.9
1	A	271/288 (94%)	0.25	20 (7%) 20 18	19, 44, 74, 100	41 (15%)
1	B	271/288 (94%)	-0.08	5 (1%) 67 64	19, 43, 77, 97	20 (7%)
All	All	542/576 (94%)	0.09	25 (4%) 37 33	19, 44, 76, 100	61 (11%)

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	214	GLU	6.0
1	A	219	ASP	4.8
1	A	209	LYS	4.2
1	A	217	VAL	4.1
1	A	155	ASN	3.9
1	B	249	GLY	3.4
1	B	251	LYS	3.3
1	A	163	LYS	3.3
1	A	191	ALA	3.3
1	A	160	PHE	3.1
1	B	223	LEU	3.1
1	A	161	PHE	3.0
1	A	188	GLN	3.0
1	A	210	PRO	3.0
1	A	189	ALA	2.7
1	A	157	ARG	2.7
1	A	192	GLU	2.5
1	A	158	ASP	2.4
1	A	218	ASN	2.3
1	A	240	LYS	2.3
1	A	19	HIS	2.2
1	B	194	LEU	2.2
1	A	221	SER	2.1
1	A	18	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	220	ILE	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](#)

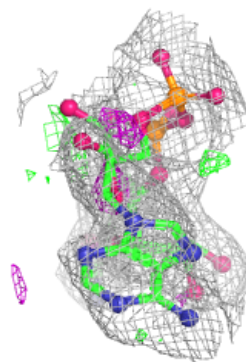
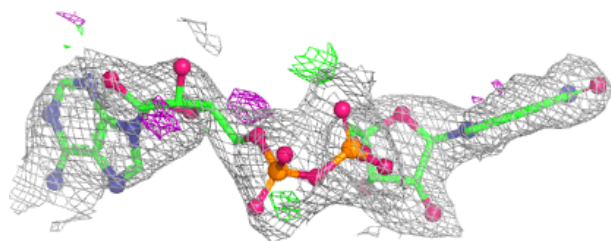
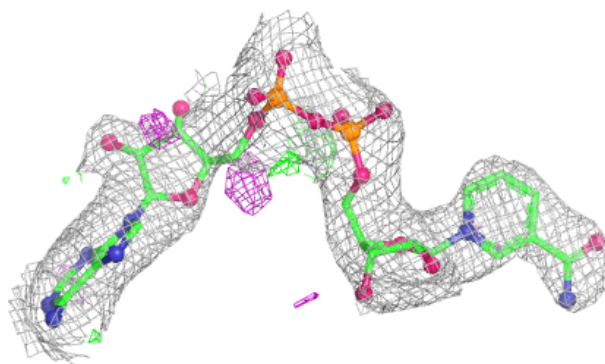
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	PO4	A	302	5/5	0.78	0.13	78,80,82,87	0
3	PO4	B	302	5/5	0.79	0.13	77,77,85,86	0
3	PO4	A	304	5/5	0.84	0.11	87,88,92,95	0
3	PO4	A	303	5/5	0.85	0.12	78,84,85,86	0
2	NAI	A	301	44/44	0.87	0.12	37,61,74,77	0
3	PO4	B	303	5/5	0.92	0.10	71,71,82,86	0
2	NAI	B	301	44/44	0.93	0.08	26,43,51,58	0

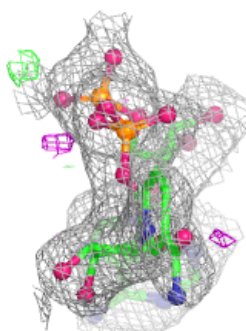
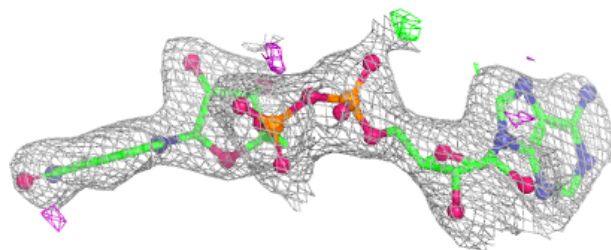
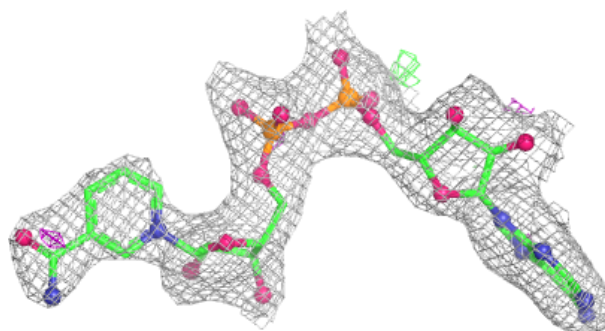
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around NAI A 301:

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

**Electron density around NAI B 301:**

$2mF_o-DF_c$ (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.