



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 01:33 PM UTC

PDB ID : 6LRG / pdb_00006lrg
Title : Crystal Structure of the Ternary Complex of AgrE with Ornithine and NAD⁺
Authors : Lee, H.; Rhee, S.
Deposited on : 2020-01-16
Resolution : 2.41 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

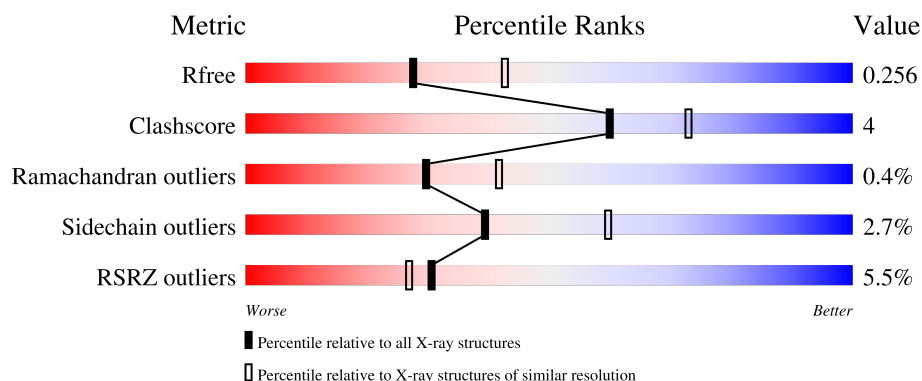
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.41 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	6062 (2.44-2.40)
Clashscore	190562	6562 (2.44-2.40)
Ramachandran outliers	187476	6481 (2.44-2.40)
Sidechain outliers	187428	6482 (2.44-2.40)
RSRZ outliers	180081	6066 (2.44-2.40)

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	703	3% 87% 10% .
1	B	703	8% 81% 15% ..

2 Entry composition [i](#)

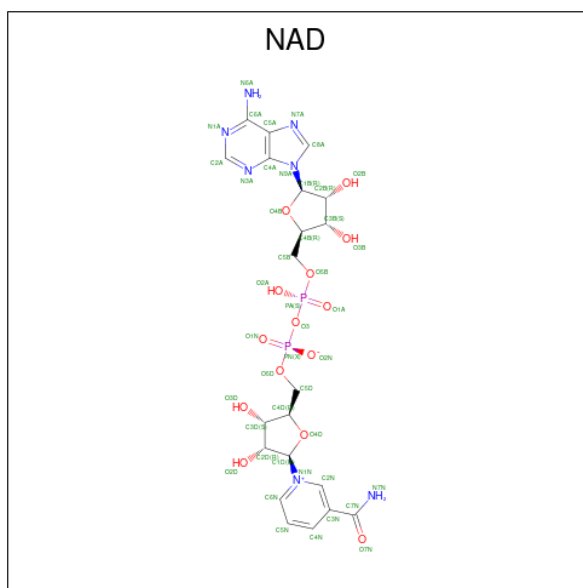
There are 4 unique types of molecules in this entry. The entry contains 10799 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Alr4995 protein.

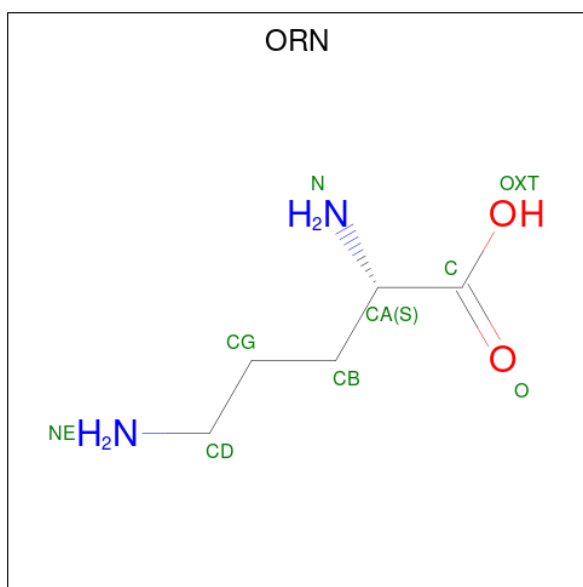
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	678	Total	C	N	O	S	0	0	0
			5286	3347	922	992	25			
1	B	681	Total	C	N	O	S	0	0	0
			5319	3363	933	998	25			

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 3 is L-ornithine (CCD ID: ORN) (formula: $C_5H_{12}N_2O_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			9	5	2	2		
3	B	1	Total	C	N	O	0	0
			9	5	2	2		

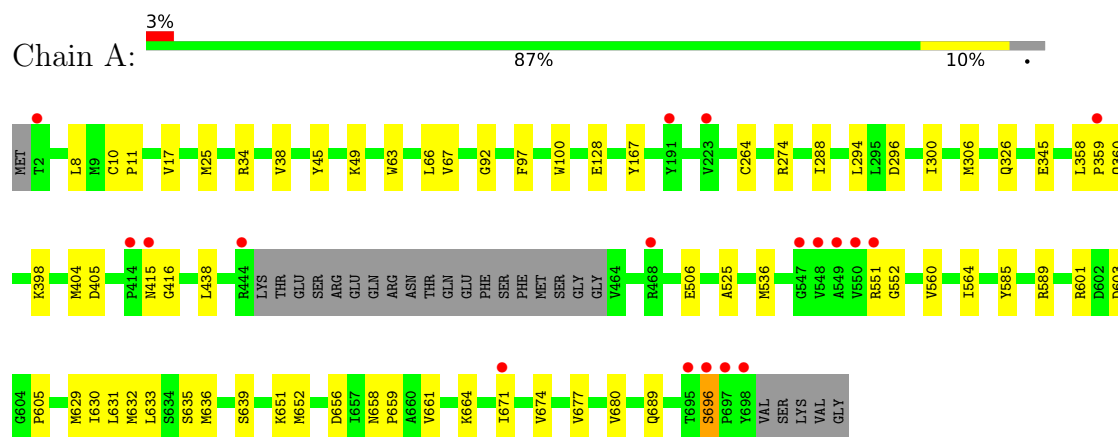
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	79	Total	O	0	0
			79	79		
4	B	53	Total	O	0	0
			53	53		

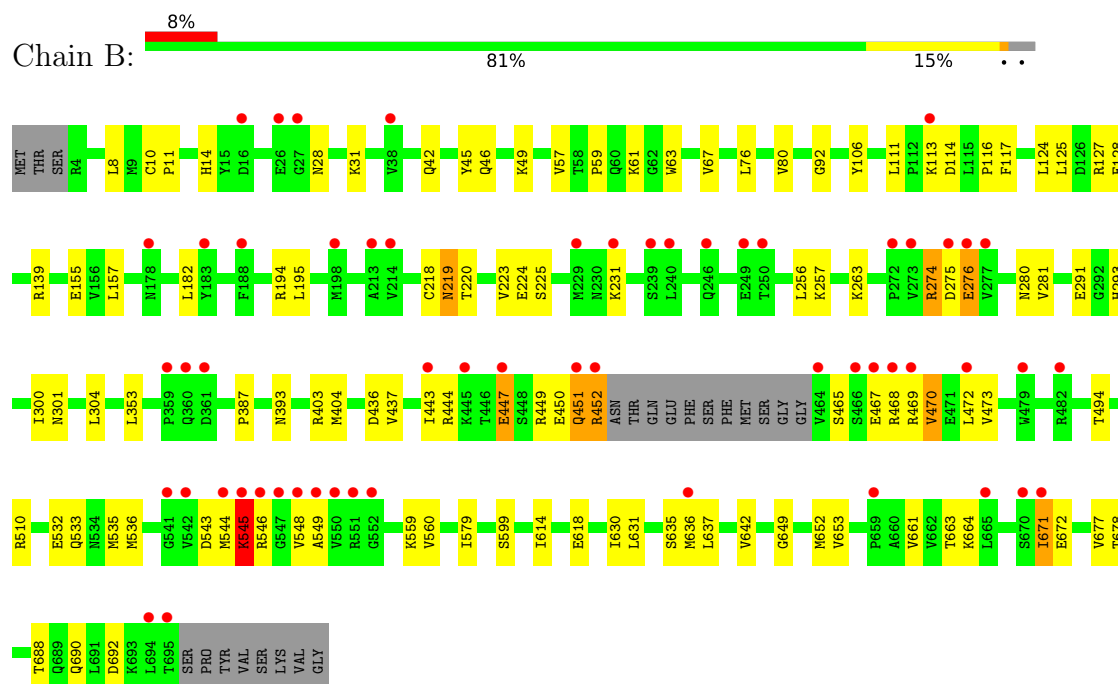
3 Residue-property plots [i](#)

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: Alr4995 protein



• Molecule 1: Alr4995 protein



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	186.90Å 201.14Å 99.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.73 – 2.41 46.73 – 2.41	Depositor EDS
% Data completeness (in resolution range)	98.6 (46.73-2.41) 98.6 (46.73-2.41)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.04 (at 2.42Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.191 , 0.251 0.197 , 0.256	Depositor DCC
R_{free} test set	2009 reflections (2.78%)	wwPDB-VP
Wilson B-factor (Å ²)	28.7	Xtriage
Anisotropy	0.452	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 30.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	10799	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.81% 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: ORN, NAD

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	0.59	0/5385	0.85	6/7302 (0.1%)
1	B	0.54	1/5416 (0.0%)	0.85	4/7339 (0.1%)
All	All	0.57	1/10801 (0.0%)	0.85	10/14641 (0.1%)

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	B	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	545	LYS	CA-C	5.02	1.58	1.52

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	416	GLY	N-CA-C	6.80	120.56	112.33
1	A	696	SER	CA-C-N	-6.74	112.73	120.89
1	A	696	SER	C-N-CA	-6.74	112.73	120.89
1	A	358	LEU	CA-C-N	5.79	127.08	119.84
1	A	358	LEU	C-N-CA	5.79	127.08	119.84
1	B	467	GLU	N-CA-C	-5.77	105.73	112.89
1	A	11	PRO	O-C-N	5.17	123.58	121.15
1	B	219	ASN	CB-CA-C	5.12	119.10	111.88
1	B	545	LYS	N-CA-C	-5.08	106.21	114.09
1	B	468	ARG	NE-CZ-NH1	-5.04	116.46	121.50

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	274	ARG	Peptide

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	5286	0	5302	33	0
1	B	5319	0	5340	59	0
2	A	44	0	26	5	0
3	A	9	0	11	2	0
3	B	9	0	11	0	0
4	A	79	0	0	0	0
4	B	53	0	0	1	0
All	All	10799	0	10690	92	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 4.

All (92) 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)
2:A:801:NAD:O4D	2:A:801:NAD:C1D	1.64	1.11
1:B:219:ASN:OD1	1:B:263:LYS:HB2	1.79	0.81
1:A:264:CYS:SG	3:A:802:ORN:NE	2.53	0.80
1:B:533:GLN:NE2	1:B:544:MET:SD	2.59	0.76
1:B:155:GLU:HG3	1:B:280:ASN:HB3	1.73	0.71
1:B:451:GLN:O	1:B:452:ARG:HB2	1.90	0.70
1:A:17:VAL:HG13	1:A:25:MET:HE2	1.74	0.68
1:B:494:THR:HG21	1:B:642:VAL:HG21	1.78	0.65
1:A:551:ARG:CG	1:A:552:GLY:H	2.09	0.65
1:A:630:ILE:HD12	1:A:652:MET:HE2	1.77	0.65
1:B:128:GLU:O	1:B:274:ARG:HD2	1.97	0.64
1:B:671:ILE:HD12	1:B:672:GLU:HG3	1.80	0.62
1:B:631:LEU:HD12	1:B:653:VAL:HB	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:469:ARG:HA	1:B:472:LEU:HD12	1.84	0.60
1:B:614:ILE:O	1:B:618:GLU:HG3	2.01	0.60
1:B:63:TRP:CH2	1:B:92:GLY:HA3	2.38	0.59
1:B:447:GLU:H	1:B:447:GLU:CD	2.10	0.58
1:B:194:ARG:HD2	1:B:536:MET:HA	1.84	0.58
1:B:113:LYS:HE3	1:B:113:LYS:HA	1.86	0.57
1:B:353:LEU:O	1:B:449:ARG:NH2	2.36	0.57
1:B:403:ARG:NH1	1:B:404:MET:O	2.36	0.57
1:B:544:MET:O	1:B:544:MET:HG2	2.05	0.56
1:B:635:SER:O	1:B:637:LEU:N	2.38	0.56
1:A:128:GLU:O	1:A:274:ARG:HD2	2.06	0.55
1:B:444:ARG:HH22	1:B:452:ARG:NH2	2.05	0.55
1:B:293:HIS:ND1	1:B:450:GLU:OE1	2.37	0.55
1:B:387:PRO:HB2	1:B:443:ILE:HG13	1.89	0.54
1:A:525:ALA:HB2	2:A:801:NAD:C2N	2.38	0.54
1:B:14:HIS:CD2	1:B:61:LYS:HG2	2.43	0.53
1:A:10:CYS:HB3	1:A:67:VAL:HA	1.90	0.53
1:A:585:TYR:OH	1:A:589:ARG:NH1	2.41	0.53
1:A:63:TRP:CH2	1:A:92:GLY:HA3	2.44	0.53
1:A:294:LEU:HD13	1:A:300:ILE:HD13	1.91	0.53
1:A:551:ARG:HG3	1:A:552:GLY:H	1.74	0.52
1:B:469:ARG:O	1:B:472:LEU:HB2	2.08	0.52
1:A:525:ALA:HB2	2:A:801:NAD:C3N	2.39	0.52
1:A:551:ARG:CG	1:A:552:GLY:N	2.73	0.52
1:B:28:ASN:HA	1:B:31:LYS:HD3	1.92	0.52
1:B:630:ILE:HD12	1:B:652:MET:HE3	1.92	0.52
1:B:157:LEU:HB3	1:B:195:LEU:HD21	1.90	0.51
1:B:300:ILE:O	1:B:304:LEU:HG	2.11	0.51
1:A:326:GLN:NE2	1:B:114:ASP:O	2.44	0.50
1:B:291:GLU:O	1:B:449:ARG:NH1	2.45	0.50
1:B:649:GLY:N	1:B:672:GLU:OE2	2.33	0.50
1:A:629:MET:HE3	1:A:651:LYS:HG2	1.94	0.49
1:A:66:LEU:HD12	1:A:97:PHE:CZ	2.47	0.49
1:B:510:ARG:NH2	1:B:692:ASP:OD1	2.45	0.49
1:B:28:ASN:HD22	1:B:257:LYS:HB3	1.77	0.49
1:B:10:CYS:HB3	1:B:67:VAL:HA	1.95	0.48
1:A:636:MET:HG3	1:A:661:VAL:HG13	1.96	0.48
1:A:34:ARG:O	1:A:38:VAL:HG23	2.13	0.47
1:B:465:SER:HB2	1:B:677:VAL:O	2.15	0.47
1:B:470:VAL:HG21	1:B:678:THR:HG21	1.97	0.47
1:B:545:LYS:O	1:B:545:LYS:HG3	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:8:LEU:HD11	1:B:57:VAL:HG23	1.98	0.46
1:A:536:MET:HE3	1:A:536:MET:HB2	1.63	0.46
1:A:603:ASP:O	1:A:605:PRO:HA	2.17	0.45
1:B:469:ARG:NH2	1:B:473:VAL:HG23	2.31	0.45
1:B:219:ASN:OD1	1:B:263:LYS:CB	2.57	0.45
1:B:548:VAL:HG12	1:B:549:ALA:H	1.82	0.45
1:A:656:ASP:O	1:A:677:VAL:HA	2.17	0.45
1:B:45:TYR:CZ	1:B:49:LYS:HD2	2.51	0.45
1:A:167:TYR:OH	3:A:802:ORN:HB2	2.16	0.44
1:B:42:GLN:O	1:B:46:GLN:HG2	2.17	0.44
1:B:124:LEU:HD23	1:B:124:LEU:HA	1.60	0.44
1:A:45:TYR:CZ	1:A:49:LYS:HD2	2.52	0.44
1:B:274:ARG:NH1	1:B:276:GLU:OE2	2.49	0.44
1:B:536:MET:HE1	1:B:559:LYS:HD3	2.00	0.44
1:B:76:LEU:HD13	1:B:125:LEU:HD21	1.99	0.43
1:B:182:LEU:HD23	1:B:218:CYS:HA	2.00	0.43
1:A:632:MET:HB3	1:A:639:SER:OG	2.18	0.43
1:B:532:GLU:HA	1:B:560:VAL:HG21	2.01	0.43
1:A:404:MET:HE3	1:A:405:ASP:OD2	2.18	0.42
1:A:633:LEU:HB3	1:A:680:VAL:HG21	2.01	0.42
1:B:224:GLU:HB2	1:B:225:SER:H	1.65	0.42
1:B:436:ASP:OD2	1:B:437:VAL:N	2.44	0.42
1:A:601:ARG:CZ	2:A:801:NAD:C5N	2.98	0.42
1:B:80:VAL:HG12	1:B:106:TYR:HB3	2.02	0.42
1:B:116:PRO:HB2	1:B:139:ARG:O	2.20	0.42
1:B:111:LEU:HD13	1:B:117:PHE:HB3	2.00	0.42
1:A:635:SER:HA	2:A:801:NAD:H52A	2.02	0.41
1:A:360:GLN:H	1:A:360:GLN:CD	2.27	0.41
1:B:127:ARG:HD3	4:B:936:HOH:O	2.19	0.41
1:B:11:PRO:HG2	1:B:59:PRO:HG3	2.02	0.41
1:A:8:LEU:HD13	1:A:100:TRP:CZ2	2.56	0.41
1:A:658:ASN:HA	1:A:659:PRO:HD3	1.93	0.41
1:B:469:ARG:HH22	1:B:473:VAL:HG23	1.85	0.41
1:A:551:ARG:HG2	1:A:552:GLY:N	2.36	0.41
1:B:452:ARG:HD3	1:B:452:ARG:HA	1.77	0.41
1:B:543:ASP:OD2	1:B:546:ARG:HG3	2.20	0.41
1:B:535:MET:CE	1:B:579:ILE:HG12	2.52	0.40
1:A:560:VAL:O	1:A:564:ILE:HG12	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	674/703 (96%)	651 (97%)	20 (3%)	3 (0%)	30	42
1	B	677/703 (96%)	641 (95%)	33 (5%)	3 (0%)	30	42
All	All	1351/1406 (96%)	1292 (96%)	53 (4%)	6 (0%)	30	42

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	636	MET
1	B	275	ASP
1	A	359	PRO
1	A	415	ASN
1	B	393	ASN
1	A	696	SER

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	573/595 (96%)	561 (98%)	12 (2%)	47	67
1	B	576/595 (97%)	557 (97%)	19 (3%)	33	53
All	All	1149/1190 (97%)	1118 (97%)	31 (3%)	39	60

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

Mol	Chain	Res	Type
1	A	288	ILE
1	A	296	ASP
1	A	306	MET
1	A	345	GLU
1	A	398	LYS
1	A	438	LEU
1	A	506	GLU
1	A	631	LEU
1	A	664	LYS
1	A	671	ILE
1	A	674	VAL
1	A	689	GLN
1	B	220	THR
1	B	223	VAL
1	B	231	LYS
1	B	256	LEU
1	B	276	GLU
1	B	281	VAL
1	B	301	ASN
1	B	447	GLU
1	B	451	GLN
1	B	452	ARG
1	B	470	VAL
1	B	545	LYS
1	B	599	SER
1	B	661	VAL
1	B	663	THR
1	B	664	LYS
1	B	671	ILE
1	B	688	THR
1	B	690	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	87	HIS
1	A	238	GLN
1	A	301	ASN
1	A	476	GLN
1	B	51	HIS
1	B	193	ASN
1	B	222	ASN
1	B	230	ASN

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Mol	Chain	Res	Type
1	B	412	GLN
1	B	432	GLN
1	B	557	HIS
1	B	590	ASN
1	B	623	HIS

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](#)

3 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	NAD	A	801	-	46,48,48	4.21	19 (41%)	64,73,73	2.29	20 (31%)
3	ORN	B	801	-	7,8,8	0.91	0	6,9,9	0.91	0
3	ORN	A	802	-	7,8,8	0.94	0	6,9,9	1.15	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	NAD	A	801	-	-	9/30/62/62	0/5/5/5
3	ORN	B	801	-	-	2/8/8/8	-
3	ORN	A	802	-	-	1/8/8/8	-

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	NAD	O4D-C1D	17.71	1.64	1.40
2	A	801	NAD	C3B-C4B	-10.58	1.26	1.53
2	A	801	NAD	C2B-C1B	-8.12	1.28	1.53
2	A	801	NAD	C7N-N7N	6.21	1.44	1.33
2	A	801	NAD	C2N-N1N	6.20	1.41	1.35
2	A	801	NAD	O4D-C4D	-5.66	1.32	1.45
2	A	801	NAD	O4B-C1B	5.37	1.54	1.42
2	A	801	NAD	O4B-C4B	5.26	1.56	1.45
2	A	801	NAD	C2B-C3B	5.15	1.67	1.53
2	A	801	NAD	PA-O3	4.93	1.64	1.59
2	A	801	NAD	C3N-C7N	4.24	1.56	1.50
2	A	801	NAD	C2A-N3A	3.45	1.40	1.33
2	A	801	NAD	C6A-N6A	3.44	1.43	1.34
2	A	801	NAD	O2D-C2D	3.06	1.50	1.43
2	A	801	NAD	C8A-N7A	2.74	1.36	1.31
2	A	801	NAD	C2N-C3N	2.58	1.43	1.39
2	A	801	NAD	PN-O3	2.39	1.62	1.59
2	A	801	NAD	C4A-N3A	2.30	1.38	1.34
2	A	801	NAD	C2A-N1A	2.17	1.37	1.33

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	NAD	N6A-C6A-N1A	-6.12	104.74	118.38
2	A	801	NAD	C4A-N9A-C1B	-6.01	112.57	126.63
2	A	801	NAD	N3A-C2A-N1A	-5.57	120.16	128.58
2	A	801	NAD	C1B-N9A-C8A	5.42	139.12	127.09
2	A	801	NAD	C5A-C4A-N3A	-5.12	119.66	126.72
2	A	801	NAD	C5A-C6A-N6A	4.75	135.05	123.29
2	A	801	NAD	N9A-C8A-N7A	-4.09	108.14	113.94
2	A	801	NAD	N3A-C4A-N9A	3.51	133.14	127.17
2	A	801	NAD	C4D-O4D-C1D	-3.39	106.82	109.92
2	A	801	NAD	C2A-N3A-C4A	3.30	119.89	111.83
2	A	801	NAD	C5A-N7A-C8A	2.88	107.97	103.45
2	A	801	NAD	C2B-C3B-C4B	2.78	107.97	102.61
2	A	801	NAD	C4B-O4B-C1B	-2.70	103.50	109.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	NAD	O2N-PN-O3	2.64	114.40	107.27
2	A	801	NAD	O7N-C7N-C3N	2.48	122.63	119.60
2	A	801	NAD	C3B-C2B-C1B	2.45	106.10	101.46
2	A	801	NAD	C4A-N9A-C8A	2.42	108.28	105.74
2	A	801	NAD	O7N-C7N-N7N	-2.34	119.23	122.62
2	A	801	NAD	C5D-C4D-C3D	-2.09	107.68	115.21
2	A	801	NAD	C6A-C5A-C4A	2.05	119.98	117.18

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	801	NAD	O4B-C4B-C5B-O5B
2	A	801	NAD	C5D-O5D-PN-O2N
2	A	801	NAD	C3B-C4B-C5B-O5B
2	A	801	NAD	O4D-C4D-C5D-O5D
2	A	801	NAD	C3D-C4D-C5D-O5D
2	A	801	NAD	C2B-C1B-N9A-C8A
2	A	801	NAD	C2B-C1B-N9A-C4A
3	A	802	ORN	NE-CD-CG-CB
2	A	801	NAD	O4B-C1B-N9A-C8A
3	B	801	ORN	O-C-CA-N
2	A	801	NAD	PA-O3-PN-O2N
3	B	801	ORN	OXT-C-CA-N

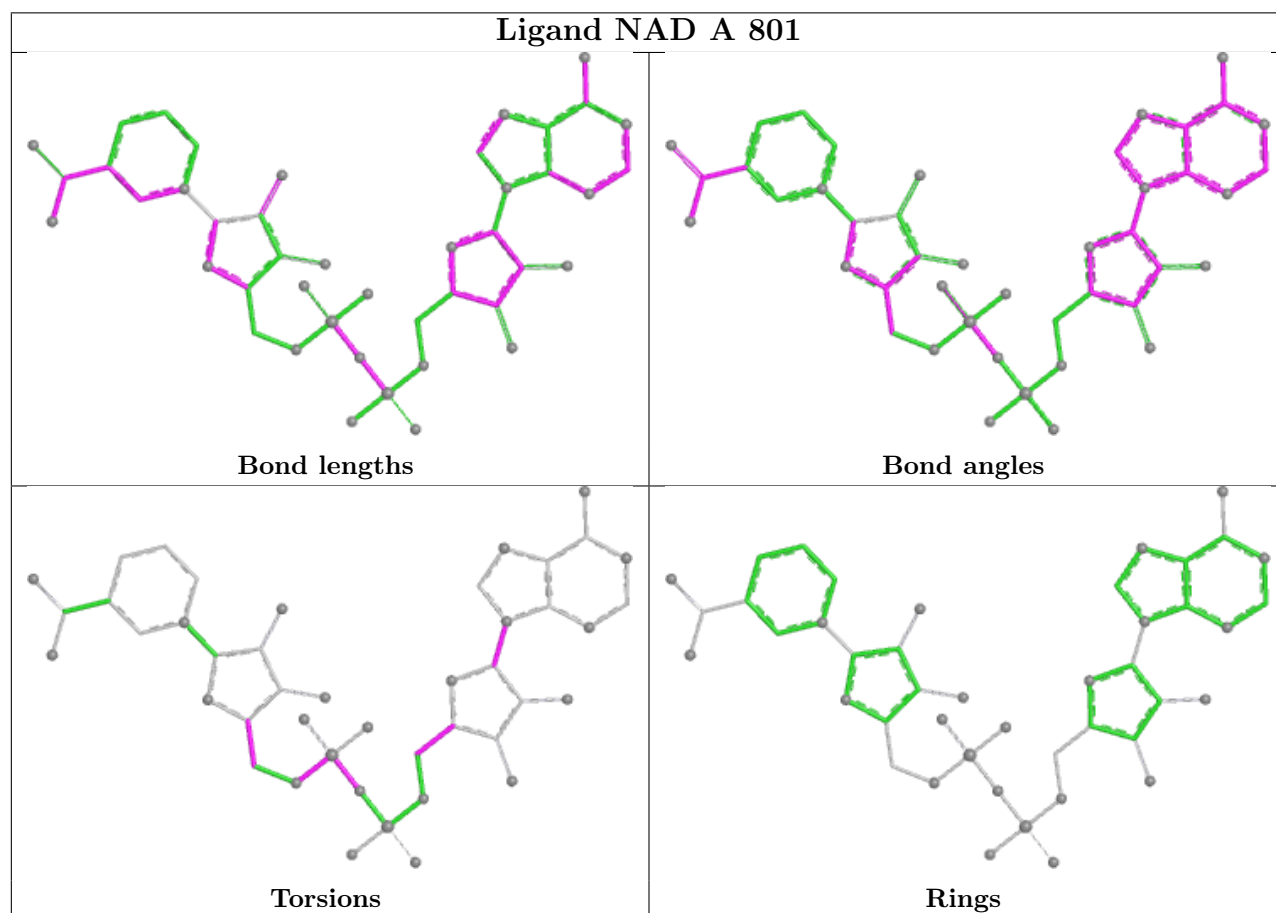
There are no ring outliers.

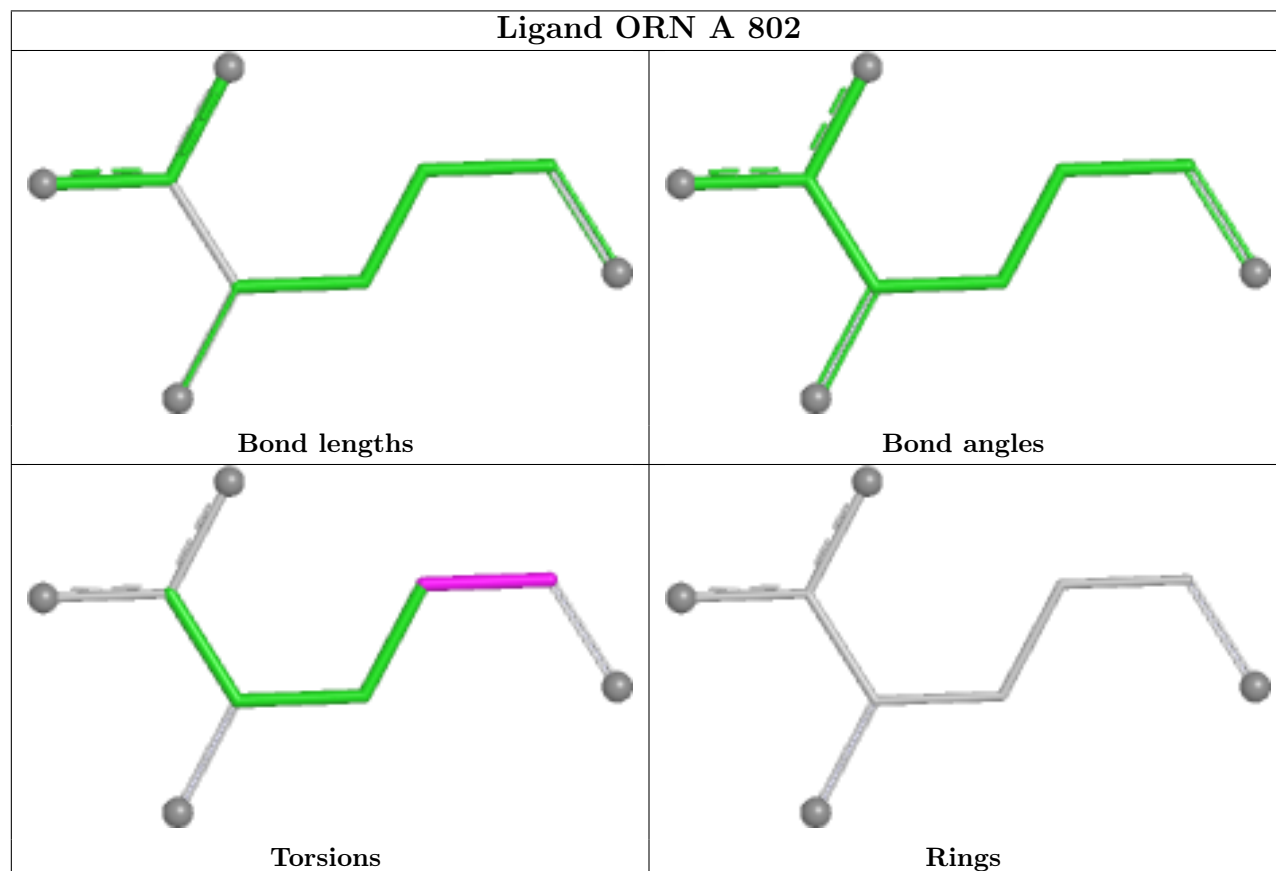
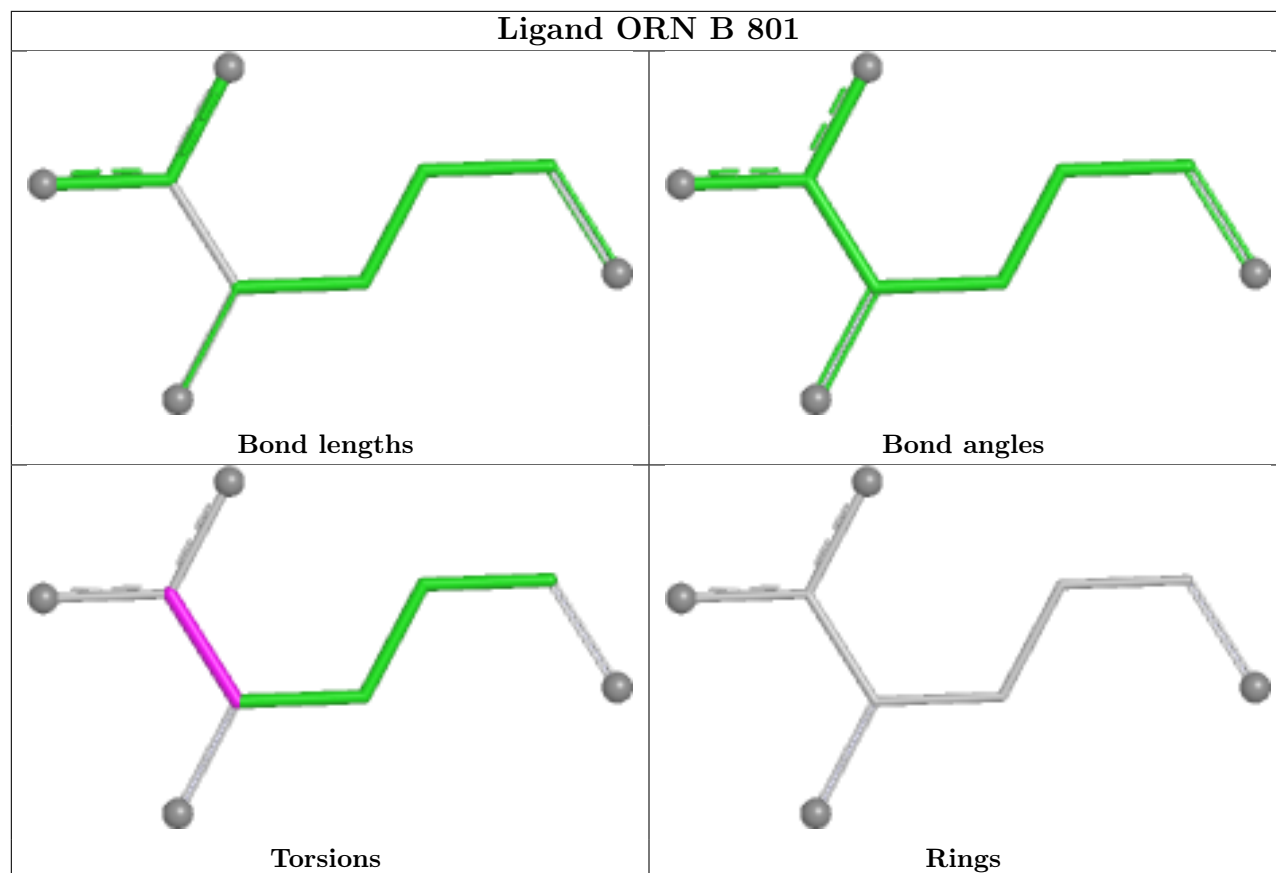
2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	NAD	5	0
3	A	802	ORN	2	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	678/703 (96%)	-0.17	18 (2%) 56 52	14, 24, 47, 75	0
1	B	681/703 (96%)	0.47	57 (8%) 17 13	20, 37, 63, 82	0
All	All	1359/1406 (96%)	0.15	75 (5%) 30 27	14, 29, 60, 82	0

All (75) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	550	VAL	6.4
1	A	2	THR	5.6
1	B	548	VAL	5.5
1	A	548	VAL	5.3
1	A	698	TYR	4.6
1	B	464	VAL	4.3
1	B	544	MET	4.3
1	B	272	PRO	4.2
1	A	551	ARG	4.2
1	B	695	THR	4.1
1	A	671	ILE	3.8
1	B	552	GLY	3.6
1	B	545	LYS	3.6
1	B	551	ARG	3.6
1	B	198	MET	3.5
1	B	452	ARG	3.4
1	B	479	TRP	3.4
1	A	414	PRO	3.3
1	B	467	GLU	3.3
1	B	273	VAL	3.2
1	B	671	ILE	3.2
1	B	275	ASP	3.2
1	A	697	PRO	3.1
1	B	276	GLU	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	550	VAL	3.1
1	A	444	ARG	3.0
1	B	468	ARG	3.0
1	A	696	SER	3.0
1	B	547	GLY	2.9
1	B	541	GLY	2.9
1	B	445	LYS	2.8
1	B	542	VAL	2.8
1	B	546	ARG	2.8
1	B	277	VAL	2.7
1	B	246	GLN	2.7
1	A	223	VAL	2.6
1	A	549	ALA	2.6
1	B	359	PRO	2.6
1	B	361	ASP	2.5
1	B	214	VAL	2.5
1	B	231	LYS	2.5
1	A	695	THR	2.5
1	B	250	THR	2.5
1	B	549	ALA	2.5
1	B	472	LEU	2.4
1	B	451	GLN	2.4
1	B	466	SER	2.3
1	A	547	GLY	2.3
1	B	229	MET	2.3
1	B	636	MET	2.3
1	B	188	PHE	2.3
1	A	468	ARG	2.3
1	B	447	GLU	2.3
1	B	239	SER	2.3
1	B	38	VAL	2.3
1	B	178	ASN	2.2
1	B	183	TYR	2.2
1	B	16	ASP	2.2
1	B	26	GLU	2.2
1	B	469	ARG	2.2
1	A	191	TYR	2.2
1	B	665	LEU	2.2
1	B	482	ARG	2.2
1	B	240	LEU	2.1
1	B	27	GLY	2.1
1	B	694	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	249	GLU	2.1
1	B	360	GLN	2.1
1	B	213	ALA	2.0
1	A	415	ASN	2.0
1	B	443	ILE	2.0
1	B	659	PRO	2.0
1	B	670	SER	2.0
1	B	113	LYS	2.0
1	A	359	PRO	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](#)

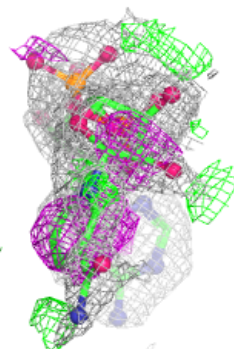
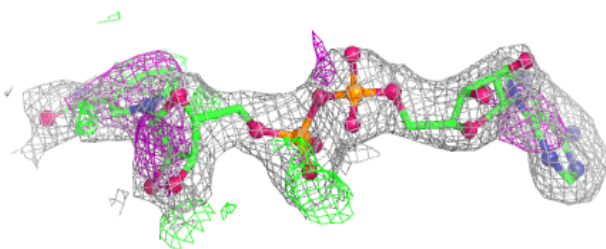
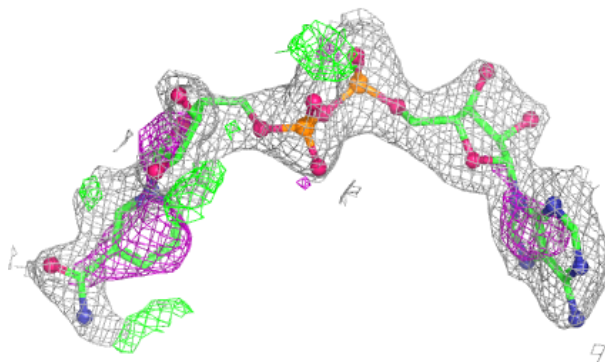
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
2	NAD	A	801	44/44	0.78	0.15	32,46,56,61	0
3	ORN	A	802	9/9	0.90	0.14	20,22,28,31	0
3	ORN	B	801	9/9	0.94	0.11	29,34,40,41	0

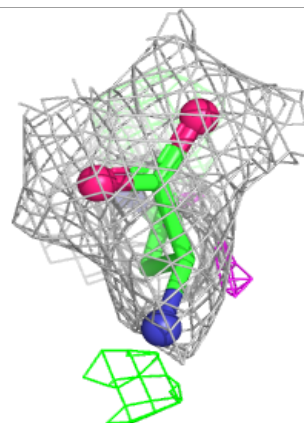
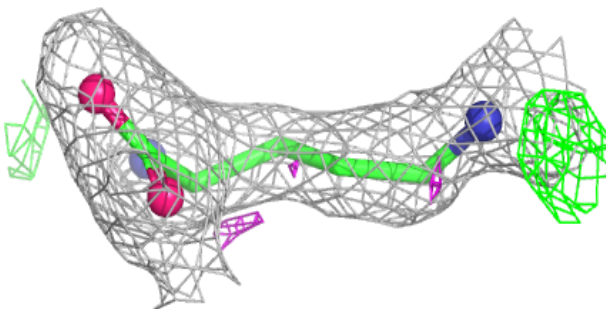
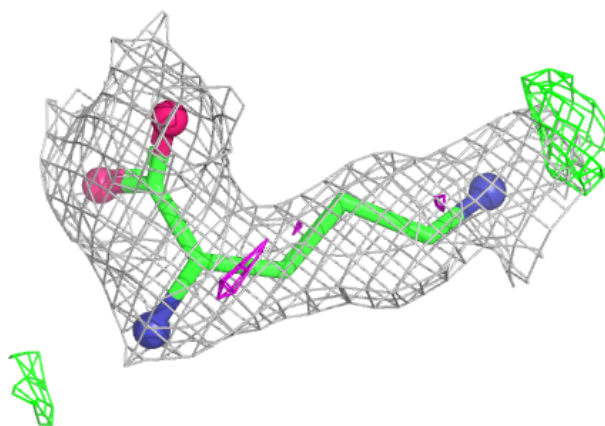
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around NAD A 801:

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

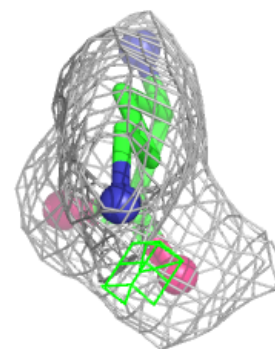
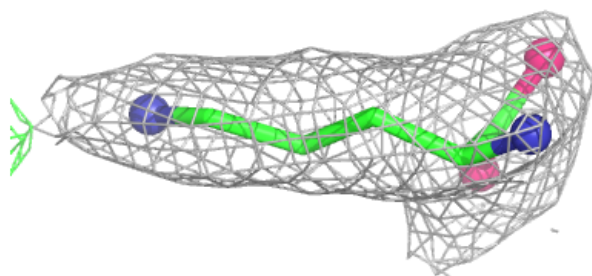
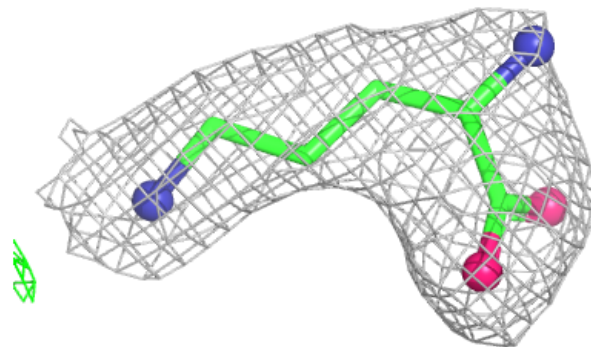
**Electron density around ORN A 802:**

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



Electron density around ORN B 801:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.