

Full wwPDB X-ray Structure Validation Report (i)

Jun 11, 2024 – 08:25 PM EDT

PDB ID : 1A4I

Title: HUMAN TETRAHYDROFOLATE DEHYDROGENASE / CYCLOHYDRO-

 $_{
m LASE}$

Authors: Allaire, M.; Li, Y.; Mackenzie, R.E.; Cygler, M.

Deposited on : 1998-01-30

Resolution : 1.50 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 (i) 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 (1)) were used in the production of this report:

MolProbity : 4.02b-467

Mogul : 2022.3.0, CSD as543be (2022)

Xtriage (Phenix) : 1.20.1

 $EDS \quad : \quad 2.36.2$

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)

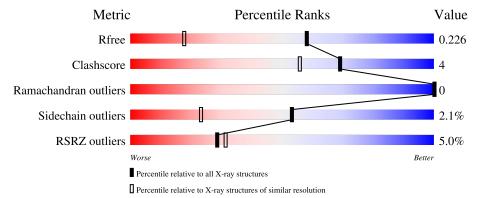
Validation Pipeline (wwPDB-VP) : 2.36.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 1.50 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	Similar resolution
Metric	$(\# ext{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	130704	2936 (1.50-1.50)
Clashscore	141614	3144 (1.50-1.50)
Ramachandran outliers	138981	3066 (1.50-1.50)
Sidechain outliers	138945	3064 (1.50-1.50)
RSRZ outliers	127900	2884 (1.50-1.50)

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 <=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	301	5% 82%	12%	• 5%
1	В	301	85%	12%	



2 Entry composition (i)

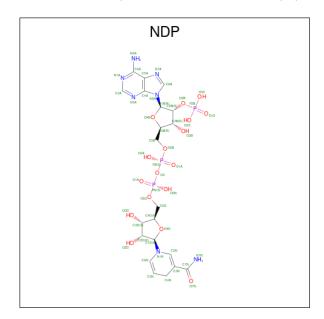
There are 3 unique types of molecules in this entry. The entry contains 4899 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 METHYLENETETRAHYDROFOLATE DEHYDROGENASE / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	A	285	Total 2159	C 1357	N 374	O 417	S 11	16	0	0
1	В	295	Total 2237	C 1404	N 390	O 432	S 11	4	0	0

• Molecule 2 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: C₂₁H₃₀N₇O₁₇P₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2	Λ	1	Total	С	N	О	Р	0	0
2	2 A	1	48	21	7	17	3	U	U
2	D	1	Total	С	N	О	Р	0	0
	Б	1	48	21	7	17	3	U	0

• Molecule 3 is water.



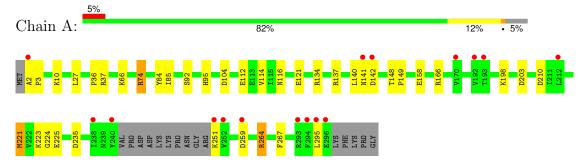
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	179	Total O 179 179	0	0
3	В	228	Total O 228 228	0	0



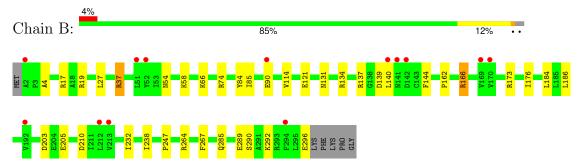
3 Residue-property plots (i)

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: METHYLENETETRAHYDROFOLATE DEHYDROGENASE / METHENYLTE TRAHYDROFOLATE CYCLOHYDROLASE



 \bullet Molecule 1: METHYLENETETRAHYDROFOLATE DEHYDROGENASE / METHENYLTE TRAHYDROFOLATE CYCLOHYDROLASE





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	67.52Å 135.84Å 61.40Å	Donositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 - 1.50	Depositor
Resolution (A)	25.41 - 1.50	EDS
% Data completeness	90.0 (20.00-1.50)	Depositor
(in resolution range)	83.0 (25.41-1.50)	EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	3.38 (at 1.50Å)	Xtriage
Refinement program	REFMAC	Depositor
D D.	0.199 , 0.235	Depositor
R, R_{free}	0.188 , 0.226	DCC
R_{free} test set	3818 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	16.5	Xtriage
Anisotropy	0.123	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.40, 45.5	EDS
L-test for twinning ²	$ < L >=0.49, < L^2>=0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4899	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.89% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

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: NDP

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		nd lengths	Bond angles		
MIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.75	1/2191 (0.0%)	1.49	$20/2973 \ (0.7\%)$	
1	В	0.75	1/2272 (0.0%)	1.47	$26/3084 \ (0.8\%)$	
All	All	0.75	2/4463 (0.0%)	1.48	$46/6057 \ (0.8\%)$	

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	Observed(Å)	Ideal(A)
1	В	296	GLU	CB-CG	7.36	1.66	1.52
1	A	251	LYS	CB-CG	-5.49	1.37	1.52

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	251	LYS	CA-CB-CG	-18.35	73.03	113.40
1	A	203	ASP	CB-CG-OD1	12.88	129.90	118.30
1	A	134	ARG	NE-CZ-NH1	12.22	126.41	120.30
1	В	19	ARG	NE-CZ-NH2	-10.55	115.03	120.30
1	В	17	ARG	CD-NE-CZ	10.43	138.21	123.60
1	В	166	ARG	NE-CZ-NH1	-10.21	115.19	120.30
1	A	251	LYS	CB-CG-CD	-9.96	85.72	111.60
1	A	235	ASP	CB-CG-OD2	-9.82	109.46	118.30
1	В	173	ARG	NE-CZ-NH2	-9.32	115.64	120.30
1	A	134	ARG	NE-CZ-NH2	-8.84	115.88	120.30
1	В	173	ARG	NE-CZ-NH1	8.80	124.70	120.30
1	A	137	ARG	NE-CZ-NH2	-8.58	116.01	120.30
1	В	264	ARG	NE-CZ-NH2	-8.57	116.01	120.30
1	A	235	ASP	CB-CG-OD1	7.99	125.49	118.30
1	A	142	ASP	CB-CA-C	-7.46	95.47	110.40
1	A	84	TYR	CB-CG-CD1	-7.44	116.53	121.00
1	A	74	ARG	NE-CZ-NH2	7.37	123.98	120.30



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Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
1	В	144	PHE	CB-CG-CD2	-7.12	115.82	120.80
1	В	134	ARG	NE-CZ-NH1	6.89	123.74	120.30
1	A	264	ARG	NE-CZ-NH2	-6.67	116.96	120.30
1	В	285	GLN	OE1-CD-NE2	6.52	136.89	121.90
1	A	210	ASP	CB-CG-OD1	-6.22	112.70	118.30
1	A	84	TYR	CB-CG-CD2	6.18	124.71	121.00
1	A	141	ASN	C-N-CA	6.16	137.11	121.70
1	В	37	ARG	NE-CZ-NH1	-6.03	117.28	120.30
1	В	203	ASP	CB-CG-OD1	6.01	123.71	118.30
1	В	210	ASP	CB-CG-OD1	-5.98	112.92	118.30
1	В	166	ARG	NH1-CZ-NH2	5.91	125.90	119.40
1	В	134	ARG	NE-CZ-NH2	-5.76	117.42	120.30
1	A	225	GLU	CA-CB-CG	5.74	126.02	113.40
1	В	139	ASP	CB-CG-OD2	-5.69	113.18	118.30
1	A	166	ARG	NE-CZ-NH2	-5.63	117.48	120.30
1	В	19	ARG	NE-CZ-NH1	5.63	123.11	120.30
1	В	139	ASP	CB-CG-OD1	5.53	123.28	118.30
1	A	203	ASP	CB-CG-OD2	-5.52	113.33	118.30
1	В	205	GLU	OE1-CD-OE2	5.46	129.86	123.30
1	A	221	MET	CA-CB-CG	5.46	122.58	113.30
1	В	267	PHE	CB-CG-CD2	-5.41	117.01	120.80
1	В	289	GLU	O-C-N	5.37	131.29	122.70
1	A	267	PHE	CB-CG-CD2	-5.28	117.11	120.80
1	В	296	GLU	CB-CG-CD	5.27	128.43	114.20
1	В	137	ARG	CD-NE-CZ	5.15	130.81	123.60
1	В	290	SER	O-C-N	5.14	130.93	122.70
1	В	4	ALA	N-CA-CB	-5.10	102.96	110.10
1	В	74	ARG	NE-CZ-NH2	-5.09	117.75	120.30
1	В	84	TYR	CB-CG-CD2	-5.03	117.98	121.00

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	2159	0	2208	19	0
1	В	2237	0	2288	14	0
2	A	48	0	26	0	0
2	В	48	0	26	1	0
3	A	179	0	0	2	1
3	В	228	0	0	3	1
All	All	4899	0	4548	33	1

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 (33) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

A 4 1	A 4 0	Interatomic	Clash
Atom-1	Atom-2	${\rm distance} \ (\rm \AA)$	overlap (Å)
1:A:2:ALA:HB3	1:A:3:PRO:HD3	1.61	0.81
1:A:37:ARG:H	1:A:95:HIS:HD2	1.33	0.75
1:B:166:ARG:HH12	1:B:232:ILE:HD12	1.54	0.72
1:A:85:ILE:HD11	1:A:114:VAL:HG13	1.73	0.69
1:A:2:ALA:HB3	1:A:3:PRO:CD	2.26	0.66
1:B:238:ILE:HD11	2:B:302:NDP:N7N	2.11	0.65
1:A:158:GLU:HG2	3:A:464:HOH:O	1.97	0.64
1:A:85:ILE:CD1	1:A:114:VAL:HG13	2.32	0.59
1:B:131:ASN:ND2	3:B:470:HOH:O	2.35	0.58
1:A:27:LEU:HD11	1:A:295:LEU:HD12	1.85	0.57
1:B:166:ARG:HH12	1:B:232:ILE:CD1	2.16	0.57
1:A:74:ARG:NE	1:A:104:ASP:OD1	2.38	0.56
1:A:112:GLU:HG2	1:A:116:ASN:HD22	1.73	0.54
1:A:37:ARG:H	1:A:95:HIS:CD2	2.20	0.53
1:B:166:ARG:NH1	1:B:232:ILE:HD12	2.25	0.51
1:B:37:ARG:CD	1:B:66:LYS:HD2	2.41	0.50
1:B:58:LYS:HE2	3:B:522:HOH:O	2.12	0.49
1:A:74:ARG:HE	1:A:104:ASP:CG	2.14	0.49
1:A:37:ARG:N	1:A:95:HIS:HD2	2.06	0.47
1:B:37:ARG:HD2	1:B:66:LYS:HD2	1.96	0.47
1:B:85:ILE:CD1	1:B:114:VAL:HG13	2.45	0.46
1:A:2:ALA:CB	1:A:3:PRO:CD	2.92	0.46
1:A:121:GLU:H	1:A:121:GLU:CD	2.20	0.45
1:A:36:PRO:HA	1:A:95:HIS:CD2	2.53	0.44
1:B:140:LEU:HD11	1:B:184:LEU:HD23	1.99	0.44
1:B:162:PRO:O	1:B:166:ARG:NE	2.51	0.43
3:A:430:HOH:O	1:B:186:LEU:HD13	2.18	0.42
1:B:27:LEU:HD11	1:B:292:LYS:HE2	2.01	0.42



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0 0 1000100000			

Atom-1	Atom-2	$egin{aligned} & ext{Interatomic} \ & ext{distance} \ & ext{(Å)} \end{aligned}$	Clash overlap (Å)
1:B:176:ILE:HG12	3:B:351:HOH:O	2.18	0.42
1:A:37:ARG:HD2	1:A:66:LYS:HE2	2.02	0.41
1:A:148:THR:HB	1:A:149:PRO:HD3	2.02	0.40
1:A:223:LYS:HA	1:A:223:LYS:HD3	1.85	0.40
1:A:224:GLY:O	1:A:264:ARG:HD2	2.21	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$egin{aligned} ext{Clash} \ ext{overlap } (ext{Å}) \end{aligned}$
3:A:389:HOH:O	3:B:502:HOH:O[3_555]	2.19	0.01

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	Perce	ntiles
1	A	281/301 (93%)	278 (99%)	3 (1%)	0	100	100
1	В	293/301 (97%)	287 (98%)	6 (2%)	0	100	100
All	All	574/602 (95%)	565 (98%)	9 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	Percentile	S
1	A	$239/253 \ (94\%)$	233 (98%)	6 (2%)	47 18	
1	В	248/253 (98%)	244 (98%)	4 (2%)	62 36	
All	All	487/506 (96%)	477 (98%)	10 (2%)	53 23	

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	LYS
1	A	92	SER
1	A	140	LEU
1	A	198	LYS
1	A	221	MET
1	A	259	ASP
1	В	54	ASN
1	В	90	GLU
1	В	121	GLU
1	В	247	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	ASN
1	A	95	HIS
1	В	22	ASN
1	В	201	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 monosaccharides in this entry.



5.6 Ligand geometry (i)

2 ligands are modelled in this entry.

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

Mol	Trme	Chain	Dec	Res Link	Bond lengths			Bond angles		
IVIOI	Type	Chain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
2	NDP	A	302	-	47,52,52	1.62	4 (8%)	61,80,80	1.57	12 (19%)
2	NDP	В	302	-	47,52,52	1.67	5 (10%)	61,80,80	1.52	12 (19%)

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	NDP	A	302	-	-	3/30/77/77	0/5/5/5
2	NDP	В	302	-	-	3/30/77/77	0/5/5/5

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(A)
2	A	302	NDP	C4N-C3N	-6.32	1.38	1.50
2	В	302	NDP	C4N-C3N	-6.19	1.38	1.50
2	В	302	NDP	C4N-C5N	-5.67	1.34	1.49
2	A	302	NDP	C4N-C5N	-5.37	1.35	1.49
2	В	302	NDP	PA-O3	-3.13	1.56	1.59
2	A	302	NDP	P2B-O2B	-2.96	1.54	1.59
2	A	302	NDP	C2N-C3N	2.73	1.42	1.35
2	В	302	NDP	C2N-C3N	2.40	1.41	1.35
2	В	302	NDP	C2A-N3A	2.28	1.35	1.32

All (24) bond angle outliers are listed below:

	Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
	2	A	302	NDP	C4B-O4B-C1B	-4.68	105.64	109.92
Ī	2	A	302	NDP	C3N-C2N-N1N	-4.62	116.42	123.20



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Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\mathrm{Ideal}(^o)$
2	В	302	NDP	C3N-C2N-N1N	-4.49	116.61	123.20
2	В	302	NDP	N3A-C2A-N1A	-3.45	124.00	128.67
2	A	302	NDP	C1D-N1N-C2N	-3.35	115.63	121.14
2	В	302	NDP	N6A-C6A-N1A	3.28	125.34	118.33
2	A	302	NDP	O4B-C1B-N9A	3.01	112.74	108.75
2	В	302	NDP	C4A-C5A-N7A	3.00	112.51	109.34
2	В	302	NDP	C1D-N1N-C2N	-2.69	116.71	121.14
2	A	302	NDP	O7N-C7N-N7N	-2.63	116.99	122.89
2	В	302	NDP	C2D-C1D-N1N	-2.58	106.96	113.31
2	A	302	NDP	C3D-C2D-C1D	-2.56	96.62	101.46
2	В	302	NDP	O7N-C7N-N7N	-2.55	117.17	122.89
2	В	302	NDP	O4D-C1D-C2D	-2.47	101.33	106.62
2	A	302	NDP	C6N-N1N-C2N	2.31	121.80	119.32
2	В	302	NDP	O2B-P2B-O1X	-2.30	101.12	109.33
2	A	302	NDP	O4B-C4B-C3B	2.24	109.60	105.15
2	В	302	NDP	O2N-PN-O1N	2.15	122.42	112.44
2	A	302	NDP	O2A-PA-O1A	2.14	122.41	112.44
2	A	302	NDP	O4B-C1B-C2B	2.13	110.24	106.61
2	В	302	NDP	C6N-N1N-C2N	2.11	121.58	119.32
2	В	302	NDP	O4B-C4B-C5B	-2.06	102.72	109.33
2	A	302	NDP	O4D-C1D-C2D	-2.04	102.25	106.62
2	A	302	NDP	O2N-PN-O1N	2.04	121.93	112.44

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	302	NDP	C3B-C2B-O2B-P2B
2	В	302	NDP	C3B-C2B-O2B-P2B
2	A	302	NDP	O4D-C1D-N1N-C2N
2	В	302	NDP	O4D-C1D-N1N-C2N
2	A	302	NDP	C1B-C2B-O2B-P2B
2	В	302	NDP	C1B-C2B-O2B-P2B

There are no ring outliers.

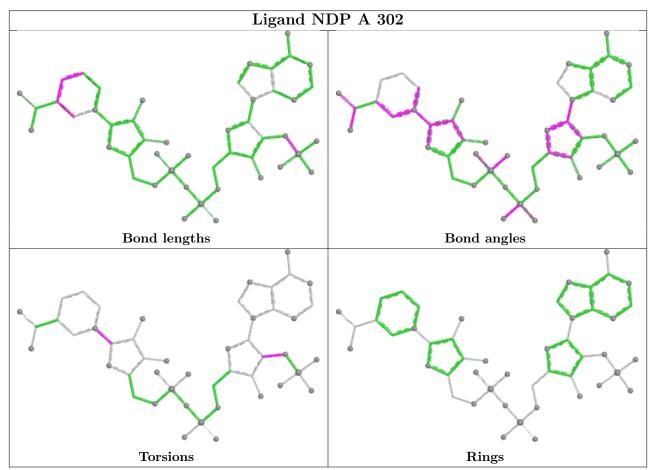
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	В	302	NDP	1	0

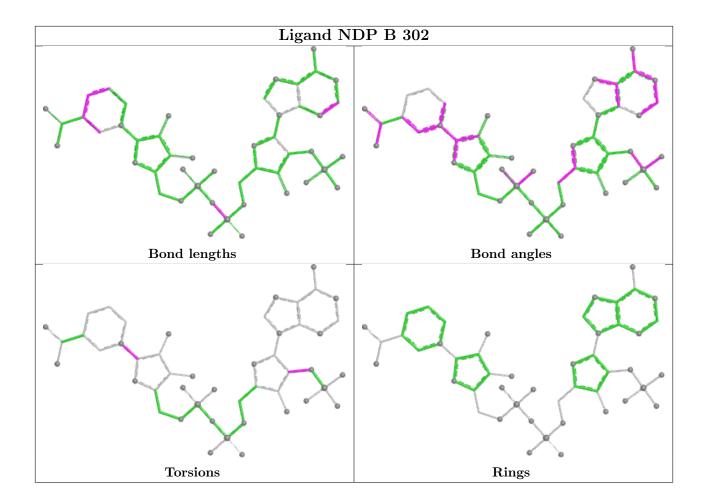
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,



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 then 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 (i)

6.1 Protein, DNA and RNA chains (i)

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, 95^{th} 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	$\langle { m RSRZ} \rangle$	$\#\mathrm{RSRZ}{>}2$		$\mathbf{OWAB}(\mathbf{\mathring{A}}^2)$	Q < 0.9
1	A	285/301 (94%)	0.32	16 (5%) 24 26	3	11, 18, 31, 48	4 (1%)
1	В	295/301~(98%)	0.29	13 (4%) 34 38	3	11, 17, 28, 42	1 (0%)
All	All	580/602 (96%)	0.30	29 (5%) 28 33	1	11, 18, 30, 48	5 (0%)

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	ALA	8.1
1	В	2	ALA	5.8
1	В	294	PHE	4.7
1	A	142	ASP	4.3
1	A	295	LEU	3.9
1	A	240	TYR	3.4
1	В	142	ASP	3.3
1	A	296	GLU	3.1
1	A	141	ASN	3.1
1	В	212	LEU	3.0
1	A	251	LYS	2.9
1	В	170	VAL	2.8
1	В	169	VAL	2.7
1	A	238	ILE	2.6
1	В	90	GLU	2.6
1	В	141	ASN	2.5
1	В	213	VAL	2.5
1	В	140	LEU	2.4
1	A	252	VAL	2.4
1	В	51	LEU	2.4
1	A	170	VAL	2.3
1	В	52	TYR	2.2
1	A	259	ASP	2.2
1	A	294	PHE	2.2



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Mol	Chain	Res	Type	RSRZ
1	A	192	VAL	2.2
1	A	193	THR	2.1
1	В	192	VAL	2.1
1	A	293	ARG	2.1
1	A	212	LEU	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 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, 95^{th} 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.

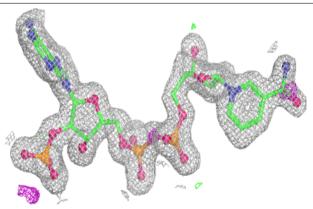
Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
2	NDP	A	302	48/48	0.97	0.08	13,21,28,32	0
2	NDP	В	302	48/48	0.97	0.07	12,16,24,29	0

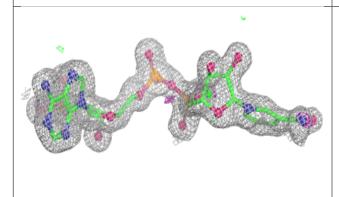
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

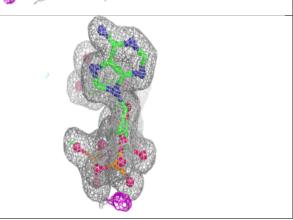


Electron density around NDP A 302:

 $2 \mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 0.7 rmsd) in gray $\mathrm{mF}_o\text{-}\mathrm{DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)

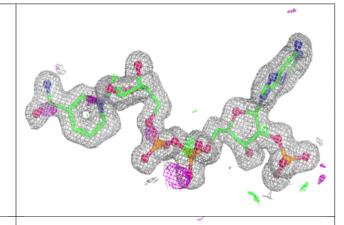


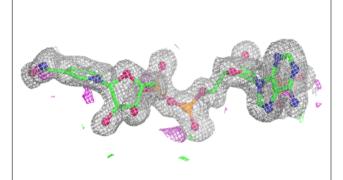


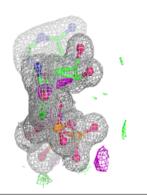


Electron density around NDP B 302:

 $2 \text{mF}_o\text{-DF}_c$ (at 0.7 rmsd) in gray $\text{mF}_o\text{-DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)









6.5 Other polymers (i)

There are no such residues in this entry.

