



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2024 – 12:09 AM EST

PDB ID : 1X15
Title : Crystal structure of E. coli transhydrogenase domain I with bound NADH
Authors : Johansson, T.; Oswald, C.; Pedersen, A.; Tornroth, S.; Okvist, M.; Karlsson, B.G.; Rydstrom, J.; Krengel, U.
Deposited on : 2005-03-31
Resolution : 2.04 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

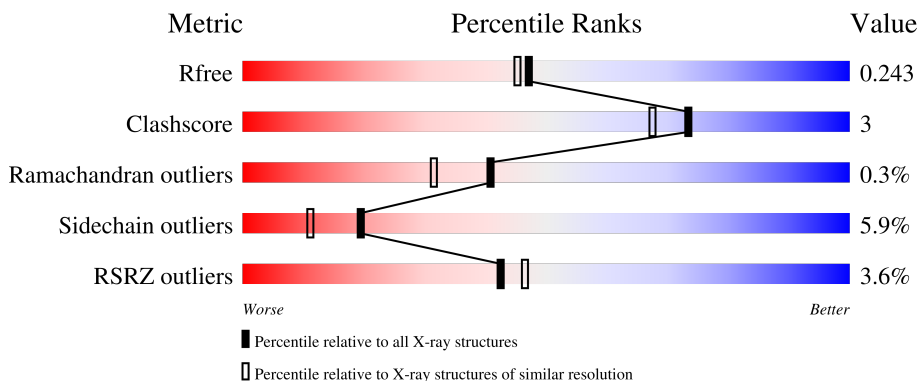
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.04 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	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

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	401	 3% 80% 12% • 8%
1	B	401	 3% 77% 11% • 10%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5730 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 NAD(P) transhydrogenase subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	370	2764	1754	467	531	12	0	0	0
1	B	360	2693	1707	458	517	11	0	0	0

There are 16 discrepancies between the modelled and reference sequences:

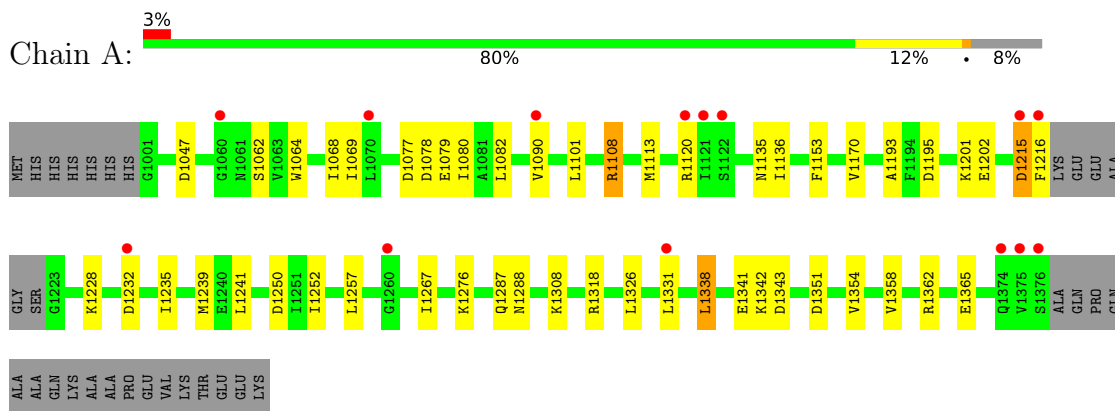
Chain	Residue	Modelled	Actual	Comment	Reference
A	994	MET	-	expression tag	UNP P07001
A	995	HIS	-	expression tag	UNP P07001
A	996	HIS	-	expression tag	UNP P07001
A	997	HIS	-	expression tag	UNP P07001
A	998	HIS	-	expression tag	UNP P07001
A	999	HIS	-	expression tag	UNP P07001
A	1000	HIS	-	expression tag	UNP P07001
A	1001	GLY	-	expression tag	UNP P07001
B	994	MET	-	expression tag	UNP P07001
B	995	HIS	-	expression tag	UNP P07001
B	996	HIS	-	expression tag	UNP P07001
B	997	HIS	-	expression tag	UNP P07001
B	998	HIS	-	expression tag	UNP P07001
B	999	HIS	-	expression tag	UNP P07001
B	1000	HIS	-	expression tag	UNP P07001
B	1001	GLY	-	expression tag	UNP P07001

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: C₂₁H₂₇N₇O₁₄P₂).

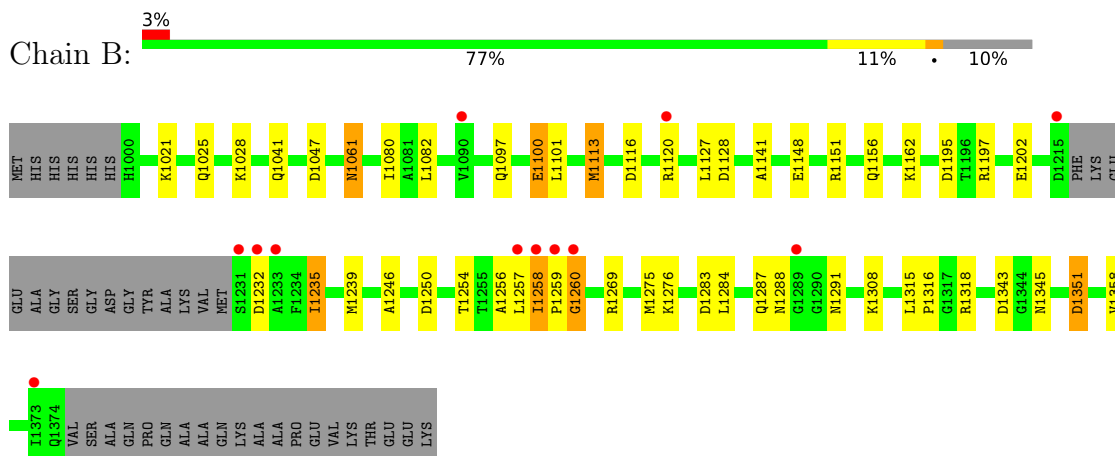
3 Residue-property plots [i](#)

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: NAD(P) transhydrogenase subunit alpha



- Molecule 1: NAD(P) transhydrogenase subunit alpha



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	38.73Å 67.09Å 76.84Å 67.22° 80.19° 81.60°	Depositor
Resolution (Å)	30.00 – 2.04 29.15 – 2.04	Depositor EDS
% Data completeness (in resolution range)	96.5 (30.00-2.04) 96.4 (29.15-2.04)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.06 (at 2.04Å)	Xtrriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.186 , 0.241 0.195 , 0.243	Depositor DCC
R_{free} test set	2215 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	27.5	Xtrriage
Anisotropy	0.408	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 42.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5730	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.53% 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:
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	0.80	0/2807	0.90	11/3812 (0.3%)
1	B	0.83	1/2735 (0.0%)	0.88	10/3716 (0.3%)
All	All	0.81	1/5542 (0.0%)	0.89	21/7528 (0.3%)

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	1113	MET	CG-SD	-7.03	1.62	1.81

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1318	ARG	NE-CZ-NH2	-9.23	115.69	120.30
1	A	1047	ASP	CB-CG-OD2	7.81	125.33	118.30
1	A	1250	ASP	CB-CG-OD2	7.09	124.69	118.30
1	A	1078	ASP	CB-CG-OD2	7.04	124.64	118.30
1	A	1195	ASP	CB-CG-OD2	6.84	124.45	118.30
1	B	1343	ASP	CB-CG-OD2	6.69	124.32	118.30
1	A	1343	ASP	CB-CG-OD2	6.62	124.26	118.30
1	A	1318	ARG	NE-CZ-NH1	6.22	123.41	120.30
1	A	1215	ASP	CB-CG-OD2	6.21	123.89	118.30
1	B	1047	ASP	CB-CG-OD2	6.19	123.88	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1351	ASP	CB-CG-OD2	6.16	123.85	118.30
1	A	1232	ASP	CB-CG-OD2	5.84	123.56	118.30
1	B	1116	ASP	CB-CG-OD2	5.76	123.49	118.30
1	B	1195	ASP	CB-CG-OD2	5.76	123.48	118.30
1	B	1269	ARG	NE-CZ-NH1	5.57	123.09	120.30
1	B	1197	ARG	NE-CZ-NH1	5.56	123.08	120.30
1	B	1128	ASP	CB-CG-OD2	5.45	123.21	118.30
1	A	1077	ASP	CB-CG-OD2	5.33	123.10	118.30
1	B	1351	ASP	CB-CG-OD2	5.16	122.94	118.30
1	B	1250	ASP	CB-CG-OD2	5.15	122.93	118.30
1	B	1127	LEU	CB-CA-C	-5.08	100.54	110.20

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	1260	GLY	Peptide

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	2764	0	2817	15	0
1	B	2693	0	2746	23	0
2	B	44	0	26	0	0
3	A	104	0	0	3	0
3	B	125	0	0	5	0
All	All	5730	0	5589	37	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 3.

All (37) 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:1151:ARG:NH2	3:B:149:HOH:O	1.90	1.03

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1151:ARG:CZ	3:B:149:HOH:O	2.10	0.98
1:B:1258:ILE:CG2	1:B:1258:ILE:O	2.39	0.71
1:B:1254:THR:HG22	1:B:1283:ASP:HA	1.79	0.65
1:B:1025:GLN:OE1	3:B:306:HOH:O	2.15	0.63
1:B:1258:ILE:O	1:B:1258:ILE:HG23	2.02	0.59
1:A:1276:LYS:NZ	3:A:129:HOH:O	2.35	0.57
1:B:1246:ALA:O	1:B:1275:MET:HG2	2.05	0.57
1:B:1100:GLU:CD	1:B:1100:GLU:H	2.08	0.55
1:B:1061:ASN:HB3	1:B:1082:LEU:HD13	1.89	0.54
1:B:1113:MET:HG2	1:B:1358:VAL:HG13	1.90	0.52
1:B:1061:ASN:ND2	3:B:37:HOH:O	2.43	0.52
1:A:1135:ASN:OD1	1:B:1156:GLN:NE2	2.44	0.51
1:B:1080:ILE:HD11	1:B:1101:LEU:HD12	1.94	0.49
1:B:1141:ALA:HB2	1:B:1284:LEU:HD11	1.94	0.48
1:B:1148:GLU:OE1	1:B:1308:LYS:NZ	2.44	0.48
1:B:1258:ILE:O	1:B:1259:PRO:C	2.52	0.48
1:A:1113:MET:HB3	1:A:1358:VAL:CG1	2.43	0.48
1:A:1064:TRP:HA	1:A:1069:ILE:HD11	1.95	0.47
1:A:1326:LEU:HD13	3:A:203:HOH:O	2.15	0.47
1:A:1079:GLU:HA	1:A:1082:LEU:HD12	1.97	0.47
1:A:1170:VAL:O	1:A:1193:ALA:HA	2.15	0.47
1:A:1287:GLN:NE2	3:A:107:HOH:O	2.48	0.46
1:B:1256:ALA:H	1:B:1291:ASN:HD21	1.64	0.45
1:A:1090:VAL:HG11	1:A:1331:LEU:HD22	1.98	0.44
1:B:1315:LEU:N	1:B:1316:PRO:CD	2.80	0.43
1:B:1254:THR:HG23	1:B:1291:ASN:HD22	1.83	0.43
1:A:1252:ILE:HG21	1:A:1267:ILE:HD11	2.01	0.43
1:A:1257:LEU:CD1	1:A:1288:ASN:HB2	2.49	0.43
1:A:1113:MET:SD	1:A:1338:LEU:HD21	2.59	0.43
1:A:1235:ILE:O	1:A:1239:MET:HG2	2.19	0.42
1:A:1080:ILE:O	1:A:1108:ARG:HD2	2.19	0.42
1:B:1235:ILE:O	1:B:1239:MET:HG2	2.21	0.41
1:A:1136:ILE:HD11	1:A:1326:LEU:HD12	2.02	0.41
1:B:1257:LEU:HD11	1:B:1288:ASN:OD1	2.21	0.41
1:B:1258:ILE:O	1:B:1258:ILE:HG22	2.19	0.41
1:B:1318:ARG:NH1	3:B:292:HOH:O	2.34	0.41

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	366/401 (91%)	357 (98%)	8 (2%)	1 (0%)	41	31
1	B	356/401 (89%)	346 (97%)	9 (2%)	1 (0%)	41	31
All	All	722/802 (90%)	703 (97%)	17 (2%)	2 (0%)	41	31

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1215	ASP
1	B	1260	GLY

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	293/317 (92%)	275 (94%)	18 (6%)	18	10
1	B	286/317 (90%)	270 (94%)	16 (6%)	21	12
All	All	579/634 (91%)	545 (94%)	34 (6%)	19	11

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1062	SER
1	A	1068	ILE
1	A	1101	LEU
1	A	1108	ARG

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Mol	Chain	Res	Type
1	A	1120	ARG
1	A	1153	PHE
1	A	1201	LYS
1	A	1202	GLU
1	A	1216	PHE
1	A	1228	LYS
1	A	1241	LEU
1	A	1308	LYS
1	A	1338	LEU
1	A	1341	GLU
1	A	1342	LYS
1	A	1354	VAL
1	A	1362	ARG
1	A	1365	GLU
1	B	1021	LYS
1	B	1028	LYS
1	B	1041	GLN
1	B	1061	ASN
1	B	1097	GLN
1	B	1100	GLU
1	B	1120	ARG
1	B	1162	LYS
1	B	1202	GLU
1	B	1232	ASP
1	B	1235	ILE
1	B	1258	ILE
1	B	1276	LYS
1	B	1287	GLN
1	B	1345	ASN
1	B	1351	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1135	ASN
1	A	1330	ASN
1	B	1012	ASN
1	B	1061	ASN
1	B	1156	GLN
1	B	1288	ASN
1	B	1291	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	B	1395	-	42,48,48	1.47	3 (7%)	50,73,73	1.64	10 (20%)

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	B	1395	-	-	6/26/62/62	0/5/5/5

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1395	NAD	C4A-N3A	6.23	1.44	1.35
2	B	1395	NAD	O4D-C1D	3.69	1.46	1.41
2	B	1395	NAD	PA-O1A	2.33	1.59	1.50

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1395	NAD	C4A-C5A-N7A	-4.35	104.86	109.40
2	B	1395	NAD	N3A-C2A-N1A	-4.35	121.88	128.68
2	B	1395	NAD	C1B-N9A-C4A	-3.08	121.22	126.64
2	B	1395	NAD	C2B-C3B-C4B	3.01	108.48	102.64
2	B	1395	NAD	C2A-N1A-C6A	2.93	123.76	118.75
2	B	1395	NAD	C3D-C2D-C1D	2.92	105.37	100.98
2	B	1395	NAD	O4B-C1B-C2B	2.81	111.03	106.93
2	B	1395	NAD	C2D-C3D-C4D	2.41	107.33	102.64
2	B	1395	NAD	C2N-N1N-C1D	-2.29	114.04	119.14
2	B	1395	NAD	C3N-C7N-N7N	2.11	120.29	117.75

There are no chirality outliers.

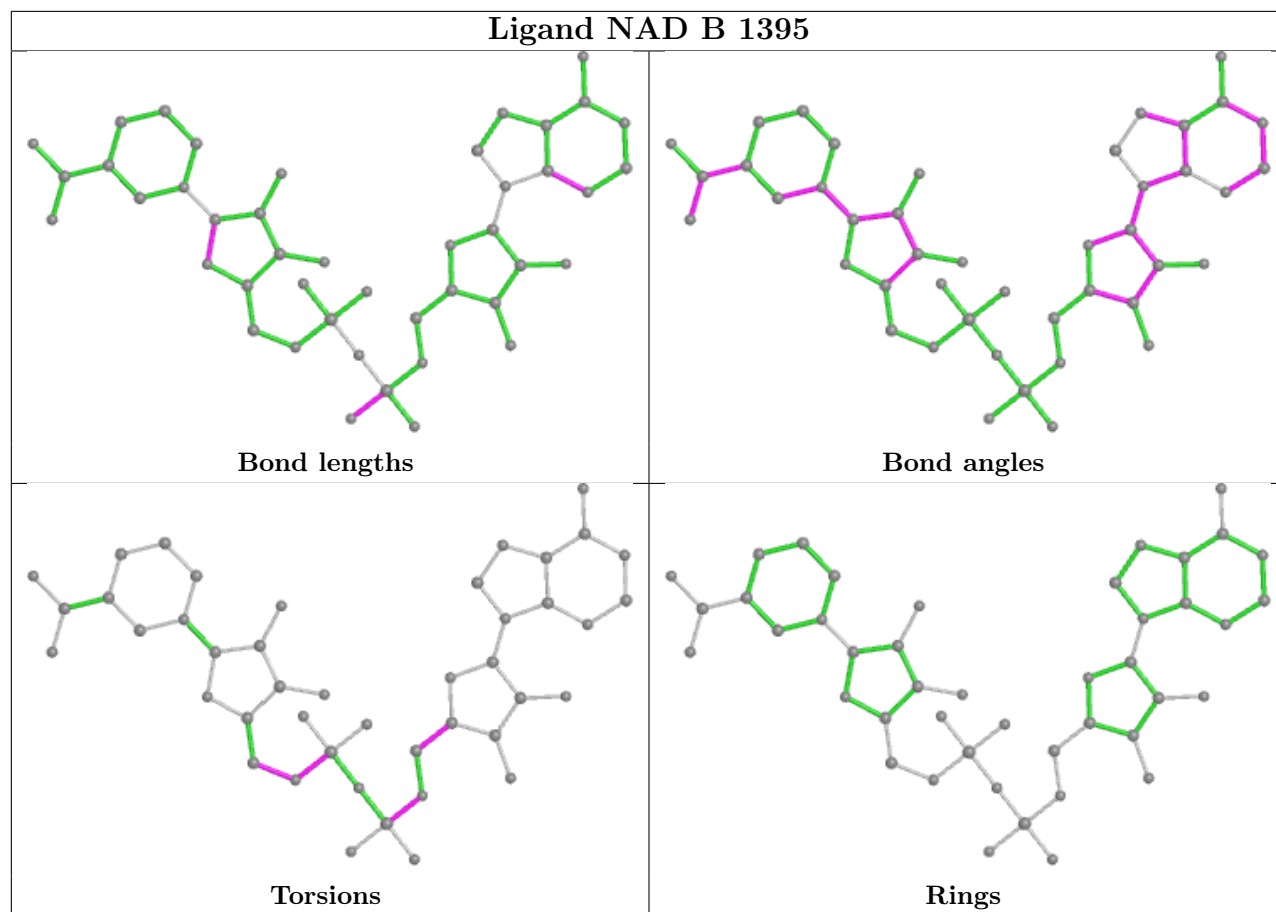
All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1395	NAD	C5D-O5D-PN-O3
2	B	1395	NAD	C5D-O5D-PN-O1N
2	B	1395	NAD	O4B-C4B-C5B-O5B
2	B	1395	NAD	C5D-O5D-PN-O2N
2	B	1395	NAD	C4D-C5D-O5D-PN
2	B	1395	NAD	C5B-O5B-PA-O1A

There are no ring outliers.

No monomer is involved in short contacts.

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	370/401 (92%)	0.12	14 (3%) 40 44	22, 37, 54, 70	0
1	B	360/401 (89%)	-0.03	12 (3%) 46 50	20, 33, 54, 72	0
All	All	730/802 (91%)	0.04	26 (3%) 42 46	20, 35, 54, 72	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1376	SER	5.1
1	B	1260	GLY	4.8
1	A	1216	PHE	4.5
1	A	1215	ASP	4.5
1	B	1258	ILE	4.4
1	B	1215	ASP	4.3
1	B	1259	PRO	3.9
1	A	1375	VAL	3.8
1	A	1374	GLN	3.2
1	A	1232	ASP	3.1
1	A	1122	SER	3.1
1	A	1060	GLY	2.8
1	B	1232	ASP	2.8
1	B	1231	SER	2.8
1	B	1257	LEU	2.7
1	A	1090	VAL	2.6
1	A	1120	ARG	2.6
1	B	1233	ALA	2.4
1	A	1070	LEU	2.4
1	B	1289	GLY	2.4
1	A	1121	ILE	2.4
1	B	1373	ILE	2.3
1	B	1090	VAL	2.2
1	A	1331	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	1260	GLY	2.1
1	B	1120	ARG	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](#)

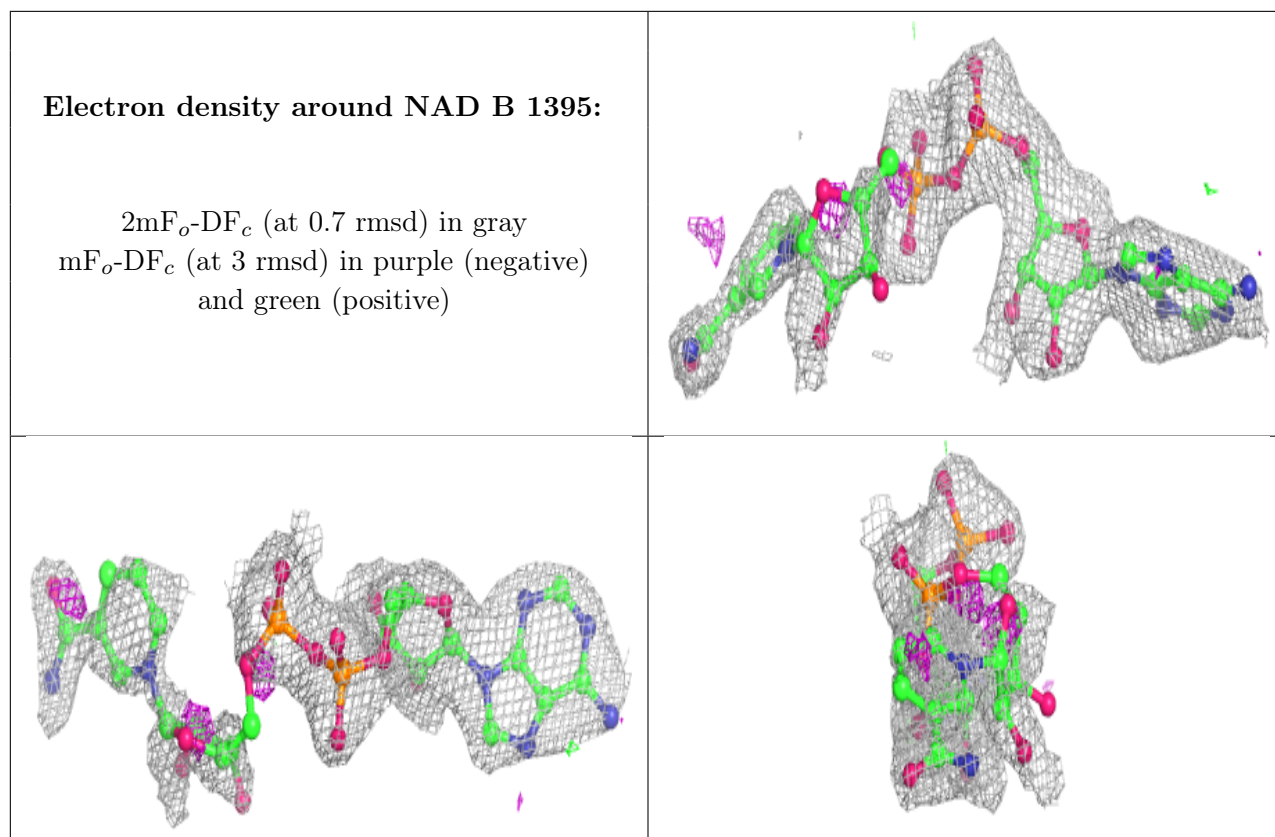
There are no monosaccharides in this entry.

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
2	NAD	B	1395	44/44	0.87	0.18	54,61,83,85	0

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



6.5 Other polymers [i](#)

There are no such residues in this entry.