



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 12:07 AM EDT

PDB ID : 1NVT / pdb_00001nvt
Title : Crystal structure of Shikimate Dehydrogenase (AROE or MJ1084) in complex with NADP+
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Deposited on : 2003-02-04
Resolution : 2.35 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

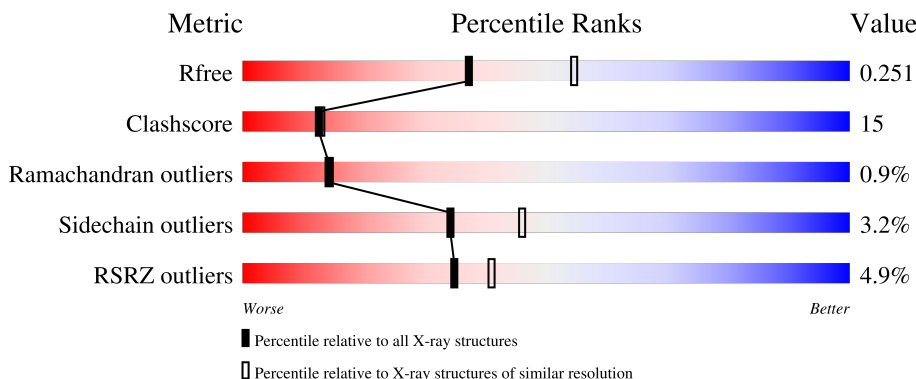
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	287	
1	B	287	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NAP	A	288	X	-	-	-
3	NAP	B	289	X	-	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4637 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 Shikimate 5'-dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	287	Total	C	N	O	S	0	0	0
			2200	1417	362	412	9			
1	B	287	Total	C	N	O	S	0	0	0
			2200	1417	362	412	9			

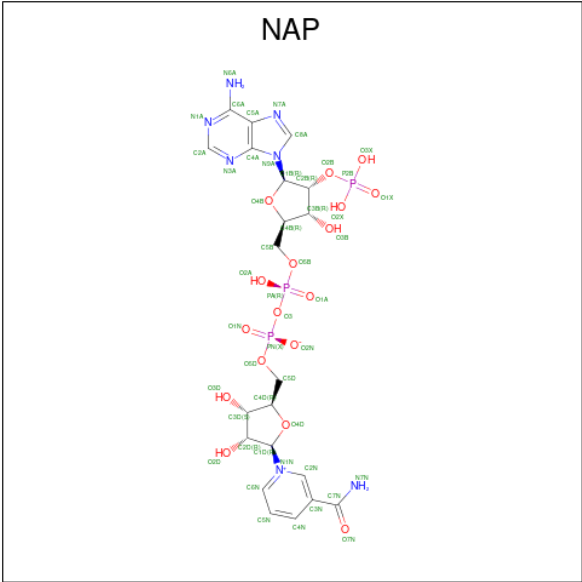
There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	cloning artifact	UNP Q58484
A	2	PRO	-	cloning artifact	UNP Q58484
A	3	LEU	-	cloning artifact	UNP Q58484
A	4	GLY	-	cloning artifact	UNP Q58484
A	5	SER	-	cloning artifact	UNP Q58484
B	1	GLY	-	cloning artifact	UNP Q58484
B	2	PRO	-	cloning artifact	UNP Q58484
B	3	LEU	-	cloning artifact	UNP Q58484
B	4	GLY	-	cloning artifact	UNP Q58484
B	5	SER	-	cloning artifact	UNP Q58484

- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		

- Molecule 3 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NAP) (formula: C₂₁H₂₈N₇O₁₇P₃).



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

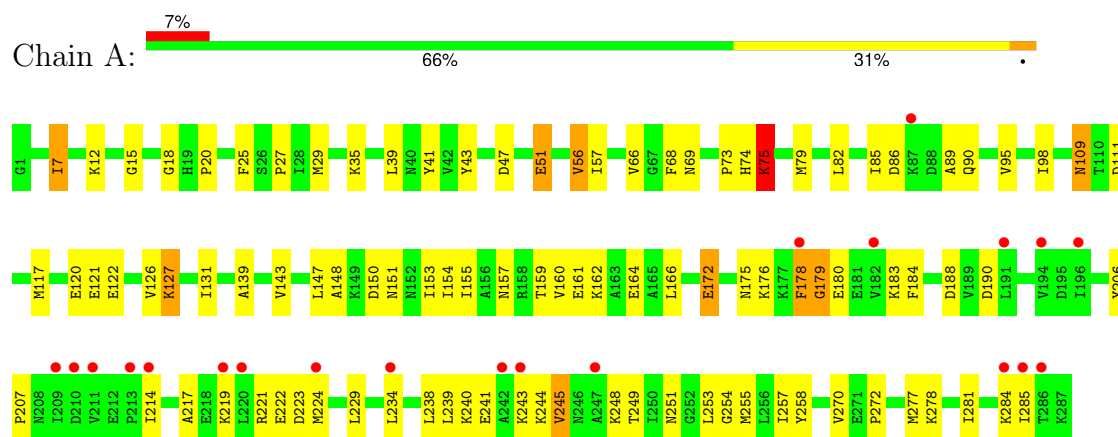
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	45	Total	O	0	0
			45	45		
4	B	94	Total	O	0	0
			94	94		

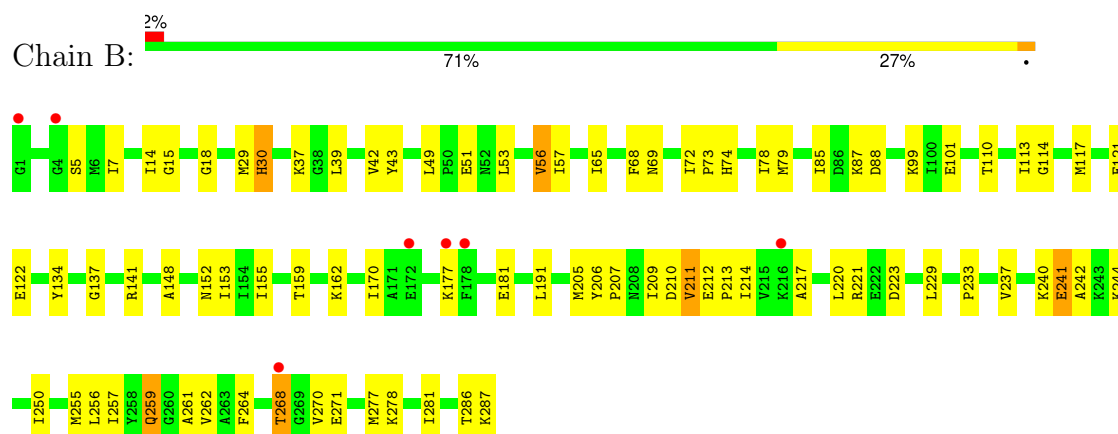
3 Residue-property plots

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: Shikimate 5'-dehydrogenase



• Molecule 1: Shikimate 5'-dehydrogenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	74.65Å 75.62Å 118.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	21.96 – 2.35 21.96 – 2.35	Depositor EDS
% Data completeness (in resolution range)	97.9 (21.96-2.35) 97.6 (21.96-2.35)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.10 (at 2.36Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.224 , 0.260 0.217 , 0.251	Depositor DCC
R_{free} test set	2616 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å ²)	37.4	Xtriage
Anisotropy	0.063	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 40.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.016 for k,h,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4637	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.14% 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: ZN, 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	0.40	0/2232	0.92	6/3012 (0.2%)
1	B	0.46	0/2232	0.96	6/3012 (0.2%)
All	All	0.43	0/4464	0.94	12/6024 (0.2%)

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	56	VAL	N-CA-C	10.37	120.28	110.53
1	A	69	ASN	N-CA-C	-9.05	95.24	109.72
1	B	69	ASN	N-CA-C	-8.51	96.10	109.72
1	A	56	VAL	N-CA-C	7.86	117.92	110.53
1	B	30	HIS	N-CA-C	7.18	119.19	111.36
1	B	65	ILE	N-CA-C	-6.35	100.50	108.89
1	A	7	ILE	N-CA-C	5.31	116.44	109.21
1	A	75	LYS	N-CA-C	5.28	118.82	112.38
1	B	241	GLU	N-CA-C	-5.26	105.22	111.69
1	B	268	THR	N-CA-C	5.04	120.27	113.72
1	A	240	LYS	N-CA-C	-5.00	105.47	111.03
1	A	66	VAL	N-CA-C	5.00	117.34	111.09

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	2200	0	2295	77	0
1	B	2200	0	2295	65	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	48	0	22	1	0
3	B	48	0	23	2	0
4	A	45	0	0	1	0
4	B	94	0	0	2	0
All	All	4637	0	4635	140	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 15.

All (140) 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:113:ILE:HG22	1:B:117:MET:HE2	1.51	0.93
1:B:261:ALA:HB2	1:B:277:MET:HE1	1.52	0.91
1:B:268:THR:HG23	1:B:270:VAL:H	1.36	0.91
1:A:127:LYS:HG3	1:A:150:ASP:HB2	1.58	0.86
1:A:79:MET:HE2	1:A:85:ILE:HD13	1.57	0.85
1:A:29:MET:HB2	1:A:281:ILE:HD11	1.64	0.79
1:A:25:PHE:HB3	1:A:281:ILE:HD12	1.64	0.79
1:A:117:MET:HE3	1:A:258:TYR:HB3	1.70	0.73
1:B:29:MET:HE2	1:B:281:ILE:HD11	1.71	0.72
1:B:257:ILE:HG23	1:B:277:MET:HE3	1.70	0.72
1:A:147:LEU:O	1:A:151:ASN:HB2	1.89	0.72
1:A:148:ALA:HB2	1:A:153:ILE:HD13	1.71	0.72
1:B:257:ILE:HD11	1:B:278:LYS:HA	1.74	0.70
1:A:75:LYS:HB3	1:A:95:VAL:O	1.92	0.69
1:B:137:GLY:O	1:B:141:ARG:HG3	1.92	0.68
1:B:211:VAL:HG22	1:B:212:GLU:H	1.59	0.68
1:B:87:LYS:HG3	1:B:88:ASP:H	1.58	0.68
1:A:272:PRO:HB2	1:A:277:MET:HE2	1.74	0.67
1:B:264:PHE:O	1:B:268:THR:HG22	1.95	0.67
1:A:12:LYS:HE2	1:A:12:LYS:HA	1.76	0.67
1:B:122:GLU:HG2	1:B:250:ILE:HG12	1.76	0.65
1:A:51:GLU:H	1:A:51:GLU:CD	2.04	0.65
1:A:239:LEU:HD22	1:A:249:THR:HB	1.78	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:ILE:HD13	1:B:42:VAL:CG2	2.28	0.64
1:B:211:VAL:HG22	1:B:212:GLU:N	2.11	0.63
1:A:126:VAL:HG12	1:A:151:ASN:HD21	1.63	0.63
1:B:134:TYR:HB3	1:B:214:ILE:HD13	1.82	0.62
1:B:220:LEU:HD13	1:B:242:ALA:HA	1.80	0.62
1:B:241:GLU:O	1:B:244:LYS:HG2	2.02	0.59
1:B:268:THR:HG23	1:B:270:VAL:N	2.14	0.59
1:A:221:ARG:H	1:A:224:MET:HE3	1.68	0.58
1:A:229:LEU:HD22	1:A:255:MET:SD	2.43	0.58
1:B:237:VAL:HA	1:B:240:LYS:HE2	1.86	0.58
1:B:53:LEU:O	1:B:56:VAL:HG22	2.04	0.57
1:A:117:MET:CE	1:A:258:TYR:HB3	2.33	0.57
1:A:206:TYR:CD1	1:A:207:PRO:HA	2.39	0.57
1:B:152:ASN:HD22	1:B:181:GLU:HA	1.70	0.57
1:B:117:MET:HE1	1:B:262:VAL:CG2	2.35	0.56
1:A:39:LEU:HD11	1:A:270:VAL:HG21	1.87	0.56
1:A:154:ILE:HG12	1:A:183:LYS:HB2	1.88	0.56
1:B:15:GLY:O	1:B:68:PHE:HA	2.07	0.55
1:A:179:GLY:O	1:A:183:LYS:HE2	2.07	0.55
1:B:148:ALA:HB2	1:B:153:ILE:HD13	1.89	0.54
1:B:206:TYR:CE2	1:B:207:PRO:HG3	2.42	0.54
1:A:122:GLU:HG3	1:A:248:LYS:NZ	2.21	0.54
1:A:217:ALA:HB2	1:A:241:GLU:OE2	2.08	0.54
1:B:221:ARG:HD2	1:B:223:ASP:OD1	2.07	0.54
1:B:53:LEU:HD11	1:B:78:ILE:HD13	1.90	0.54
1:B:177:LYS:N	1:B:177:LYS:HD2	2.24	0.53
1:A:117:MET:HE3	1:A:258:TYR:CD1	2.44	0.52
1:B:114:GLY:HA2	1:B:117:MET:HE3	1.90	0.52
1:B:37:LYS:HB3	1:B:39:LEU:HG	1.92	0.52
1:A:126:VAL:HG12	1:A:151:ASN:ND2	2.26	0.51
1:B:134:TYR:HB3	1:B:214:ILE:CD1	2.40	0.51
1:B:30:HIS:HE1	4:B:292:HOH:O	1.94	0.50
1:B:191:LEU:O	1:B:221:ARG:NH2	2.44	0.50
1:B:117:MET:HE1	1:B:262:VAL:HG21	1.93	0.49
1:A:109:ASN:C	1:A:109:ASN:HD22	2.20	0.49
1:A:184:PHE:C	1:A:184:PHE:CD1	2.90	0.49
1:B:7:ILE:HD12	1:B:7:ILE:N	2.28	0.49
1:B:177:LYS:HA	1:B:177:LYS:HE3	1.95	0.48
1:A:120:GLU:C	1:A:122:GLU:H	2.21	0.48
1:A:175:ASN:O	1:A:176:LYS:HD2	2.14	0.47
1:B:79:MET:HE2	1:B:85:ILE:HD13	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:127:LYS:NZ	1:A:127:LYS:HB3	2.28	0.47
1:A:175:ASN:C	1:A:176:LYS:HD2	2.39	0.47
1:A:254:GLY:O	1:A:258:TYR:HD2	1.98	0.47
1:B:99:LYS:HE2	1:B:101:GLU:OE2	2.14	0.47
1:A:117:MET:HE3	1:A:258:TYR:CB	2.43	0.47
1:A:86:ASP:O	1:A:89:ALA:HB3	2.15	0.46
1:A:120:GLU:C	1:A:122:GLU:N	2.72	0.46
1:A:85:ILE:HG22	1:A:90:GLN:HG2	1.98	0.46
1:A:15:GLY:O	1:A:68:PHE:HA	2.14	0.46
1:B:29:MET:HE1	1:B:256:LEU:HG	1.98	0.46
1:A:243:LYS:C	1:A:245:VAL:H	2.23	0.45
1:A:272:PRO:CB	1:A:277:MET:HE2	2.46	0.45
1:A:109:ASN:HD21	1:A:111:ASP:HB2	1.81	0.45
1:A:131:ILE:O	1:A:153:ILE:HA	2.16	0.45
1:A:120:GLU:O	1:A:122:GLU:N	2.49	0.45
1:A:172:GLU:OE1	1:A:172:GLU:C	2.60	0.45
1:B:257:ILE:CG2	1:B:277:MET:HE3	2.43	0.45
1:A:18:GLY:HA2	1:A:74:HIS:CD2	2.51	0.45
1:B:286:THR:O	1:B:287:LYS:C	2.59	0.45
1:A:253:LEU:HG	1:A:257:ILE:HD12	1.99	0.45
1:A:234:LEU:HD11	1:A:285:ILE:HD13	1.99	0.44
1:A:178:PHE:C	1:A:180:GLU:H	2.26	0.44
1:A:190:ASP:HA	1:A:219:LYS:NZ	2.33	0.44
1:A:253:LEU:HG	1:A:257:ILE:CD1	2.47	0.44
1:B:209:ILE:HG21	1:B:233:PRO:HG3	2.00	0.44
1:B:211:VAL:CG2	1:B:212:GLU:H	2.28	0.44
1:B:155:ILE:HD11	1:B:170:ILE:HD12	2.00	0.44
1:B:18:GLY:HA2	1:B:74:HIS:CD2	2.52	0.44
1:A:39:LEU:HB3	1:A:41:TYR:HD2	1.81	0.44
1:A:164:GLU:HG3	1:A:184:PHE:CE2	2.53	0.44
1:B:122:GLU:HG2	1:B:250:ILE:CG1	2.47	0.44
1:B:159:THR:O	1:B:162:LYS:HB3	2.18	0.44
1:A:148:ALA:HB2	1:A:153:ILE:CD1	2.45	0.43
1:A:79:MET:HE3	1:A:95:VAL:HG23	2.00	0.43
1:A:272:PRO:CG	1:A:277:MET:CE	2.96	0.43
1:B:217:ALA:HB2	1:B:241:GLU:HG3	1.98	0.43
1:B:229:LEU:HD22	1:B:255:MET:SD	2.58	0.43
1:A:139:ALA:O	1:A:143:VAL:HG23	2.18	0.43
1:B:49:LEU:HD13	1:B:51:GLU:OE2	2.18	0.43
1:B:213:PRO:HG3	1:B:237:VAL:CG2	2.48	0.43
1:A:178:PHE:O	1:A:180:GLU:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:214:ILE:HG22	1:A:238:LEU:HD13	2.00	0.43
1:B:110:THR:OG1	1:B:259:GLN:HG2	2.19	0.43
1:A:157:ASN:ND2	4:A:296:HOH:O	2.52	0.42
1:A:122:GLU:HG3	1:A:248:LYS:HZ1	1.82	0.42
1:B:14:ILE:O	1:B:43:TYR:HA	2.19	0.42
1:B:113:ILE:CG2	1:B:117:MET:HE2	2.37	0.42
1:B:72:ILE:HD11	3:B:289:NAP:O1N	2.18	0.42
1:B:214:ILE:HG12	1:B:214:ILE:O	2.20	0.42
1:A:82:LEU:HD21	1:A:98:ILE:HD13	2.02	0.42
1:A:222:GLU:C	1:A:224:MET:H	2.28	0.42
1:B:56:VAL:HG23	1:B:57:ILE:N	2.34	0.42
1:A:20:PRO:HA	1:A:47:ASP:OD1	2.20	0.42
1:A:244:LYS:O	1:A:245:VAL:HG13	2.19	0.42
1:B:211:VAL:CG2	1:B:212:GLU:N	2.79	0.41
1:A:160:VAL:HG23	1:A:161:GLU:N	2.36	0.41
1:B:217:ALA:N	1:B:241:GLU:OE1	2.45	0.41
1:A:27:PRO:HA	1:A:43:TYR:CD2	2.55	0.41
1:B:29:MET:CE	1:B:256:LEU:HG	2.50	0.41
1:B:217:ALA:HB2	1:B:241:GLU:CD	2.46	0.41
1:A:234:LEU:N	1:A:234:LEU:HD12	2.36	0.41
1:A:251:ASN:HD21	1:A:253:LEU:HB2	1.86	0.41
1:A:253:LEU:HD21	1:A:278:LYS:HG3	2.01	0.41
1:A:272:PRO:HG2	1:A:277:MET:CE	2.51	0.41
1:B:5:SER:O	1:B:7:ILE:HD12	2.20	0.41
1:A:7:ILE:CD1	1:B:42:VAL:CG2	2.98	0.41
1:A:86:ASP:O	1:A:90:GLN:HG3	2.21	0.41
1:B:213:PRO:HG3	1:B:237:VAL:HB	2.03	0.41
1:A:223:ASP:OD2	1:A:223:ASP:N	2.54	0.41
1:B:205:MET:HE2	4:B:363:HOH:O	2.20	0.40
1:A:39:LEU:HB3	1:A:41:TYR:CD2	2.56	0.40
1:A:56:VAL:HG23	1:A:57:ILE:N	2.36	0.40
1:A:155:ILE:HD13	1:A:166:LEU:HD23	2.02	0.40
1:B:205:MET:HE1	3:B:289:NAP:O2D	2.22	0.40
1:A:159:THR:HG23	3:A:288:NAP:O2X	2.22	0.40
1:A:85:ILE:CG2	1:A:90:GLN:HG2	2.52	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	285/287 (99%)	258 (90%)	23 (8%)	4 (1%)	9	7
1	B	285/287 (99%)	265 (93%)	19 (7%)	1 (0%)	30	34
All	All	570/574 (99%)	523 (92%)	42 (7%)	5 (1%)	14	14

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	178	PHE
1	A	179	GLY
1	A	121	GLU
1	A	245	VAL
1	B	211	VAL

5.3.2 Protein sidechains [i](#)

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	233/233 (100%)	223 (96%)	10 (4%)	26	34
1	B	233/233 (100%)	228 (98%)	5 (2%)	47	61
All	All	466/466 (100%)	451 (97%)	15 (3%)	34	46

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	35	LYS

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Mol	Chain	Res	Type
1	A	51	GLU
1	A	73	PRO
1	A	75	LYS
1	A	109	ASN
1	A	127	LYS
1	A	162	LYS
1	A	172	GLU
1	A	188	ASP
1	A	284	LYS
1	B	73	PRO
1	B	121	GLU
1	B	210	ASP
1	B	259	GLN
1	B	271	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	HIS
1	A	40	ASN
1	A	52	ASN
1	A	109	ASN
1	A	130	ASN
1	A	152	ASN
1	A	157	ASN
1	A	232	ASN
1	A	259	GLN
1	A	279	ASN
1	B	30	HIS
1	B	52	ASN
1	B	152	ASN
1	B	157	ASN
1	B	175	ASN
1	B	208	ASN
1	B	232	ASN

5.3.3 RNA ⓘ

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](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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	B	289	-	50,52,52	3.17	14 (28%)	71,80,80	3.30	17 (23%)
3	NAP	A	288	-	50,52,52	3.31	14 (28%)	71,80,80	3.22	19 (26%)

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	B	289	-	1/1/12/12	11/35/67/67	0/5/5/5
3	NAP	A	288	-	1/1/12/12	13/35/67/67	0/5/5/5

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	289	NAP	O7N-C7N	10.26	1.43	1.24
3	A	288	NAP	O7N-C7N	10.19	1.43	1.24
3	A	288	NAP	PN-O3	-9.34	1.49	1.59
3	B	289	NAP	C2N-N1N	9.19	1.45	1.35
3	A	288	NAP	PA-O3	-8.86	1.49	1.59
3	A	288	NAP	C2N-N1N	8.67	1.44	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	288	NAP	C5N-C4N	7.66	1.52	1.38
3	B	289	NAP	C5N-C4N	7.65	1.52	1.38
3	B	289	NAP	PA-O3	-7.31	1.51	1.59
3	B	289	NAP	PN-O3	-7.17	1.51	1.59
3	B	289	NAP	C6N-C5N	6.25	1.51	1.38
3	A	288	NAP	C6N-C5N	5.85	1.50	1.38
3	A	288	NAP	C6N-N1N	4.89	1.46	1.35
3	B	289	NAP	C6N-N1N	4.81	1.46	1.35
3	B	289	NAP	C4N-C3N	4.10	1.45	1.39
3	A	288	NAP	C4N-C3N	3.98	1.45	1.39
3	A	288	NAP	C2N-C3N	2.97	1.43	1.39
3	B	289	NAP	C4A-N3A	2.84	1.39	1.34
3	A	288	NAP	C4A-N3A	2.66	1.39	1.34
3	B	289	NAP	C2A-N1A	2.60	1.38	1.33
3	B	289	NAP	C2N-C3N	2.59	1.43	1.39
3	A	288	NAP	C2A-N1A	2.54	1.38	1.33
3	B	289	NAP	C8A-N7A	2.45	1.36	1.31
3	A	288	NAP	C1B-N9A	-2.39	1.39	1.46
3	B	289	NAP	C7N-N7N	2.36	1.37	1.33
3	B	289	NAP	O4D-C1D	2.22	1.43	1.40
3	A	288	NAP	O4D-C1D	2.11	1.43	1.40
3	A	288	NAP	C8A-N7A	2.05	1.35	1.31

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	289	NAP	P2B-O2B-C2B	-14.55	84.58	123.43
3	A	288	NAP	P2B-O2B-C2B	-13.79	86.61	123.43
3	B	289	NAP	C2B-C1B-N9A	12.50	134.33	113.75
3	A	288	NAP	C2B-C1B-N9A	11.69	132.99	113.75
3	A	288	NAP	C6N-N1N-C1D	-8.42	103.21	119.73
3	B	289	NAP	C6N-N1N-C1D	-8.13	103.77	119.73
3	B	289	NAP	O5D-C5D-C4D	7.44	134.32	108.99
3	A	288	NAP	O5D-C5D-C4D	7.18	133.45	108.99
3	A	288	NAP	C2N-N1N-C1D	6.83	134.20	119.13
3	B	289	NAP	C2N-N1N-C1D	6.55	133.60	119.13
3	A	288	NAP	N3A-C2A-N1A	-5.82	119.77	128.58
3	B	289	NAP	C5A-C4A-N3A	-5.74	118.82	126.72
3	B	289	NAP	N3A-C2A-N1A	-5.69	119.96	128.58
3	A	288	NAP	C5A-C4A-N3A	-5.45	119.22	126.72
3	B	289	NAP	O3X-P2B-O2B	5.18	126.02	105.85
3	A	288	NAP	O3X-P2B-O2B	5.13	125.84	105.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	289	NAP	N3A-C4A-N9A	4.89	135.48	127.17
3	A	288	NAP	N3A-C4A-N9A	4.78	135.29	127.17
3	A	288	NAP	PN-O5D-C5D	4.74	148.51	121.35
3	B	289	NAP	PN-O5D-C5D	4.59	147.64	121.35
3	A	288	NAP	C2A-N3A-C4A	3.96	121.50	111.83
3	B	289	NAP	C2A-N3A-C4A	3.96	121.50	111.83
3	A	288	NAP	C1B-N9A-C8A	-2.77	120.94	127.09
3	B	289	NAP	O4B-C1B-N9A	-2.73	102.85	108.09
3	B	289	NAP	C6N-C5N-C4N	-2.65	115.63	119.45
3	A	288	NAP	C6N-C5N-C4N	-2.63	115.65	119.45
3	B	289	NAP	C3B-C2B-C1B	-2.54	97.94	102.81
3	A	288	NAP	O4B-C1B-N9A	-2.50	103.29	108.09
3	B	289	NAP	C1B-N9A-C8A	-2.37	121.84	127.09
3	B	289	NAP	C6A-C5A-C4A	2.33	120.36	117.18
3	A	288	NAP	C3B-C2B-C1B	-2.24	98.52	102.81
3	A	288	NAP	N9A-C8A-N7A	-2.20	110.81	113.94
3	A	288	NAP	C6A-C5A-C4A	2.19	120.17	117.18
3	B	289	NAP	C6A-C5A-N7A	-2.09	128.06	132.09
3	A	288	NAP	O2X-P2B-O2B	-2.05	97.87	105.85
3	A	288	NAP	C4A-N9A-C8A	2.02	107.86	105.74

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	288	NAP	C1D
3	B	289	NAP	C1D

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	288	NAP	C5B-O5B-PA-O1A
3	A	288	NAP	C5B-O5B-PA-O3
3	A	288	NAP	C5D-O5D-PN-O3
3	A	288	NAP	C5D-O5D-PN-O1N
3	A	288	NAP	C5D-O5D-PN-O2N
3	A	288	NAP	O4D-C1D-N1N-C2N
3	A	288	NAP	O4D-C1D-N1N-C6N
3	B	289	NAP	C5B-O5B-PA-O3
3	B	289	NAP	C5D-O5D-PN-O3
3	B	289	NAP	C5D-O5D-PN-O2N
3	B	289	NAP	O4D-C1D-N1N-C2N
3	B	289	NAP	O4D-C1D-N1N-C6N

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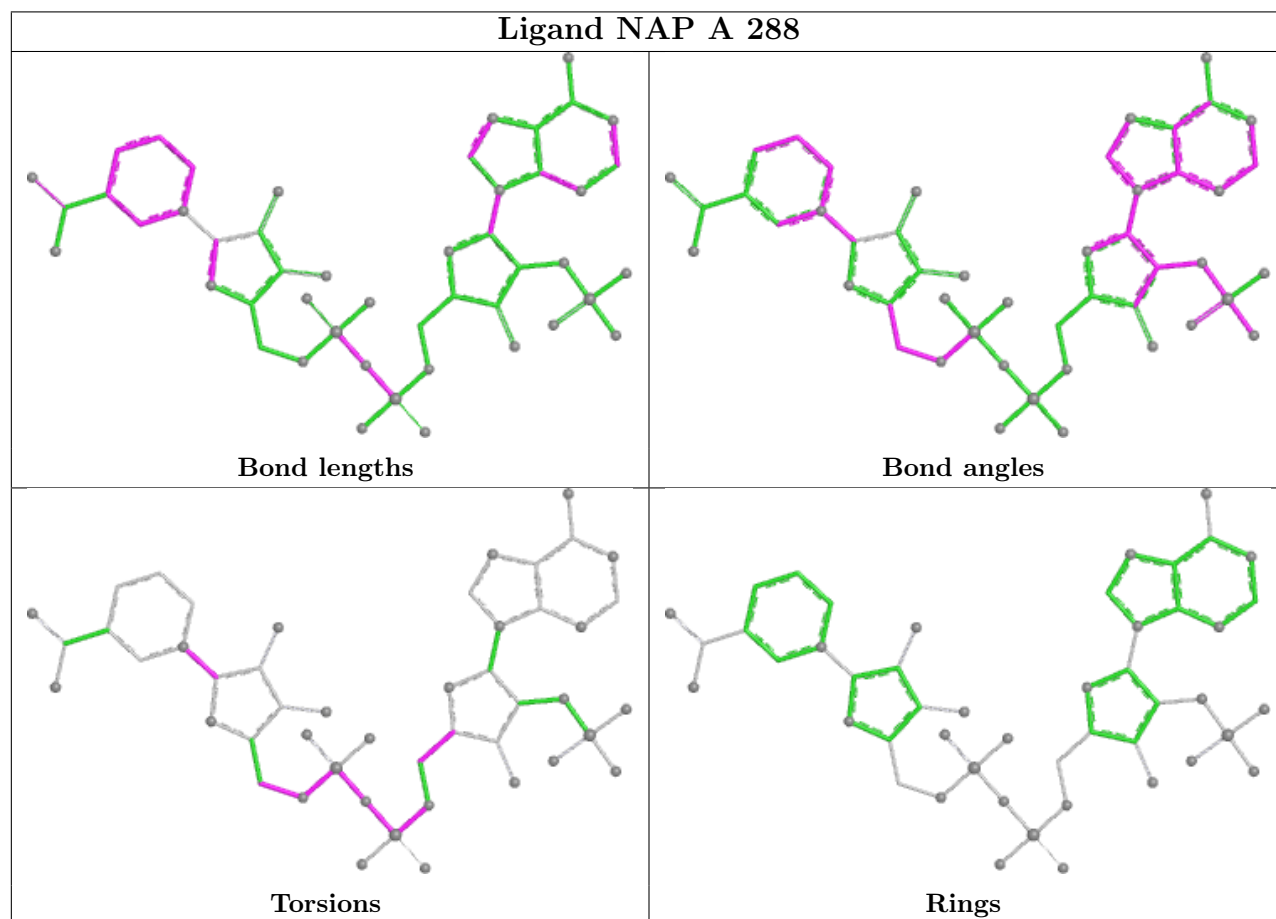
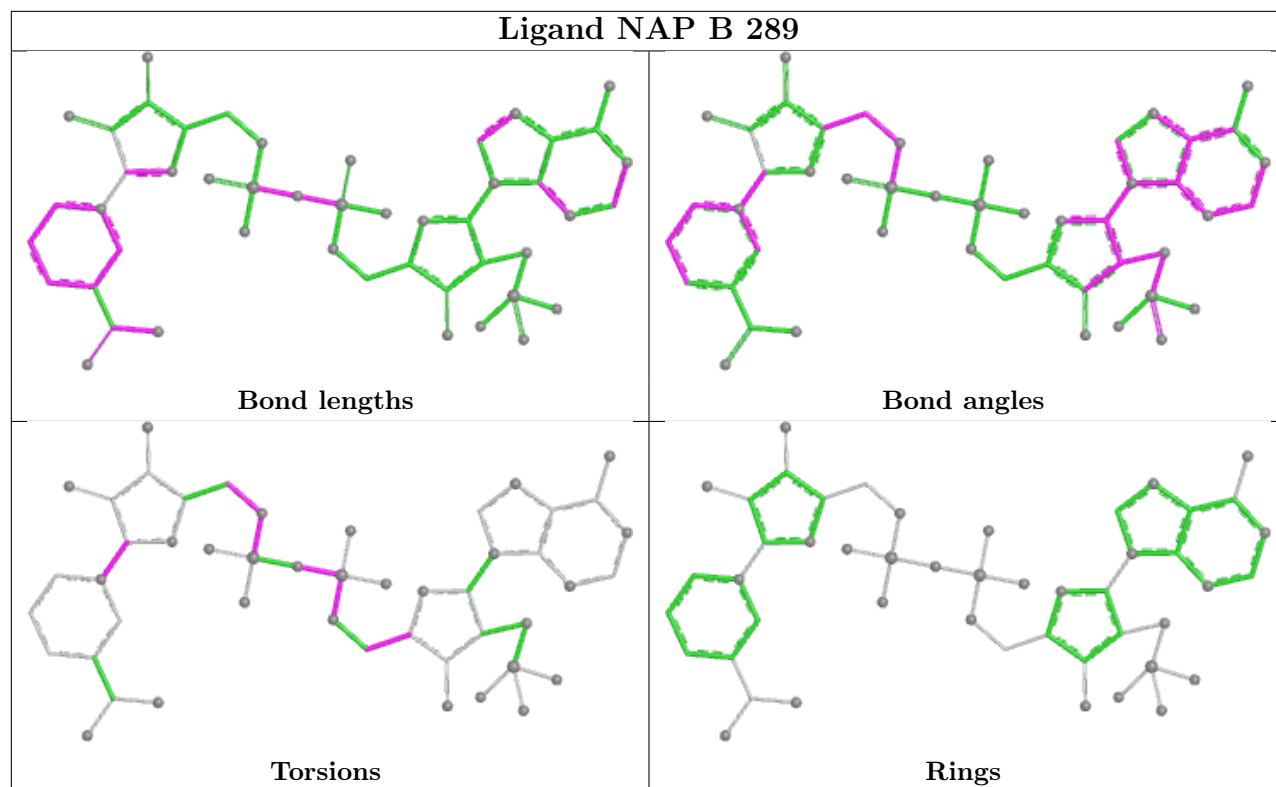
Mol	Chain	Res	Type	Atoms
3	A	288	NAP	O4B-C4B-C5B-O5B
3	B	289	NAP	O4B-C4B-C5B-O5B
3	A	288	NAP	C3B-C4B-C5B-O5B
3	B	289	NAP	C3B-C4B-C5B-O5B
3	B	289	NAP	C4D-C5D-O5D-PN
3	A	288	NAP	PA-O3-PN-O5D
3	A	288	NAP	PN-O3-PA-O2A
3	B	289	NAP	PN-O3-PA-O2A
3	B	289	NAP	C5B-O5B-PA-O1A
3	B	289	NAP	C5D-O5D-PN-O1N
3	A	288	NAP	C4D-C5D-O5D-PN
3	A	288	NAP	PN-O3-PA-O1A

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	289	NAP	2	0
3	A	288	NAP	1	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	287/287 (100%)	0.62	21 (7%) 21 24	23, 49, 81, 92	0
1	B	287/287 (100%)	0.10	7 (2%) 59 66	19, 34, 60, 70	0
All	All	574/574 (100%)	0.36	28 (4%) 35 41	19, 42, 77, 92	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	194	VAL	3.4
1	A	247	ALA	3.1
1	A	210	ASP	3.0
1	A	191	LEU	2.9
1	A	234	LEU	2.9
1	A	211	VAL	2.9
1	A	209	ILE	2.8
1	A	285	ILE	2.8
1	B	1	GLY	2.6
1	A	286	THR	2.6
1	A	220	LEU	2.4
1	A	182	VAL	2.4
1	A	224	MET	2.3
1	A	196	ILE	2.3
1	A	214	ILE	2.3
1	B	177	LYS	2.3
1	A	213	PRO	2.2
1	B	4	GLY	2.2
1	A	284	LYS	2.2
1	A	178	PHE	2.2
1	A	219	LYS	2.2
1	B	216	LYS	2.2
1	B	172	GLU	2.1
1	A	243	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	178	PHE	2.1
1	B	268	THR	2.0
1	A	242	ALA	2.0
1	A	87	LYS	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

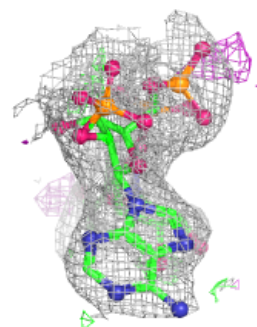
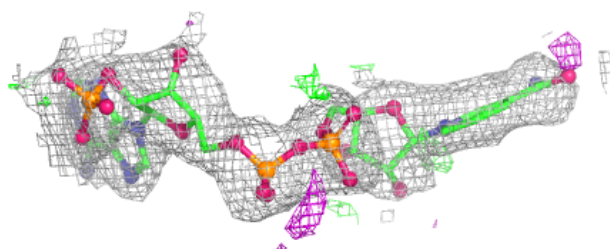
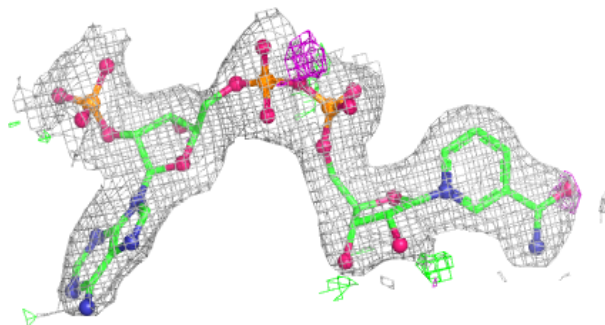
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	NAP	B	289	48/48	0.88	0.12	50,64,68,69	0
3	NAP	A	288	48/48	0.92	0.11	38,48,54,55	0
2	ZN	A	290	1/1	0.98	0.04	46,46,46,46	0
2	ZN	B	291	1/1	0.98	0.04	36,36,36,36	0

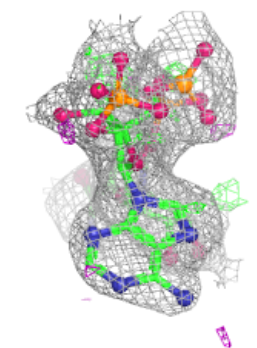
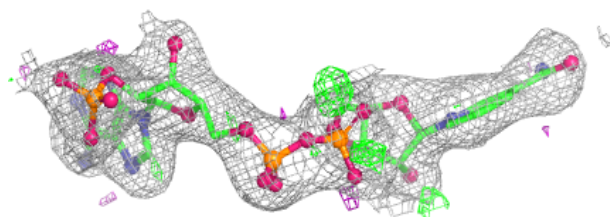
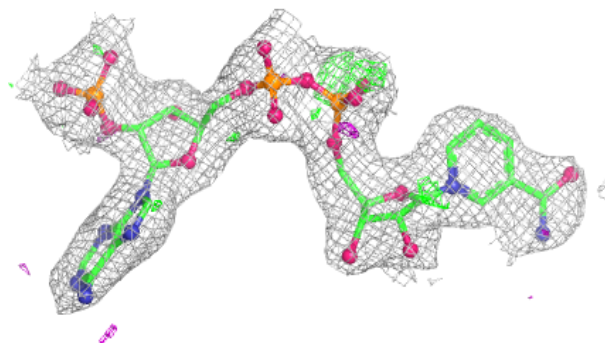
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around NAP B 289:

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

**Electron density around NAP A 288:**

$2mF_o-DF_c$ (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.