



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 4, 2026 – 06:08 PM EDT

PDB ID : 1AI2 / pdb_00001ai2
Title : ISOCITRATE DEHYDROGENASE COMPLEXED WITH ISOCITRATE,
NADP+, AND CALCIUM (FLASH-COOLED)
Authors : Stoddard, B.L.; Mesecar, A.; Koshland Junior, D.E.
Deposited on : 1997-04-30
Resolution : 1.90 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

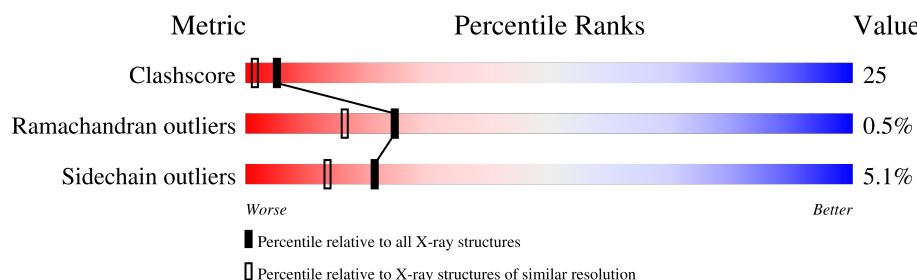
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)

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
2	NAP	A	417	-	-	X	-
3	ICT	A	418	-	X	-	-

2 Entry composition [i](#)

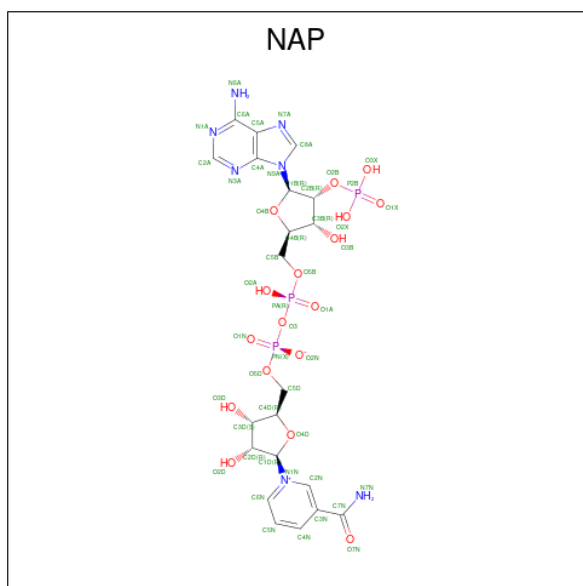
There are 5 unique types of molecules in this entry. The entry contains 3562 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ISOCITRATE DEHYDROGENASE.

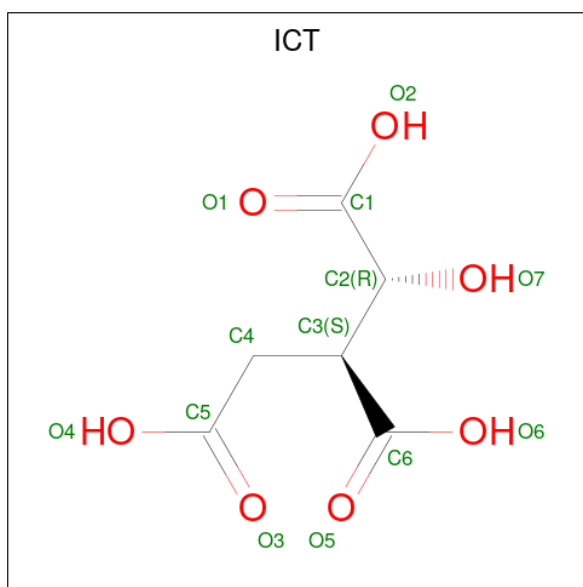
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	414	3196	2035	538	605	18	0	0	0

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NAP) (formula: C₂₁H₂₈N₇O₁₇P₃).



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

- Molecule 3 is ISOCITRIC ACID (CCD ID: ICT) (formula: C₆H₈O₇).



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

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Ca	0	0
			1	1		

- Molecule 5 is water.

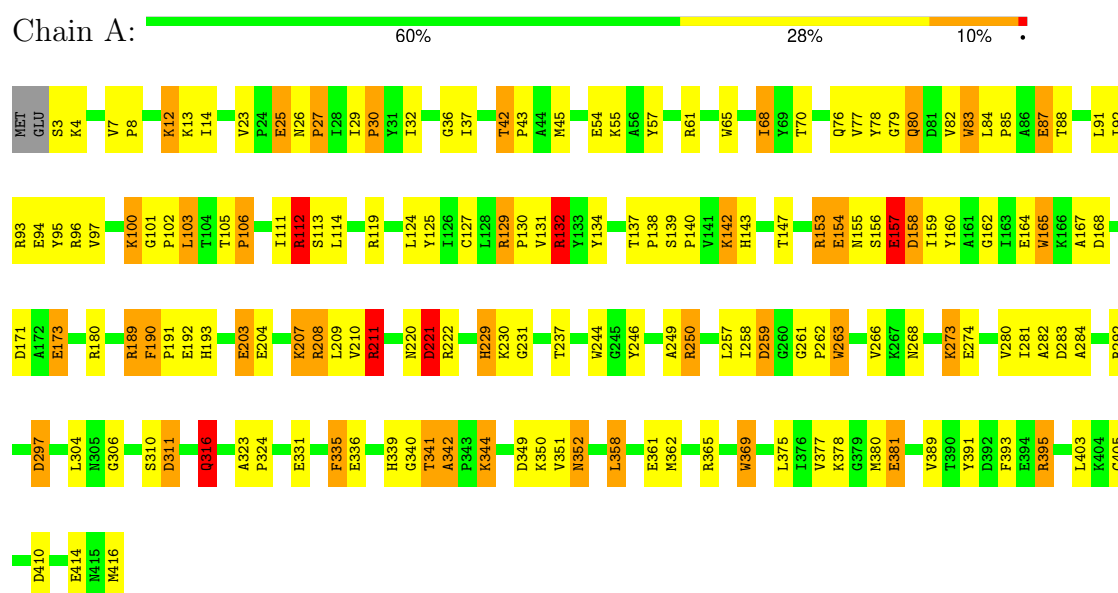
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	304	Total	O	0	0
			304	304		

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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



4 Data and refinement statistics

Xtriage (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	102.30Å 102.30Å 150.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 1.90	Depositor
% Data completeness (in resolution range)	98.6 (50.00-1.90)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
Refinement program	X-PLOR 3.8	Depositor
R, R_{free}	0.191 , 0.215	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3562	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ICT, CA, NAP

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.51	44/3257 (1.4%)	1.88	94/4405 (2.1%)

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	A	0	9

All (44) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	154	GLU	C-N	24.09	1.70	1.33
1	A	165	TRP	C-N	-12.01	1.16	1.33
1	A	83	TRP	NE1-CE2	10.52	1.49	1.37
1	A	65	TRP	NE1-CE2	10.49	1.49	1.37
1	A	165	TRP	NE1-CE2	10.44	1.49	1.37
1	A	369	TRP	NE1-CE2	10.41	1.49	1.37
1	A	263	TRP	NE1-CE2	10.39	1.48	1.37
1	A	244	TRP	NE1-CE2	10.38	1.48	1.37
1	A	210	VAL	C-N	-10.18	1.20	1.33
1	A	164	GLU	C-N	9.69	1.47	1.33
1	A	129	ARG	C-N	-9.37	1.24	1.33
1	A	29	ILE	C-N	-8.79	1.24	1.33
1	A	190	PHE	C-N	-8.25	1.23	1.34
1	A	7	VAL	C-N	-7.92	1.24	1.33
1	A	311	ASP	C-N	7.72	1.44	1.33
1	A	143	HIS	C-N	-7.68	1.24	1.33
1	A	137	THR	C-N	-7.60	1.25	1.33
1	A	352	ASN	C-N	-7.19	1.27	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	92	ILE	C-N	6.74	1.43	1.34
1	A	101	GLY	C-N	-6.35	1.25	1.33
1	A	23	VAL	C-N	-6.27	1.25	1.33
1	A	262	PRO	C-N	6.21	1.41	1.33
1	A	306	GLY	C-N	6.11	1.41	1.33
1	A	139	SER	C-N	-6.06	1.26	1.34
1	A	237	THR	C-N	5.93	1.41	1.33
1	A	173	GLU	C-N	-5.91	1.25	1.33
1	A	403	LEU	C-N	5.87	1.42	1.33
1	A	105	THR	C-N	-5.83	1.25	1.33
1	A	114	LEU	C-N	5.78	1.41	1.33
1	A	377	VAL	C-N	-5.77	1.26	1.33
1	A	54	GLU	C-N	-5.72	1.26	1.33
1	A	229	HIS	C-N	-5.72	1.25	1.33
1	A	268	ASN	C-N	-5.63	1.25	1.33
1	A	310	SER	C-N	-5.60	1.26	1.33
1	A	84	LEU	C-N	-5.41	1.26	1.33
1	A	280	VAL	C-N	-5.40	1.27	1.33
1	A	147	THR	C-N	-5.30	1.25	1.34
1	A	191	PRO	C-N	5.18	1.40	1.33
1	A	282	ALA	C-N	5.17	1.41	1.34
1	A	65	TRP	C-N	-5.15	1.26	1.33
1	A	83	TRP	C-N	-5.07	1.27	1.33
1	A	249	ALA	C-N	5.06	1.40	1.33
1	A	323	ALA	C-N	-5.04	1.27	1.33
1	A	102	PRO	C-N	-5.00	1.26	1.33

All (94) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	157	GLU	O-C-N	-28.87	85.62	123.15
1	A	190	PHE	CA-C-N	10.08	129.88	119.19
1	A	190	PHE	C-N-CA	10.08	129.88	119.19
1	A	342	ALA	O-C-N	-9.82	117.01	121.53
1	A	164	GLU	O-C-N	-9.82	112.91	123.42
1	A	164	GLU	CA-C-N	9.36	137.51	122.81
1	A	164	GLU	C-N-CA	9.36	137.51	122.81
1	A	132	ARG	O-C-N	-8.95	112.34	123.17
1	A	311	ASP	O-C-N	-8.47	113.15	122.12
1	A	292	ARG	CA-C-N	8.36	128.33	119.05
1	A	292	ARG	C-N-CA	8.36	128.33	119.05
1	A	139	SER	CA-C-N	8.18	127.82	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	139	SER	C-N-CA	8.18	127.82	119.56
1	A	342	ALA	CA-C-N	8.01	128.09	119.28
1	A	342	ALA	C-N-CA	8.01	128.09	119.28
1	A	84	LEU	CA-C-N	7.79	127.79	119.76
1	A	84	LEU	C-N-CA	7.79	127.79	119.76
1	A	143	HIS	CA-C-N	7.71	127.76	119.28
1	A	143	HIS	C-N-CA	7.71	127.76	119.28
1	A	323	ALA	CA-C-N	7.38	127.34	120.03
1	A	323	ALA	C-N-CA	7.38	127.34	120.03
1	A	210	VAL	CA-C-N	7.34	130.44	120.38
1	A	210	VAL	C-N-CA	7.34	130.44	120.38
1	A	101	GLY	CA-C-N	7.29	127.27	119.76
1	A	101	GLY	C-N-CA	7.29	127.27	119.76
1	A	105	THR	CA-C-N	7.09	127.09	119.78
1	A	105	THR	C-N-CA	7.09	127.09	119.78
1	A	26	ASN	CA-C-N	6.98	127.53	119.99
1	A	26	ASN	C-N-CA	6.98	127.53	119.99
1	A	282	ALA	O-C-N	-6.94	114.87	122.09
1	A	157	GLU	CA-C-N	6.93	134.78	121.54
1	A	157	GLU	C-N-CA	6.93	134.78	121.54
1	A	23	VAL	CA-C-N	6.93	127.33	119.92
1	A	23	VAL	C-N-CA	6.93	127.33	119.92
1	A	68	ILE	CA-C-N	-6.85	111.94	122.62
1	A	68	ILE	C-N-CA	-6.85	111.94	122.62
1	A	154	GLU	CA-C-N	-6.79	111.69	122.29
1	A	154	GLU	C-N-CA	-6.79	111.69	122.29
1	A	3	SER	O-C-N	-6.75	112.19	123.00
1	A	42	THR	CA-C-N	6.68	126.93	119.32
1	A	42	THR	C-N-CA	6.68	126.93	119.32
1	A	221	ASP	CA-C-N	-6.38	109.97	122.02
1	A	221	ASP	C-N-CA	-6.38	109.97	122.02
1	A	259	ASP	CB-CA-C	-6.27	109.36	116.63
1	A	352	ASN	CA-C-N	6.12	127.24	120.45
1	A	352	ASN	C-N-CA	6.12	127.24	120.45
1	A	82	VAL	N-CA-C	6.09	112.73	106.21
1	A	131	VAL	CA-C-N	-5.99	112.50	122.21
1	A	131	VAL	C-N-CA	-5.99	112.50	122.21
1	A	80	GLN	O-C-N	-5.93	114.70	122.59
1	A	316	GLN	O-C-N	-5.90	114.32	122.46
1	A	268	ASN	CA-C-N	5.89	126.31	119.47
1	A	268	ASN	C-N-CA	5.89	126.31	119.47
1	A	30	PRO	N-CA-CB	5.87	108.23	103.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	132	ARG	CD-NE-CZ	-5.86	116.20	124.40
1	A	266	VAL	CA-C-N	-5.83	113.17	121.50
1	A	266	VAL	C-N-CA	-5.83	113.17	121.50
1	A	211	ARG	CD-NE-CZ	-5.80	116.28	124.40
1	A	130	PRO	N-CA-CB	5.80	107.94	103.30
1	A	42	THR	O-C-N	-5.72	115.86	120.38
1	A	231	GLY	O-C-N	-5.72	116.22	122.68
1	A	138	PRO	N-CA-CB	5.70	108.24	103.17
1	A	207	LYS	CA-C-N	-5.68	111.21	121.14
1	A	207	LYS	C-N-CA	-5.68	111.21	121.14
1	A	106	PRO	N-CA-CB	5.58	108.20	103.35
1	A	137	THR	CA-C-N	5.58	126.45	119.98
1	A	137	THR	C-N-CA	5.58	126.45	119.98
1	A	208	ARG	CD-NE-CZ	-5.50	116.69	124.40
1	A	102	PRO	N-CA-CB	5.47	108.18	103.31
1	A	85	PRO	N-CA-CB	5.45	108.16	103.31
1	A	79	GLY	CA-C-N	5.38	131.81	121.54
1	A	79	GLY	C-N-CA	5.38	131.81	121.54
1	A	112	ARG	CD-NE-CZ	-5.34	116.92	124.40
1	A	129	ARG	CA-C-N	5.33	126.79	120.23
1	A	129	ARG	C-N-CA	5.33	126.79	120.23
1	A	78	TYR	O-C-N	-5.22	115.49	122.49
1	A	93	ARG	CD-NE-CZ	-5.22	117.09	124.40
1	A	229	HIS	CA-CB-CG	-5.20	108.60	113.80
1	A	7	VAL	CA-C-N	5.18	125.42	119.83
1	A	7	VAL	C-N-CA	5.18	125.42	119.83
1	A	189	ARG	CD-NE-CZ	-5.17	117.16	124.40
1	A	119	ARG	CD-NE-CZ	-5.13	117.21	124.40
1	A	292	ARG	CD-NE-CZ	-5.12	117.23	124.40
1	A	153	ARG	CD-NE-CZ	-5.11	117.24	124.40
1	A	190	PHE	O-C-N	-5.10	115.26	121.02
1	A	395	ARG	CD-NE-CZ	-5.09	117.28	124.40
1	A	180	ARG	CD-NE-CZ	-5.07	117.31	124.40
1	A	335	PHE	O-C-N	-5.06	117.39	123.06
1	A	129	ARG	CD-NE-CZ	-5.06	117.31	124.40
1	A	365	ARG	CD-NE-CZ	-5.06	117.31	124.40
1	A	8	PRO	N-CA-CB	5.02	107.79	103.27
1	A	130	PRO	O-C-N	-5.02	117.70	123.03
1	A	250	ARG	CD-NE-CZ	-5.01	117.38	124.40
1	A	27	PRO	N-CA-CB	5.00	107.94	103.19

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	132	ARG	Mainchain
1	A	157	GLU	Mainchain
1	A	211	ARG	Mainchain
1	A	230	LYS	Mainchain
1	A	297	ASP	Mainchain
1	A	311	ASP	Mainchain
1	A	316	GLN	Mainchain
1	A	331	GLU	Mainchain
1	A	350	LYS	Mainchain

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	3196	0	3221	157	3
2	A	48	0	24	21	0
3	A	13	0	4	2	0
4	A	1	0	0	0	0
5	A	304	0	0	23	0
All	All	3562	0	3249	160	3

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 25.

All (160) 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:154:GLU:C	1:A:155:ASN:N	1.70	1.50
1:A:344:LYS:CE	5:A:470:HOH:O	1.77	1.25
1:A:37:ILE:HD12	1:A:351:VAL:CG1	1.69	1.22
1:A:37:ILE:CD1	1:A:351:VAL:HG11	1.79	1.11
1:A:36:GLY:HA3	1:A:341:THR:HG23	1.30	1.06
1:A:220:ASN:OD1	5:A:610:HOH:O	1.73	1.06
1:A:203:GLU:OE1	5:A:599:HOH:O	1.73	1.05
1:A:37:ILE:CG2	1:A:351:VAL:HG21	1.87	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:344:LYS:HE2	5:A:470:HOH:O	1.43	1.04
1:A:220:ASN:OD1	1:A:220:ASN:O	1.75	1.03
1:A:156:SER:OG	5:A:686:HOH:O	1.76	1.02
1:A:220:ASN:ND2	5:A:711:HOH:O	1.71	1.01
1:A:87:GLU:HA	1:A:87:GLU:OE1	1.66	0.93
1:A:273:LYS:HZ2	1:A:273:LYS:HA	1.35	0.90
1:A:341:THR:H	2:A:417:NAP:C5D	1.85	0.90
1:A:395:ARG:NE	5:A:483:HOH:O	1.99	0.89
1:A:157:GLU:O	1:A:158:ASP:CB	2.18	0.88
1:A:37:ILE:CB	1:A:351:VAL:HG21	2.02	0.87
1:A:36:GLY:HA3	1:A:341:THR:CG2	2.04	0.87
1:A:87:GLU:OE1	1:A:87:GLU:CA	2.23	0.86
1:A:283:ASP:OD1	1:A:284:ALA:N	2.09	0.85
1:A:250:ARG:HB3	1:A:250:ARG:NH1	1.90	0.85
1:A:273:LYS:HA	1:A:273:LYS:NZ	1.92	0.85
1:A:142:LYS:HB2	1:A:142:LYS:HZ3	1.42	0.84
1:A:341:THR:HB	2:A:417:NAP:H52N	1.57	0.84
1:A:37:ILE:HB	1:A:351:VAL:HG21	1.59	0.83
1:A:100:LYS:HE3	1:A:336:GLU:HB2	1.61	0.82
1:A:273:LYS:HD2	5:A:638:HOH:O	1.77	0.82
1:A:37:ILE:HG21	1:A:351:VAL:HG21	1.60	0.80
1:A:339:HIS:CE1	2:A:417:NAP:H61A	1.98	0.80
1:A:36:GLY:CA	1:A:341:THR:HG23	2.11	0.79
1:A:87:GLU:OE1	1:A:87:GLU:O	2.01	0.79
1:A:395:ARG:NH2	5:A:483:HOH:O	2.13	0.79
1:A:13:LYS:HE2	1:A:94:GLU:O	1.83	0.78
1:A:142:LYS:HB2	1:A:142:LYS:NZ	1.99	0.77
1:A:351:VAL:HG23	5:A:486:HOH:O	1.87	0.75
1:A:341:THR:N	2:A:417:NAP:C5D	2.51	0.74
1:A:352:ASN:HB3	2:A:417:NAP:N1A	2.02	0.73
1:A:165:TRP:CD1	1:A:171:ASP:HB3	2.23	0.73
1:A:154:GLU:C	1:A:155:ASN:CA	2.62	0.73
1:A:209:LEU:C	1:A:209:LEU:HD13	2.13	0.73
1:A:273:LYS:HA	1:A:273:LYS:CE	2.15	0.72
1:A:37:ILE:HD12	1:A:351:VAL:HG11	0.83	0.72
1:A:273:LYS:HE3	1:A:274:GLU:N	2.05	0.71
1:A:211:ARG:HD2	5:A:613:HOH:O	1.92	0.70
1:A:250:ARG:HB3	1:A:250:ARG:HH11	1.54	0.69
1:A:37:ILE:HG21	1:A:351:VAL:CG2	2.23	0.68
1:A:341:THR:CB	2:A:417:NAP:H52N	2.23	0.68
1:A:324:PRO:HB3	1:A:358:LEU:HB3	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:341:THR:N	2:A:417:NAP:H51N	2.09	0.68
1:A:341:THR:HB	2:A:417:NAP:C5D	2.26	0.66
2:A:417:NAP:H4N	3:A:418:ICT:H2	1.76	0.66
1:A:37:ILE:CG2	1:A:351:VAL:CG2	2.71	0.66
1:A:273:LYS:HE3	1:A:274:GLU:H	1.61	0.66
1:A:342:ALA:H	2:A:417:NAP:H51N	1.62	0.65
1:A:112:ARG:CG	1:A:112:ARG:HH11	2.09	0.65
1:A:87:GLU:OE1	1:A:87:GLU:C	2.40	0.65
1:A:132:ARG:NH1	1:A:134:TYR:OH	2.30	0.64
2:A:417:NAP:C4N	3:A:418:ICT:H2	2.28	0.64
1:A:344:LYS:CD	5:A:470:HOH:O	2.24	0.64
1:A:341:THR:H	2:A:417:NAP:C4D	2.10	0.64
1:A:250:ARG:NH1	1:A:250:ARG:CB	2.59	0.63
1:A:42:THR:N	1:A:43:PRO:HD2	2.14	0.63
1:A:157:GLU:O	1:A:158:ASP:HB3	1.99	0.63
1:A:127:CYS:HB3	1:A:153:ARG:HB3	1.82	0.62
1:A:344:LYS:HD3	5:A:470:HOH:O	1.94	0.62
1:A:12:LYS:NZ	1:A:12:LYS:HB2	2.15	0.62
1:A:127:CYS:HB2	1:A:155:ASN:OD1	2.01	0.61
1:A:157:GLU:O	1:A:158:ASP:HB2	2.01	0.61
1:A:395:ARG:HH22	2:A:417:NAP:P2B	2.23	0.61
1:A:221:ASP:N	1:A:221:ASP:OD1	2.34	0.60
1:A:220:ASN:C	1:A:221:ASP:OD1	2.45	0.60
1:A:258:ILE:O	1:A:259:ASP:HB2	2.01	0.59
1:A:37:ILE:CD1	1:A:351:VAL:CG1	2.59	0.59
1:A:410:ASP:O	1:A:414:GLU:HG3	2.03	0.58
1:A:395:ARG:CZ	5:A:483:HOH:O	2.34	0.58
1:A:70:THR:CG2	1:A:103:LEU:HD21	2.34	0.57
1:A:220:ASN:C	1:A:221:ASP:CG	2.72	0.57
1:A:341:THR:H	2:A:417:NAP:H51N	1.61	0.57
1:A:106:PRO:HG2	1:A:111:ILE:HD12	1.87	0.57
1:A:112:ARG:HG3	1:A:112:ARG:NH1	2.19	0.57
1:A:162:GLY:HA2	5:A:755:HOH:O	2.05	0.57
1:A:160:TYR:HE1	1:A:304:LEU:HD12	1.69	0.56
1:A:208:ARG:HA	1:A:211:ARG:NH1	2.21	0.56
1:A:220:ASN:CG	1:A:222:ARG:HD3	2.31	0.55
1:A:273:LYS:CE	1:A:274:GLU:H	2.18	0.55
1:A:250:ARG:CB	1:A:250:ARG:CZ	2.85	0.54
1:A:160:TYR:HE1	1:A:304:LEU:CD1	2.21	0.54
1:A:167:ALA:O	1:A:168:ASP:HB2	2.07	0.54
1:A:57:TYR:CE1	1:A:61:ARG:NH1	2.75	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:4:LYS:HD2	1:A:77:VAL:HG13	1.90	0.53
1:A:358:LEU:HD22	1:A:380:MET:HE2	1.89	0.53
1:A:142:LYS:NZ	1:A:142:LYS:CB	2.67	0.53
1:A:32:ILE:HB	1:A:100:LYS:CB	2.39	0.53
1:A:45:MET:SD	1:A:45:MET:C	2.92	0.52
1:A:273:LYS:CE	1:A:273:LYS:CA	2.85	0.52
1:A:100:LYS:HE3	1:A:336:GLU:CB	2.38	0.51
1:A:57:TYR:CG	1:A:61:ARG:HD2	2.46	0.51
1:A:209:LEU:C	1:A:209:LEU:CD1	2.82	0.50
1:A:160:TYR:CE1	1:A:304:LEU:CD1	2.94	0.50
1:A:30:PRO:HD2	1:A:97:VAL:O	2.11	0.49
1:A:381:GLU:HB3	5:A:569:HOH:O	2.11	0.49
1:A:95:TYR:O	1:A:96:ARG:HB2	2.12	0.49
1:A:55:LYS:HD3	1:A:375:LEU:HD13	1.93	0.49
1:A:369:TRP:CD1	1:A:369:TRP:N	2.81	0.49
1:A:155:ASN:O	5:A:529:HOH:O	2.20	0.48
1:A:283:ASP:OD1	1:A:283:ASP:C	2.52	0.48
1:A:160:TYR:CE1	1:A:304:LEU:HD12	2.46	0.48
1:A:341:THR:CA	2:A:417:NAP:H52N	2.43	0.48
1:A:125:TYR:C	1:A:155:ASN:HB2	2.38	0.48
1:A:124:LEU:O	1:A:155:ASN:HB3	2.14	0.48
1:A:344:LYS:HE3	5:A:470:HOH:O	1.73	0.48
1:A:13:LYS:CE	1:A:94:GLU:O	2.59	0.48
1:A:158:ASP:OD1	1:A:159:ILE:N	2.42	0.47
1:A:391:TYR:O	1:A:395:ARG:HG2	2.15	0.47
1:A:273:LYS:NZ	1:A:274:GLU:H	2.13	0.47
1:A:209:LEU:HD13	1:A:209:LEU:O	2.16	0.46
1:A:12:LYS:HB2	1:A:12:LYS:HZ3	1.79	0.46
1:A:70:THR:HG21	1:A:103:LEU:HD21	1.96	0.46
1:A:263:TRP:CD1	1:A:263:TRP:N	2.81	0.46
1:A:341:THR:CG2	1:A:341:THR:O	2.63	0.46
1:A:156:SER:HB3	5:A:545:HOH:O	2.16	0.46
1:A:211:ARG:HD2	1:A:211:ARG:HH11	1.59	0.46
1:A:349:ASP:OD1	1:A:405:CYS:HB3	2.15	0.46
1:A:220:ASN:ND2	5:A:590:HOH:O	2.49	0.46
1:A:378:LYS:HD3	1:A:416:MET:OXT	2.15	0.46
1:A:165:TRP:CD1	1:A:171:ASP:CB	2.97	0.45
2:A:417:NAP:H6N	2:A:417:NAP:H2D	1.73	0.45
1:A:257:LEU:HD11	1:A:261:GLY:CA	2.46	0.45
1:A:341:THR:O	1:A:342:ALA:C	2.59	0.45
1:A:156:SER:C	5:A:530:HOH:O	2.60	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:192:GLU:O	1:A:193:HIS:C	2.60	0.45
1:A:342:ALA:H	2:A:417:NAP:C5D	2.27	0.44
1:A:335:PHE:CD1	1:A:335:PHE:N	2.85	0.44
1:A:342:ALA:N	2:A:417:NAP:C5D	2.81	0.44
1:A:246:TYR:O	1:A:250:ARG:HG3	2.17	0.43
1:A:339:HIS:HB2	2:A:417:NAP:N7A	2.33	0.43
1:A:32:ILE:HB	1:A:100:LYS:HB2	2.00	0.43
1:A:76:GLN:OE1	1:A:76:GLN:CA	2.66	0.43
1:A:83:TRP:CE2	1:A:106:PRO:HG3	2.53	0.43
1:A:203:GLU:OE1	1:A:207:LYS:HD2	2.18	0.43
1:A:173:GLU:HG2	5:A:465:HOH:O	2.19	0.42
1:A:324:PRO:HB2	1:A:362:MET:SD	2.59	0.42
1:A:207:LYS:O	1:A:211:ARG:CB	2.68	0.42
1:A:340:GLY:HA2	2:A:417:NAP:N1N	2.33	0.42
1:A:389:VAL:HG21	1:A:393:PHE:HB3	2.00	0.42
1:A:112:ARG:HH11	1:A:112:ARG:HG3	1.81	0.42
1:A:112:ARG:O	1:A:113:SER:C	2.63	0.42
1:A:129:ARG:HH11	1:A:129:ARG:HD2	1.64	0.42
1:A:358:LEU:HD12	1:A:358:LEU:HA	1.75	0.42
1:A:4:LYS:CD	1:A:77:VAL:HG13	2.49	0.41
1:A:13:LYS:HG2	1:A:14:ILE:O	2.20	0.41
1:A:339:HIS:CG	2:A:417:NAP:H61A	2.38	0.41
1:A:112:ARG:NH1	5:A:746:HOH:O	2.50	0.41
1:A:68:ILE:HD12	1:A:88:THR:HG23	2.01	0.41
1:A:222:ARG:HB3	1:A:297:ASP:OD2	2.21	0.41
1:A:358:LEU:CD1	1:A:380:MET:HG3	2.52	0.40
1:A:229:HIS:O	1:A:281:ILE:HA	2.22	0.40
1:A:25:GLU:C	1:A:27:PRO:HD3	2.46	0.40
1:A:358:LEU:O	1:A:361:GLU:HB3	2.22	0.40

All (3) 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:190:PHE:CE1	1:A:204:GLU:OE1[7_555]	1.96	0.24
1:A:140:PRO:O	1:A:142:LYS:NZ[7_555]	2.08	0.12
1:A:157:GLU:OE2	1:A:189:ARG:CB[7_555]	2.11	0.09

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	412/416 (99%)	394 (96%)	16 (4%)	2 (0%)	24	16

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	158	ASP
1	A	80	GLN

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	336/338 (99%)	319 (95%)	17 (5%)	21	13

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	LYS
1	A	25	GLU
1	A	87	GLU
1	A	91	LEU
1	A	100	LYS
1	A	103	LEU
1	A	112	ARG
1	A	132	ARG
1	A	142	LYS

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Mol	Chain	Res	Type
1	A	203	GLU
1	A	221	ASP
1	A	273	LYS
1	A	316	GLN
1	A	341	THR
1	A	344	LYS
1	A	358	LEU
1	A	381	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	GLN
1	A	220	ASN
1	A	247	GLN

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](#)

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
2	NAP	A	417	-	50,52,52	3.48	19 (38%)	71,80,80	3.91	23 (32%)
3	ICT	A	418	4	12,12,12	2.81	6 (50%)	13,16,16	1.54	2 (15%)

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	NAP	A	417	-	-	14/35/67/67	0/5/5/5
3	ICT	A	418	4	-	10/16/16/16	-

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	417	NAP	PA-O3	-10.68	1.48	1.59
2	A	417	NAP	C4N-C3N	10.67	1.55	1.39
2	A	417	NAP	O2D-C2D	7.64	1.61	1.43
2	A	417	NAP	C5D-C4D	6.70	1.71	1.51
2	A	417	NAP	C5N-C4N	6.30	1.49	1.38
3	A	418	ICT	C3-C2	-6.27	1.46	1.54
2	A	417	NAP	O5D-C5D	-5.82	1.22	1.44
2	A	417	NAP	PN-O5D	5.26	1.80	1.59
2	A	417	NAP	O4D-C4D	-4.77	1.34	1.45
2	A	417	NAP	C2N-N1N	4.26	1.39	1.35
3	A	418	ICT	C4-C5	-4.19	1.40	1.51
2	A	417	NAP	O4D-C1D	-4.06	1.35	1.40
2	A	417	NAP	PN-O3	4.05	1.63	1.59
3	A	418	ICT	C3-C6	3.70	1.57	1.51
2	A	417	NAP	O2B-C2B	3.70	1.56	1.44
2	A	417	NAP	C3B-C4B	-3.68	1.43	1.53
2	A	417	NAP	O5B-C5B	3.35	1.57	1.44
2	A	417	NAP	C3N-C7N	-2.76	1.46	1.50
3	A	418	ICT	O4-C5	-2.66	1.22	1.30
2	A	417	NAP	C2N-C3N	2.49	1.42	1.39
2	A	417	NAP	C2D-C3D	2.22	1.59	1.53
2	A	417	NAP	PA-O1A	2.19	1.58	1.50
2	A	417	NAP	PA-O2A	-2.16	1.45	1.55
3	A	418	ICT	O2-C1	-2.15	1.23	1.30
3	A	418	ICT	C4-C3	-2.07	1.49	1.53

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	417	NAP	C4D-O4D-C1D	19.13	127.45	109.92
2	A	417	NAP	C5N-C4N-C3N	-17.02	103.63	120.36
2	A	417	NAP	C2N-C3N-C4N	8.56	128.22	118.26
2	A	417	NAP	C6N-C5N-C4N	6.38	128.65	119.45
2	A	417	NAP	C5D-C4D-C3D	5.28	134.20	115.21
2	A	417	NAP	O3-PA-O1A	5.12	126.11	110.70
2	A	417	NAP	O3D-C3D-C4D	4.84	124.98	111.08
2	A	417	NAP	C2B-C1B-N9A	4.55	121.23	113.75
2	A	417	NAP	C6N-N1N-C1D	-4.49	110.91	119.73
2	A	417	NAP	C2N-N1N-C1D	4.17	128.33	119.13
2	A	417	NAP	O3B-C3B-C4B	4.02	122.63	111.08
3	A	418	ICT	C3-C4-C5	4.00	121.43	113.95
2	A	417	NAP	O2N-PN-O3	3.82	117.59	107.27
2	A	417	NAP	C4N-C3N-C7N	-3.82	110.66	121.06
2	A	417	NAP	C3B-C2B-C1B	-3.78	95.57	102.81
2	A	417	NAP	O7N-C7N-N7N	-3.75	117.19	122.62
2	A	417	NAP	C2B-C3B-C4B	3.47	109.44	101.99
2	A	417	NAP	O2D-C2D-C3D	3.45	122.87	111.82
2	A	417	NAP	O4D-C4D-C3D	-3.10	99.01	105.15
2	A	417	NAP	O2B-C2B-C1B	-2.85	100.02	110.05
2	A	417	NAP	C3N-C7N-N7N	2.35	120.63	117.74
3	A	418	ICT	O5-C6-C3	-2.15	117.93	123.01
2	A	417	NAP	O5D-PN-O1N	-2.11	100.56	108.94
2	A	417	NAP	O7N-C7N-C3N	2.11	122.17	119.60
2	A	417	NAP	O4B-C4B-C3B	-2.08	101.03	105.15

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	417	NAP	C5D-O5D-PN-O1N
2	A	417	NAP	C5D-O5D-PN-O2N
2	A	417	NAP	O4D-C1D-N1N-C2N
2	A	417	NAP	O4D-C1D-N1N-C6N
2	A	417	NAP	C2D-C1D-N1N-C2N
2	A	417	NAP	C2D-C1D-N1N-C6N
3	A	418	ICT	C1-C2-C3-C4
3	A	418	ICT	C1-C2-C3-C6
3	A	418	ICT	O7-C2-C3-C4
3	A	418	ICT	C4-C3-C6-O5
2	A	417	NAP	C3B-C4B-C5B-O5B

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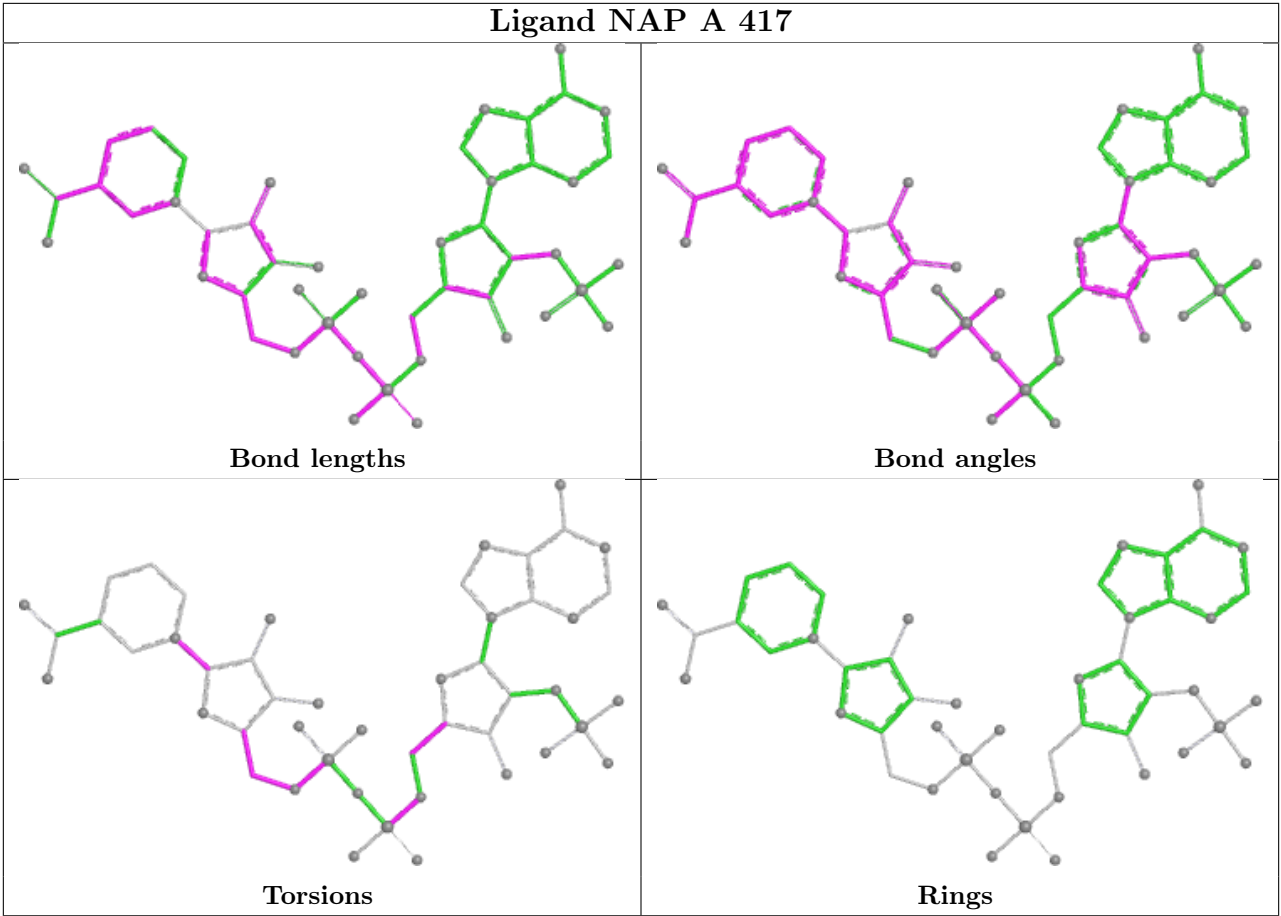
Mol	Chain	Res	Type	Atoms
2	A	417	NAP	O4D-C4D-C5D-O5D
2	A	417	NAP	C4D-C5D-O5D-PN
2	A	417	NAP	C3D-C4D-C5D-O5D
2	A	417	NAP	O4B-C4B-C5B-O5B
3	A	418	ICT	O1-C1-C2-C3
3	A	418	ICT	C6-C3-C4-C5
3	A	418	ICT	C4-C3-C6-O6
3	A	418	ICT	O7-C2-C3-C6
3	A	418	ICT	O2-C1-C2-C3
2	A	417	NAP	C5B-O5B-PA-O1A
2	A	417	NAP	C5B-O5B-PA-O2A
2	A	417	NAP	C5D-O5D-PN-O3
3	A	418	ICT	C2-C3-C4-C5

There are no ring outliers.

2 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	417	NAP	21	0
3	A	418	ICT	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 ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	154:GLU	C	155:ASN	N	1.70
1	A	165:TRP	C	166:LYS	N	1.16

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.