



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 23, 2021 – 09:29 AM EDT

PDB ID : 1IDE
Title : ISOCITRATE DEHYDROGENASE Y160F MUTANT STEADY-STATE INTERMEDIATE COMPLEX (LAUE DETERMINATION)
Authors : Bolduc, J.M.; Dyer, D.H.; Scott, W.G.; Singer, P.; Sweet, R.M.; Koshland Junior, D.E.; Stoddard, B.L.
Deposited on : 1995-01-18
Resolution : 2.50 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The 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)
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

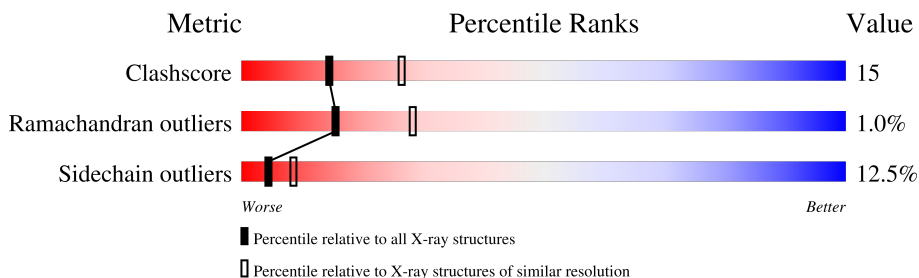
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	416	

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
4	NAP	A	419	X	-	-	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3954 atoms, of which 695 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 ISOCITRATE DEHYDROGENASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	414	3879	2035	684	538	604	18	0	0	0

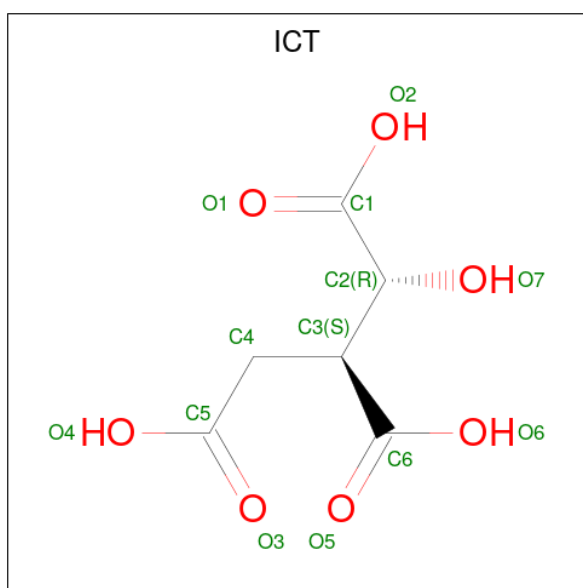
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	160	PHE	TYR	engineered mutation	UNP P08200

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

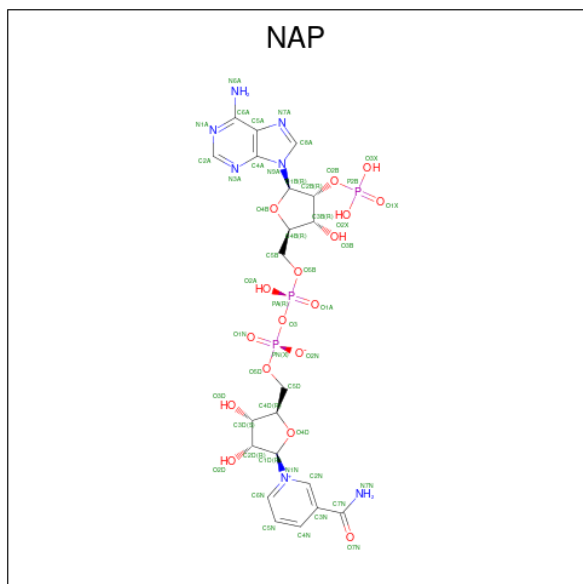
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is ISOCITRIC ACID (three-letter code: ICT) (formula: C₆H₈O₇).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			13	6	7		

- Molecule 4 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: $C_{21}H_{28}N_7O_{17}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
4	A	1	Total	C	H	N	O	P	0	0
			55	21	7	7	17	3		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	2	Total	H	O	0	0
			6	4	2		

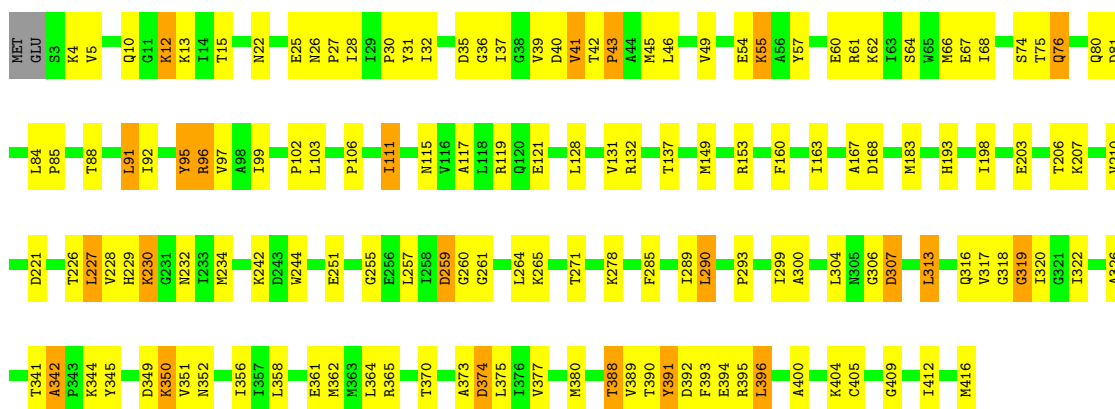
3 Residue-property plots [i](#)

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. 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. 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.

Note EDS was not executed.

- Molecule 1: ISOCITRATE DEHYDROGENASE

Chain A:  64% 30% 5%



4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	105.10Å 105.10Å 150.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.50	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.50)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.192 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	3954	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

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: MG, NAP, ICT

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	0.39	0/3256	0.88	7/4403 (0.2%)

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

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

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	396	LEU	CA-CB-CG	7.92	133.52	115.30
1	A	307	ASP	CB-CG-OD1	7.24	124.81	118.30
1	A	290	LEU	CA-CB-CG	6.54	130.34	115.30
1	A	304	LEU	CA-CB-CG	5.54	128.04	115.30
1	A	230	LYS	N-CA-C	-5.46	96.26	111.00
1	A	46	LEU	CA-CB-CG	5.39	127.70	115.30
1	A	388	THR	N-CA-C	-5.37	96.50	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	95	TYR	Sidechain

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	3195	684	3222	100	1
2	A	1	0	0	0	0
3	A	13	0	4	0	1
4	A	48	7	24	0	0
5	A	2	4	0	0	0
All	All	3259	695	3250	100	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 15.

All (100) 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:A:342:ALA:HB1	1:A:345:TYR:HD2	1.30	0.95
1:A:37:ILE:HG12	1:A:341:THR:HA	1.50	0.89
1:A:37:ILE:HD12	1:A:351:VAL:HG21	1.55	0.88
1:A:5:VAL:HG11	1:A:91:LEU:HD21	1.55	0.87
1:A:37:ILE:H	1:A:341:THR:HB	1.40	0.85
1:A:35:ASP:O	1:A:341:THR:HG21	1.80	0.81
1:A:37:ILE:N	1:A:341:THR:HB	1.97	0.79
1:A:37:ILE:HG23	1:A:341:THR:O	1.83	0.78
1:A:41:VAL:HG13	1:A:356:ILE:HG21	1.66	0.77
1:A:106:PRO:HG2	1:A:111:ILE:HD13	1.66	0.76
1:A:102:PRO:HB2	1:A:341:THR:HG23	1.68	0.76
1:A:75:THR:HB	1:A:80:GLN:HA	1.68	0.75
1:A:37:ILE:CD1	1:A:351:VAL:HG21	2.17	0.74
1:A:389:VAL:HG22	1:A:390:THR:H	1.54	0.71
1:A:342:ALA:HB1	1:A:345:TYR:CD2	2.21	0.71
1:A:257:LEU:HD11	1:A:261:GLY:HA2	1.74	0.70
1:A:361:GLU:HG3	1:A:377:VAL:HG12	1.74	0.67
1:A:389:VAL:HG22	1:A:390:THR:N	2.13	0.64
1:A:394:GLU:HG2	1:A:400:ALA:HB3	1.80	0.64
1:A:342:ALA:CB	1:A:345:TYR:HD2	2.08	0.63
1:A:349:ASP:OD1	1:A:405:CYS:HB3	2.00	0.62
1:A:389:VAL:HG21	1:A:393:PHE:CD2	2.34	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:26:ASN:HA	1:A:62:LYS:O	2.01	0.60
1:A:37:ILE:HG12	1:A:341:THR:CA	2.25	0.60
1:A:255:GLY:HA2	1:A:265:LYS:O	2.01	0.60
1:A:37:ILE:HG21	1:A:351:VAL:HG11	1.83	0.60
1:A:68:ILE:HD12	1:A:88:THR:HG23	1.83	0.60
1:A:40:ASP:O	1:A:43:PRO:HD2	2.02	0.60
1:A:36:GLY:O	1:A:39:VAL:HG12	2.01	0.59
1:A:319:GLY:HA3	1:A:322:ILE:HG12	1.85	0.59
1:A:76:GLN:HE21	1:A:76:GLN:HA	1.68	0.58
1:A:388:THR:HG23	1:A:388:THR:O	2.04	0.58
1:A:41:VAL:HG13	1:A:356:ILE:CG2	2.34	0.58
1:A:289:ILE:O	1:A:293:PRO:HB3	2.04	0.58
1:A:374:ASP:HA	1:A:377:VAL:HG13	1.86	0.58
1:A:57:TYR:O	1:A:60:GLU:HG2	2.05	0.57
1:A:365:ARG:HH21	1:A:373:ALA:HB1	1.71	0.56
1:A:163:ILE:HB	1:A:198:ILE:HB	1.88	0.55
1:A:203:GLU:HG2	1:A:244:TRP:CE2	2.41	0.55
1:A:37:ILE:HD12	1:A:351:VAL:CG2	2.34	0.55
1:A:30:PRO:HD2	1:A:97:VAL:O	2.06	0.55
1:A:102:PRO:HB2	1:A:341:THR:CG2	2.36	0.54
1:A:358:LEU:HD21	1:A:380:MET:HE1	1.90	0.54
1:A:32:ILE:HG12	1:A:68:ILE:HG13	1.91	0.53
1:A:37:ILE:HG12	1:A:341:THR:HG22	1.91	0.53
1:A:326:ALA:HB2	1:A:362:MET:HE3	1.91	0.52
1:A:404:LYS:HZ2	1:A:404:LYS:HB2	1.74	0.52
1:A:358:LEU:O	1:A:361:GLU:HB3	2.09	0.52
1:A:389:VAL:CG2	1:A:390:THR:H	2.21	0.52
1:A:227:LEU:HD12	1:A:300:ALA:HB3	1.93	0.50
1:A:115:ASN:O	1:A:119:ARG:HD3	2.11	0.50
1:A:12:LYS:O	1:A:27:PRO:HA	2.12	0.49
1:A:37:ILE:CG1	1:A:341:THR:HA	2.32	0.49
1:A:102:PRO:CB	1:A:341:THR:HG23	2.38	0.49
1:A:55:LYS:HE2	1:A:416:MET:O	2.13	0.49
1:A:391:TYR:CG	1:A:392:ASP:N	2.80	0.49
1:A:285:PHE:CZ	1:A:299:ILE:HD13	2.48	0.49
1:A:358:LEU:HD21	1:A:380:MET:CE	2.43	0.49
1:A:285:PHE:HZ	1:A:299:ILE:CD1	2.26	0.48
1:A:74:SER:OG	1:A:85:PRO:HD3	2.13	0.48
1:A:10:GLN:O	1:A:26:ASN:ND2	2.47	0.48
1:A:37:ILE:HG21	1:A:351:VAL:CG1	2.43	0.48
1:A:5:VAL:HG11	1:A:91:LEU:CD2	2.36	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:257:LEU:HD11	1:A:261:GLY:CA	2.44	0.47
1:A:45:MET:O	1:A:49:VAL:HG23	2.15	0.46
1:A:389:VAL:CG2	1:A:390:THR:N	2.79	0.46
1:A:88:THR:O	1:A:92:ILE:HG13	2.15	0.46
1:A:206:THR:O	1:A:210:VAL:HG23	2.15	0.45
1:A:149:MET:SD	1:A:313:LEU:HD21	2.57	0.45
1:A:117:ALA:O	1:A:121:GLU:HB2	2.18	0.45
1:A:203:GLU:HG2	1:A:244:TRP:NE1	2.32	0.44
1:A:153:ARG:HG3	1:A:306:GLY:HA3	1.99	0.44
1:A:167:ALA:O	1:A:168:ASP:HB2	2.17	0.44
1:A:326:ALA:HB2	1:A:362:MET:CE	2.46	0.44
1:A:389:VAL:HG21	1:A:393:PHE:HD2	1.82	0.44
1:A:352:ASN:HA	1:A:390:THR:HG21	1.99	0.44
1:A:28:ILE:HA	1:A:64:SER:O	2.19	0.43
1:A:30:PRO:HA	1:A:66:MET:O	2.18	0.43
1:A:31:TYR:CE1	1:A:67:GLU:HG3	2.54	0.43
1:A:229:HIS:CE1	1:A:242:LYS:HD3	2.54	0.42
1:A:350:LYS:HG2	1:A:350:LYS:O	2.19	0.42
1:A:313:LEU:O	1:A:317:VAL:HG22	2.19	0.42
1:A:230:LYS:HD2	1:A:230:LYS:HA	1.65	0.42
1:A:75:THR:HB	1:A:80:GLN:CA	2.43	0.42
1:A:111:ILE:HD12	1:A:111:ILE:H	1.84	0.42
1:A:149:MET:HE1	1:A:313:LEU:HD11	2.02	0.42
1:A:45:MET:HE2	1:A:99:ILE:HD13	2.01	0.41
1:A:226:THR:HA	1:A:278:LYS:O	2.21	0.41
1:A:259:ASP:HB3	1:A:260:GLY:H	1.71	0.41
1:A:285:PHE:HZ	1:A:299:ILE:HD13	1.84	0.41
1:A:409:GLY:HA2	1:A:412:ILE:HD12	2.02	0.41
1:A:203:GLU:O	1:A:207:LYS:HB2	2.21	0.41
1:A:37:ILE:HG12	1:A:341:THR:CB	2.50	0.41
1:A:41:VAL:HG12	1:A:42:THR:N	2.36	0.41
1:A:318:GLY:O	1:A:320:ILE:N	2.54	0.41
1:A:95:TYR:O	1:A:96:ARG:HB2	2.20	0.41
1:A:12:LYS:HD2	1:A:13:LYS:N	2.37	0.41
1:A:341:THR:O	1:A:342:ALA:O	2.39	0.40
1:A:375:LEU:HD12	1:A:375:LEU:HA	1.67	0.40
1:A:62:LYS:HB2	1:A:62:LYS:HE3	1.81	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	Interatomic distance (Å)	Clash overlap (Å)
1:A:232:ASN:HD21	3:A:418:ICT:O4[7_555]	1.38	0.22

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	412/416 (99%)	362 (88%)	46 (11%)	4 (1%)	15 28

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	81	ASP
1	A	319	GLY
1	A	41	VAL
1	A	342	ALA

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	336/338 (99%)	294 (88%)	42 (12%)	4 8

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LYS
1	A	12	LYS

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Mol	Chain	Res	Type
1	A	15	THR
1	A	22	ASN
1	A	25	GLU
1	A	43	PRO
1	A	54	GLU
1	A	55	LYS
1	A	61	ARG
1	A	76	GLN
1	A	84	LEU
1	A	91	LEU
1	A	96	ARG
1	A	103	LEU
1	A	111	ILE
1	A	128	LEU
1	A	131	VAL
1	A	132	ARG
1	A	137	THR
1	A	160	PHE
1	A	183	MET
1	A	193	HIS
1	A	221	ASP
1	A	227	LEU
1	A	228	VAL
1	A	234	MET
1	A	251	GLU
1	A	259	ASP
1	A	264	LEU
1	A	271	THR
1	A	290	LEU
1	A	307	ASP
1	A	313	LEU
1	A	316	GLN
1	A	344	LYS
1	A	350	LYS
1	A	364	LEU
1	A	370	THR
1	A	374	ASP
1	A	391	TYR
1	A	395	ARG
1	A	396	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	76	GLN
1	A	305	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](#)

Of 3 ligands modelled in this entry, 1 is 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	ICT	A	418	2	2,12,12	0.74	0	5,16,16	2.13	3 (60%)
4	NAP	A	419	-	45,52,52	1.73	8 (17%)	56,80,80	1.72	13 (23%)

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	ICT	A	418	2	-	3/6/16/16	-
4	NAP	A	419	-	1/1/12/12	13/31/67/67	0/5/5/5

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	419	NAP	C3N-C7N	-6.15	1.41	1.50
4	A	419	NAP	C2N-C3N	4.22	1.45	1.39
4	A	419	NAP	C7N-N7N	3.70	1.40	1.33
4	A	419	NAP	O4D-C4D	-2.69	1.39	1.45
4	A	419	NAP	C4N-C3N	2.60	1.43	1.39
4	A	419	NAP	O4B-C4B	-2.23	1.40	1.45
4	A	419	NAP	P2B-O3X	-2.23	1.46	1.54
4	A	419	NAP	C8A-N7A	-2.20	1.30	1.34

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	419	NAP	C3B-C2B-C1B	-4.76	93.94	102.89
4	A	419	NAP	N3A-C2A-N1A	-3.52	123.17	128.68
4	A	419	NAP	C3N-C7N-N7N	3.37	121.80	117.75
4	A	419	NAP	O7N-C7N-N7N	-3.31	117.87	122.58
4	A	419	NAP	O4B-C1B-C2B	-2.99	101.41	106.59
4	A	419	NAP	C6N-N1N-C2N	-2.96	119.27	121.97
3	A	418	ICT	C1-C2-C3	-2.84	109.05	112.25
3	A	418	ICT	O7-C2-C3	2.72	116.19	108.56
4	A	419	NAP	O4D-C4D-C5D	2.55	117.78	109.37
4	A	419	NAP	O3B-C3B-C4B	2.51	118.29	111.05
3	A	418	ICT	O7-C2-C1	-2.43	105.26	111.10
4	A	419	NAP	O4B-C4B-C3B	-2.42	100.33	105.11
4	A	419	NAP	O5D-C5D-C4D	2.27	116.82	108.99
4	A	419	NAP	C3D-C2D-C1D	2.25	104.36	100.98
4	A	419	NAP	O3B-C3B-C2B	2.22	117.48	111.17
4	A	419	NAP	C4A-C5A-N7A	2.01	111.50	109.40

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	A	419	NAP	C3D

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	419	NAP	C5D-O5D-PN-O3
4	A	419	NAP	O4D-C4D-C5D-O5D
4	A	419	NAP	O4D-C1D-N1N-C2N
4	A	419	NAP	O4D-C1D-N1N-C6N

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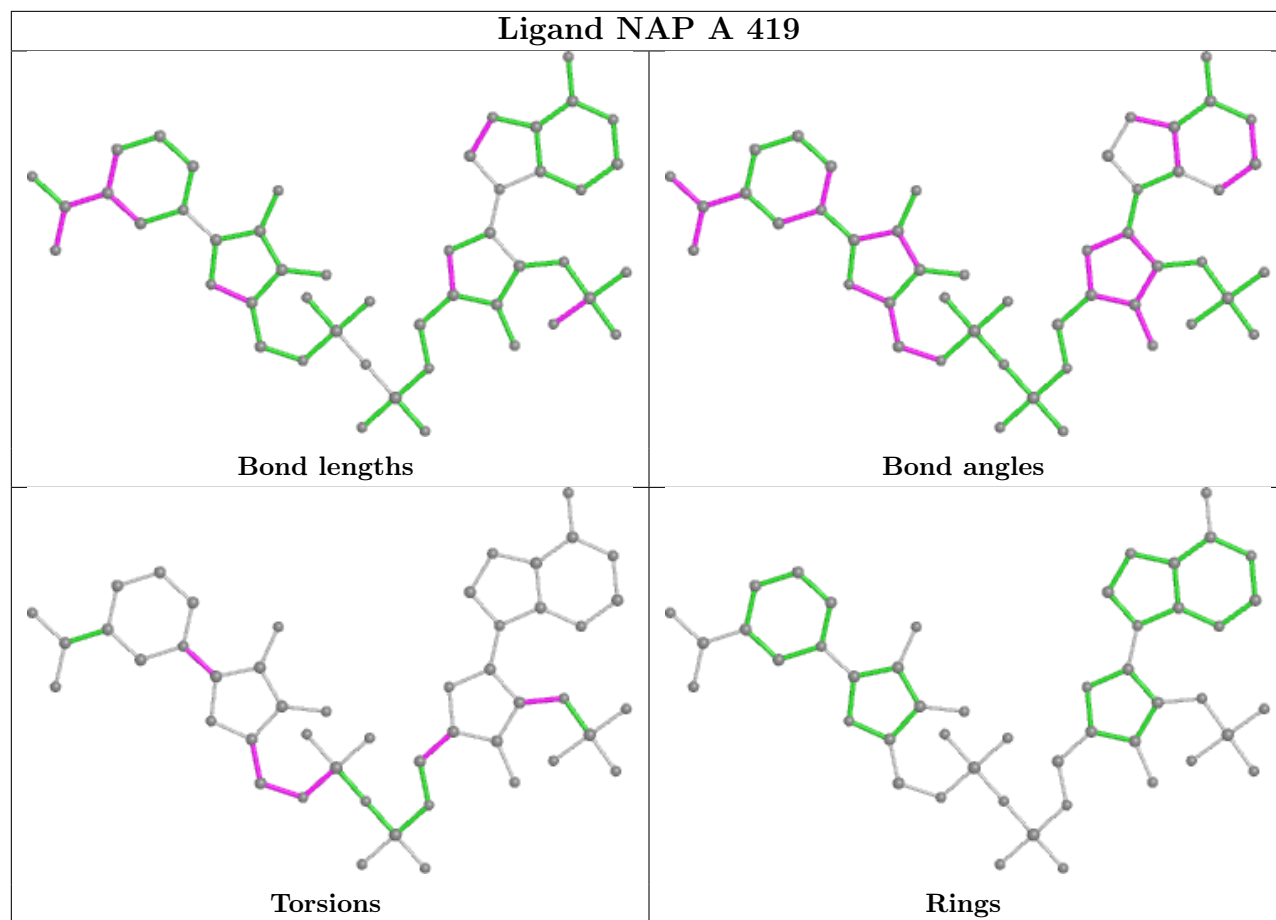
Mol	Chain	Res	Type	Atoms
4	A	419	NAP	C2D-C1D-N1N-C2N
4	A	419	NAP	C2D-C1D-N1N-C6N
4	A	419	NAP	C3D-C4D-C5D-O5D
4	A	419	NAP	C3B-C2B-O2B-P2B
4	A	419	NAP	C1B-C2B-O2B-P2B
4	A	419	NAP	C4D-C5D-O5D-PN
4	A	419	NAP	C5D-O5D-PN-O1N
4	A	419	NAP	C5D-O5D-PN-O2N
3	A	418	ICT	O7-C2-C3-C6
3	A	418	ICT	C1-C2-C3-C6
4	A	419	NAP	O4B-C4B-C5B-O5B
3	A	418	ICT	C6-C3-C4-C5

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	418	ICT	0	1

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.