



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 11:57 AM UTC

PDB ID : 1HIV / pdb_00001hiv
Title : CRYSTAL STRUCTURE OF A COMPLEX OF HIV-1 PROTEASE WITH
A DIHYDROETHYLENE-CONTAINING INHIBITOR: COMPARISONS
WITH MOLECULAR MODELING
Authors : Thanki, N.; Wlodawer, A.
Deposited on : 1992-02-12
Resolution : 2.00 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)
Xtrriage (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)	:	2.49

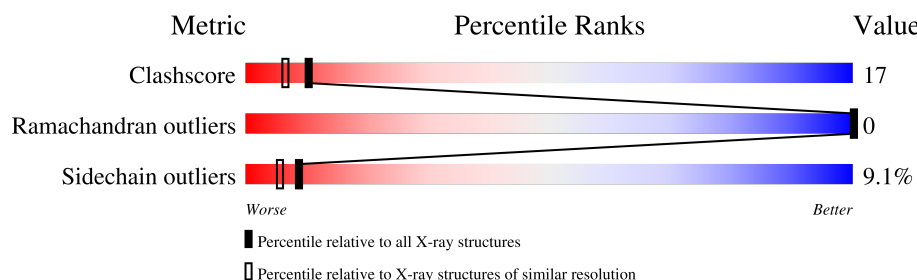
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)

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	99	37% 52% 7% .
1	B	99	45% 44% 9% .

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	1ZK	A	100	-	-	X	-

2 Entry composition (i)

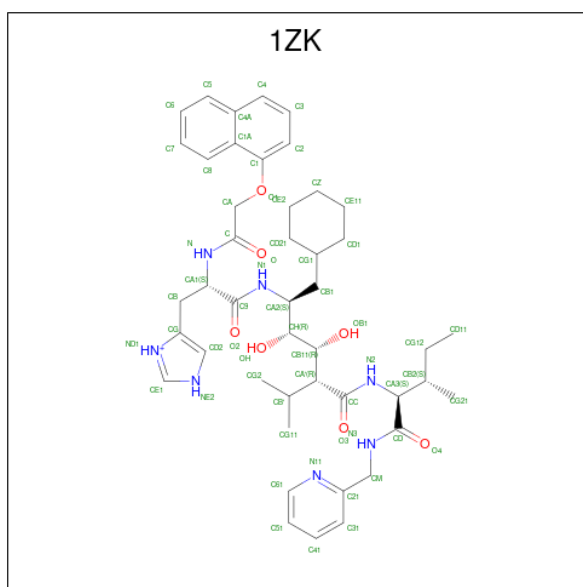
There are 3 unique types of molecules in this entry. The entry contains 1665 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 HIV-1 PROTEASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	99	Total 758	C 488	N 130	O 136	S 4	0	0	0
1	B	99	Total 758	C 488	N 130	O 136	S 4	0	0	0

- Molecule 2 is 4-[(2R)-3-[(1S,2S,3R,4S)-1-(cyclohexylmethyl)-2,3-dihydroxy-5-methyl-4-[(1S,2R)-2-methyl-1-[(pyridin-2-ylmethyl)carbamoyl]butyl]carbamoyl]hexyl]amino}-2-[(naphthalen-1-yloxy)acetyl]amino}-3-oxopropyl]-1H-imidazol-3-ium (CCD ID: 1ZK) (formula: C₄₅H₆₂N₇O₇).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			59	45	7	7		

- Molecule 3 is water.

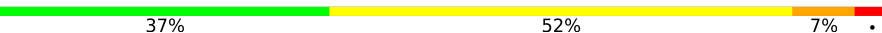
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	49	Total 49	O 49	0	0
3	B	41	Total 41	O 41	0	0

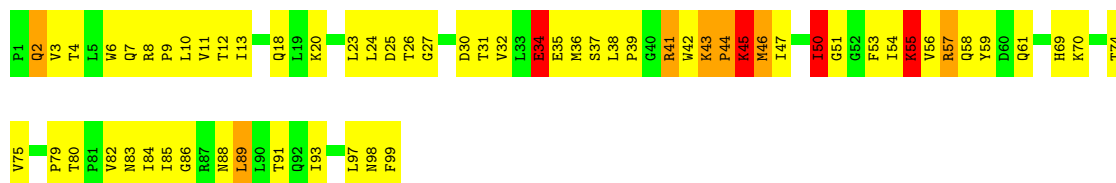
3 Residue-property plots

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.

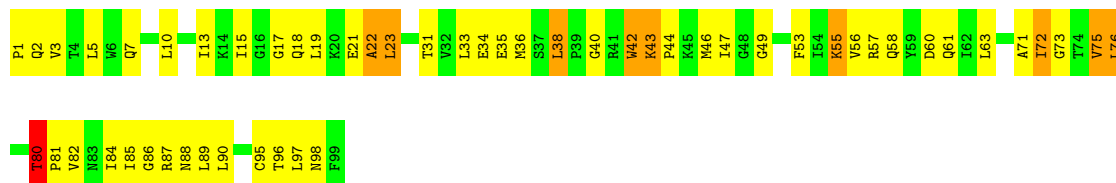
• Molecule 1: HIV-1 PROTEASE

Chain A: 



• Molecule 1: HIV-1 PROTEASE

Chain B: 



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	52.00Å 58.60Å 61.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.00	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.00)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.169 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1665	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: 1ZK, CSO

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	1.54	7/763 (0.9%)	2.68	73/1031 (7.1%)
1	B	1.52	2/763 (0.3%)	2.61	64/1031 (6.2%)
All	All	1.53	9/1526 (0.6%)	2.65	137/2062 (6.6%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	75	VAL	N-CA	6.42	1.53	1.46
1	A	31	THR	CA-CB	6.03	1.61	1.53
1	A	91	THR	CA-CB	6.02	1.62	1.53
1	A	93	ILE	C-N	-5.81	1.27	1.33
1	A	86	GLY	N-CA	5.64	1.50	1.44
1	A	74	THR	CA-CB	5.22	1.61	1.53
1	A	25	ASP	C-O	5.10	1.29	1.24
1	B	56	VAL	N-CA	5.07	1.52	1.46
1	A	80	THR	CA-CB	5.01	1.61	1.53

All (137) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	25	ASP	N-CA-CB	-11.25	93.73	110.84
1	A	85	ILE	CA-C-N	-10.68	112.92	122.43
1	A	85	ILE	C-N-CA	-10.68	112.92	122.43
1	B	84	ILE	O-C-N	10.22	134.04	123.20
1	A	88	ASN	OD1-CG-ND2	-9.76	112.84	122.60
1	A	50	ILE	CA-CB-CG2	9.13	126.02	110.50
1	A	61	GLN	OE1-CD-NE2	9.05	131.65	122.60
1	A	57	ARG	CD-NE-CZ	8.55	136.37	124.40
1	A	11	VAL	O-C-N	8.51	132.36	123.00
1	A	13	ILE	O-C-N	8.27	131.85	123.00

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	85	ILE	CA-C-N	-7.92	115.39	122.43
1	B	85	ILE	C-N-CA	-7.92	115.39	122.43
1	B	90	LEU	CA-C-O	-7.82	112.26	120.55
1	B	73	GLY	O-C-N	7.72	131.33	123.92
1	B	95	CYS	O-C-N	-7.71	113.45	122.93
1	B	33	LEU	O-C-N	7.71	132.87	123.16
1	A	89	LEU	CA-C-O	-7.69	110.72	119.41
1	B	80	THR	N-CA-CB	7.55	121.14	110.11
1	A	93	ILE	CA-C-N	7.53	134.88	120.66
1	A	93	ILE	C-N-CA	7.53	134.88	120.66
1	B	2	GLN	CA-C-O	-7.50	112.52	120.40
1	B	36	MET	CA-CB-CG	7.49	129.09	114.10
1	A	47	ILE	CA-C-O	-7.43	114.28	121.63
1	B	84	ILE	CA-C-O	-7.39	112.70	120.39
1	B	7	GLN	CB-CG-CD	7.36	125.12	112.60
1	B	53	PHE	CA-C-O	-7.29	112.94	121.46
1	B	80	THR	O-C-N	7.12	129.36	121.53
1	B	87	ARG	NE-CZ-NH2	7.01	125.51	119.20
1	A	43	LYS	O-C-N	6.91	128.49	121.72
1	A	31	THR	CA-CB-OG1	-6.84	99.34	109.60
1	B	23	LEU	O-C-N	6.83	131.08	123.16
1	A	53	PHE	CA-CB-CG	-6.82	106.98	113.80
1	B	7	GLN	CA-C-N	6.81	129.80	120.67
1	B	7	GLN	C-N-CA	6.81	129.80	120.67
1	B	40	GLY	CA-C-O	6.78	127.83	122.33
1	A	50	ILE	CA-C-O	-6.74	111.49	119.85
1	A	47	ILE	CA-C-N	6.71	126.81	122.18
1	A	47	ILE	C-N-CA	6.71	126.81	122.18
1	A	2	GLN	N-CA-CB	6.70	121.08	110.55
1	A	12	THR	CA-CB-OG1	-6.68	99.58	109.60
1	A	10	LEU	O-C-N	6.64	130.79	123.22
1	A	45	LYS	CA-C-O	-6.63	114.13	121.23
1	A	50	ILE	O-C-N	6.63	130.74	122.05
1	A	91	THR	CA-CB-OG1	-6.63	99.66	109.60
1	B	72	ILE	CA-C-N	-6.61	111.79	120.91
1	B	72	ILE	C-N-CA	-6.61	111.79	120.91
1	B	80	THR	CB-CA-C	-6.60	98.64	109.27
1	A	6	TRP	N-CA-C	-6.59	104.14	111.71
1	A	30	ASP	O-C-N	6.57	132.33	122.94
1	B	46	MET	CA-CB-CG	-6.52	101.06	114.10
1	B	31	THR	CA-CB-OG1	-6.52	99.82	109.60
1	A	58	GLN	OE1-CD-NE2	-6.39	116.21	122.60

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	7	GLN	CA-C-O	-6.37	113.89	121.60
1	B	87	ARG	CA-C-N	6.36	129.44	120.28
1	B	87	ARG	C-N-CA	6.36	129.44	120.28
1	A	97	LEU	CA-C-O	-6.33	113.81	121.28
1	A	88	ASN	CA-CB-CG	6.33	118.93	112.60
1	A	8	ARG	NE-CZ-NH2	6.32	124.89	119.20
1	B	95	CYS	CA-C-O	6.28	128.03	120.81
1	B	90	LEU	O-C-N	6.27	128.77	122.12
1	B	89	LEU	CA-C-O	-6.25	112.17	119.24
1	B	97	LEU	CA-C-O	-6.13	113.75	120.43
1	A	18	GLN	CA-C-O	-6.10	114.11	120.70
1	B	75	VAL	N-CA-CB	-6.09	101.45	111.44
1	A	38	LEU	CB-CA-C	6.08	117.99	108.63
1	A	35	GLU	CG-CD-OE2	-6.06	104.45	118.40
1	A	98	ASN	CB-CG-ND2	6.05	125.47	116.40
1	A	34	GLU	CA-CB-CG	5.99	126.08	114.10
1	B	75	VAL	CA-CB-CG1	5.99	120.58	110.40
1	A	39	PRO	CB-CA-C	5.93	118.72	110.95
1	A	3	VAL	CA-C-O	5.93	126.55	120.39
1	B	88	ASN	CB-CG-ND2	5.90	125.26	116.40
1	A	9	PRO	O-C-N	-5.88	114.69	122.64
1	A	75	VAL	CB-CA-C	5.88	118.91	110.33
1	B	35	GLU	CG-CD-OE2	-5.84	104.96	118.40
1	B	87	ARG	NH1-CZ-NH2	-5.77	111.80	119.30
1	A	31	THR	O-C-N	5.76	129.75	123.13
1	A	11	VAL	CA-C-O	-5.71	115.85	121.67
1	A	41	ARG	NE-CZ-NH2	5.71	124.34	119.20
1	B	58	GLN	CA-C-O	-5.70	114.27	120.36
1	A	13	ILE	CA-C-O	-5.69	114.68	121.28
1	A	44	PRO	CA-C-O	-5.66	114.52	121.31
1	A	38	LEU	N-CA-C	-5.65	102.32	110.40
1	B	76	LEU	CA-C-N	5.62	130.43	123.12
1	B	76	LEU	C-N-CA	5.62	130.43	123.12
1	B	61	GLN	CA-C-N	-5.59	115.89	122.93
1	B	61	GLN	C-N-CA	-5.59	115.89	122.93
1	B	95	CYS	CB-CA-C	5.58	118.82	109.89
1	A	70	LYS	CA-C-O	5.57	127.40	121.05
1	B	86	GLY	O-C-N	5.55	128.75	122.86
1	A	55	LYS	CA-C-O	-5.54	114.65	120.80
1	B	44	PRO	CB-CA-C	-5.50	103.78	110.98
1	B	56	VAL	CA-C-O	-5.49	116.26	121.64
1	B	7	GLN	OE1-CD-NE2	-5.49	117.11	122.60

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	24	LEU	CA-C-N	-5.48	115.07	122.86
1	A	24	LEU	C-N-CA	-5.48	115.07	122.86
1	A	43	LYS	CA-C-O	-5.48	113.60	120.23
1	A	98	ASN	OD1-CG-ND2	-5.44	117.16	122.60
1	B	2	GLN	O-C-N	5.42	130.27	123.12
1	B	47	ILE	O-C-N	5.42	128.62	122.98
1	A	41	ARG	NE-CZ-NH1	-5.40	116.10	121.50
1	B	19	LEU	CA-C-O	-5.39	114.82	120.80
1	A	32	VAL	CA-C-O	-5.37	114.81	120.39
1	A	74	THR	CA-CB-CG2	5.37	119.62	110.50
1	B	53	PHE	N-CA-C	5.30	118.22	109.85
1	A	74	THR	CA-CB-OG1	-5.28	101.68	109.60
1	B	38	LEU	CA-C-O	-5.28	115.76	120.19
1	A	46	MET	N-CA-CB	5.27	119.18	110.69
1	B	3	VAL	CA-CB-CG2	5.27	119.36	110.40
1	B	40	GLY	N-CA-C	5.23	117.39	111.85
1	A	38	LEU	O-C-N	5.21	127.54	121.39
1	A	69	HIS	CA-CB-CG	-5.20	108.60	113.80
1	A	23	LEU	CA-C-O	-5.19	114.95	120.92
1	A	59	TYR	N-CA-CB	5.19	118.72	110.57
1	B	17	GLY	CA-C-N	5.18	130.30	122.99
1	B	17	GLY	C-N-CA	5.18	130.30	122.99
1	B	60	ASP	CA-C-O	-5.17	115.31	121.16
1	A	88	ASN	CB-CG-ND2	5.17	124.15	116.40
1	A	30	ASP	CA-CB-CG	-5.16	107.44	112.60
1	A	45	LYS	CG-CD-CE	5.15	123.14	111.30
1	B	58	GLN	CB-CG-CD	-5.15	103.85	112.60
1	B	42	TRP	O-C-N	5.14	129.83	122.74
1	A	53	PHE	CA-C-N	-5.13	115.53	122.92
1	A	53	PHE	C-N-CA	-5.13	115.53	122.92
1	B	21	GLU	CA-C-O	-5.13	115.02	120.92
1	A	26	THR	CA-CB-OG1	-5.10	101.95	109.60
1	A	89	LEU	O-C-N	5.10	129.60	122.36
1	B	5	LEU	N-CA-CB	-5.08	102.80	110.92
1	A	34	GLU	N-CA-CB	5.07	117.61	110.36
1	A	56	VAL	O-C-N	5.07	128.58	122.95
1	B	19	LEU	CB-CA-C	5.07	117.99	109.48
1	B	34	GLU	CB-CA-C	-5.06	100.56	109.62
1	A	43	LYS	CA-C-N	5.05	124.81	119.76
1	A	43	LYS	C-N-CA	5.05	124.81	119.76
1	B	82	VAL	CA-C-N	-5.03	114.30	121.50
1	B	82	VAL	C-N-CA	-5.03	114.30	121.50

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	22	ALA	CA-C-O	-5.02	115.36	120.99

There are no chirality outliers.

There are no planarity outliers.

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	758	0	803	24	0
1	B	758	0	803	14	0
2	A	59	0	61	24	0
3	A	49	0	0	1	1
3	B	41	0	0	1	0
All	All	1665	0	1667	55	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 17.

All (55) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:100:1ZK:HD22	2:A:100:1ZK:CD21	0.97	1.12
2:A:100:1ZK:HE13	2:A:100:1ZK:CE11	0.97	1.12
2:A:100:1ZK:CD11	2:A:100:1ZK:HD14	0.97	1.10
2:A:100:1ZK:CD11	2:A:100:1ZK:HD11	0.97	1.08
2:A:100:1ZK:CD11	2:A:100:1ZK:HD15	0.97	1.06
2:A:100:1ZK:CE11	2:A:100:1ZK:HE12	0.97	1.06
2:A:100:1ZK:CD21	2:A:100:1ZK:HD23	0.97	1.05
2:A:100:1ZK:HD22	2:A:100:1ZK:HD23	1.56	0.88
2:A:100:1ZK:HE13	2:A:100:1ZK:HE12	1.56	0.88
2:A:100:1ZK:HD11	2:A:100:1ZK:CG12	2.04	0.86
2:A:100:1ZK:HD15	2:A:100:1ZK:CG12	2.04	0.86
2:A:100:1ZK:HD14	2:A:100:1ZK:CG12	2.04	0.86
2:A:100:1ZK:HD11	2:A:100:1ZK:HD15	1.58	0.85
2:A:100:1ZK:HD22	2:A:100:1ZK:CG1	2.05	0.85

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:100:1ZK:HE12	2:A:100:1ZK:CZ	2.06	0.85
2:A:100:1ZK:HD23	2:A:100:1ZK:CG1	2.05	0.85
2:A:100:1ZK:HE13	2:A:100:1ZK:CZ	2.06	0.85
2:A:100:1ZK:HD14	2:A:100:1ZK:HD15	1.58	0.84
2:A:100:1ZK:HD14	2:A:100:1ZK:HD11	1.58	0.83
2:A:100:1ZK:HD23	2:A:100:1ZK:CE2	2.08	0.83
2:A:100:1ZK:HD22	2:A:100:1ZK:CE2	2.08	0.82
2:A:100:1ZK:HE12	2:A:100:1ZK:CD1	2.09	0.81
2:A:100:1ZK:HE13	2:A:100:1ZK:CD1	2.09	0.80
1:B:80:THR:HG22	1:B:81:PRO:HD2	1.70	0.73
1:A:50:ILE:HD12	1:A:51:GLY:N	2.09	0.68
1:B:43:LYS:HD2	1:B:43:LYS:N	2.11	0.66
1:A:2:GLN:HE21	1:B:98:ASN:HD21	1.46	0.62
1:A:99:PHE:CZ	1:B:1:PRO:HG2	2.40	0.57
1:A:54:ILE:HD12	1:A:79:PRO:HD2	1.86	0.57
1:A:50:ILE:HD11	1:B:49:GLY:HA3	1.87	0.56
1:A:27:GLY:HA2	1:B:23:LEU:HD21	1.91	0.53
1:A:41:ARG:HG2	1:A:43:LYS:HZ3	1.74	0.53
1:A:41:ARG:HG2	1:A:43:LYS:NZ	2.26	0.51
1:A:20:LYS:HE3	1:A:36:MET:SD	2.52	0.49
1:A:44:PRO:CB	1:A:55:LYS:HE2	2.43	0.48
1:A:50:ILE:HD11	1:B:49:GLY:CA	2.43	0.48
1:A:34:GLU:HG3	3:A:363:HOH:O	2.14	0.48
1:A:34:GLU:HG2	1:A:83:ASN:OD1	2.13	0.48
1:A:42:TRP:CD2	1:A:57:ARG:HD2	2.50	0.47
1:A:44:PRO:HB3	1:A:55:LYS:HE2	1.98	0.46
1:B:63:LEU:HD12	1:B:71:ALA:O	2.16	0.46
1:A:50:ILE:HD12	1:A:51:GLY:H	1.81	0.46
1:A:50:ILE:HG12	2:A:100:1ZK:HD15	1.98	0.45
1:A:46:MET:SD	1:A:55:LYS:HG2	2.57	0.45
1:B:42:TRP:CD1	1:B:42:TRP:N	2.85	0.44
1:A:41:ARG:CG	1:A:43:LYS:NZ	2.81	0.44
1:A:46:MET:HB3	1:A:46:MET:HE3	1.67	0.44
1:B:57:ARG:O	1:B:76:LEU:HA	2.18	0.43
1:B:13:ILE:HD13	1:B:22:ALA:HB2	2.02	0.42
1:B:15:ILE:O	1:B:18:GLN:HB2	2.20	0.42
1:B:55:LYS:NZ	3:B:379:HOH:O	2.41	0.42
1:A:4:THR:HG22	1:B:96:THR:HG22	2.01	0.41
1:A:44:PRO:O	1:A:45:LYS:HE2	2.20	0.41
1:A:50:ILE:H	1:A:50:ILE:HG13	1.65	0.40
1:A:41:ARG:CG	1:A:43:LYS:HZ3	2.33	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)
3:A:316:HOH:O	3:A:386:HOH:O[2_455]	2.15	0.05

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	96/99 (97%)	95 (99%)	1 (1%)	0	100	100
1	B	96/99 (97%)	93 (97%)	3 (3%)	0	100	100
All	All	192/198 (97%)	188 (98%)	4 (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	Percentiles	
1	A	82/82 (100%)	74 (90%)	8 (10%)	7	5
1	B	82/82 (100%)	75 (92%)	7 (8%)	10	7
All	All	164/164 (100%)	149 (91%)	15 (9%)	9	6

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	GLU
1	A	37	SER
1	A	45	LYS
1	A	50	ILE
1	A	55	LYS
1	A	82	VAL
1	A	84	ILE
1	A	89	LEU
1	B	10	LEU
1	B	38	LEU
1	B	43	LYS
1	B	55	LYS
1	B	72	ILE
1	B	75	VAL
1	B	80	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2	GLN
1	A	61	GLN
1	A	88	ASN
1	A	98	ASN
1	B	2	GLN
1	B	88	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	CSO	B	67	1	3,6,7	0.67	0	1,6,8	0.81	0
1	CSO	A	67	1	3,6,7	0.80	0	1,6,8	1.67	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	CSO	B	67	1	-	0/1/5/7	-
1	CSO	A	67	1	-	0/1/5/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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	1ZK	A	100	-	63,63,63	1.05	3 (4%)	78,85,85	1.92	20 (25%)

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	1ZK	A	100	-	-	6/64/72/72	0/5/5/5

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	100	1ZK	OB1-CB11	-2.88	1.35	1.43
2	A	100	1ZK	CD2-NE2	2.58	1.43	1.36
2	A	100	1ZK	CM-N3	-2.07	1.42	1.46

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	100	1ZK	CM-N3-CD	6.10	130.66	122.29
2	A	100	1ZK	OH-CH-CA2	4.84	120.87	109.28
2	A	100	1ZK	CA-O1-C1	3.86	124.90	116.68
2	A	100	1ZK	CB2-CA3-N2	3.76	119.10	111.35
2	A	100	1ZK	CG12-CB2-CA3	3.72	120.51	111.17
2	A	100	1ZK	CE11-CD1-CG1	-3.44	104.85	112.08
2	A	100	1ZK	CB-CA1-N	3.43	117.17	110.64
2	A	100	1ZK	CB-CG-CD2	3.29	136.06	129.33
2	A	100	1ZK	CA1-CB-CG	-3.25	106.12	113.75
2	A	100	1ZK	CM-C21-N11	3.25	123.24	116.30
2	A	100	1ZK	CD-CA3-N2	-3.10	101.89	110.32
2	A	100	1ZK	C51-C41-C31	-2.95	116.60	120.24
2	A	100	1ZK	CG21-CB2-CG12	-2.79	104.77	111.81
2	A	100	1ZK	OB1-CB11-CA'	2.56	114.28	108.76
2	A	100	1ZK	CA-C-N	2.53	120.79	116.41
2	A	100	1ZK	CM-C21-C31	-2.48	115.95	121.47
2	A	100	1ZK	OH-CH-CB11	-2.43	103.78	109.46
2	A	100	1ZK	CA3-CD-N3	2.19	119.98	116.38
2	A	100	1ZK	O1-C1-C2	-2.14	119.74	124.45
2	A	100	1ZK	CA1-N-C	2.01	126.72	121.68

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	100	1ZK	N1-C9-CA1-N

Continued on next page...

Continued from previous page...

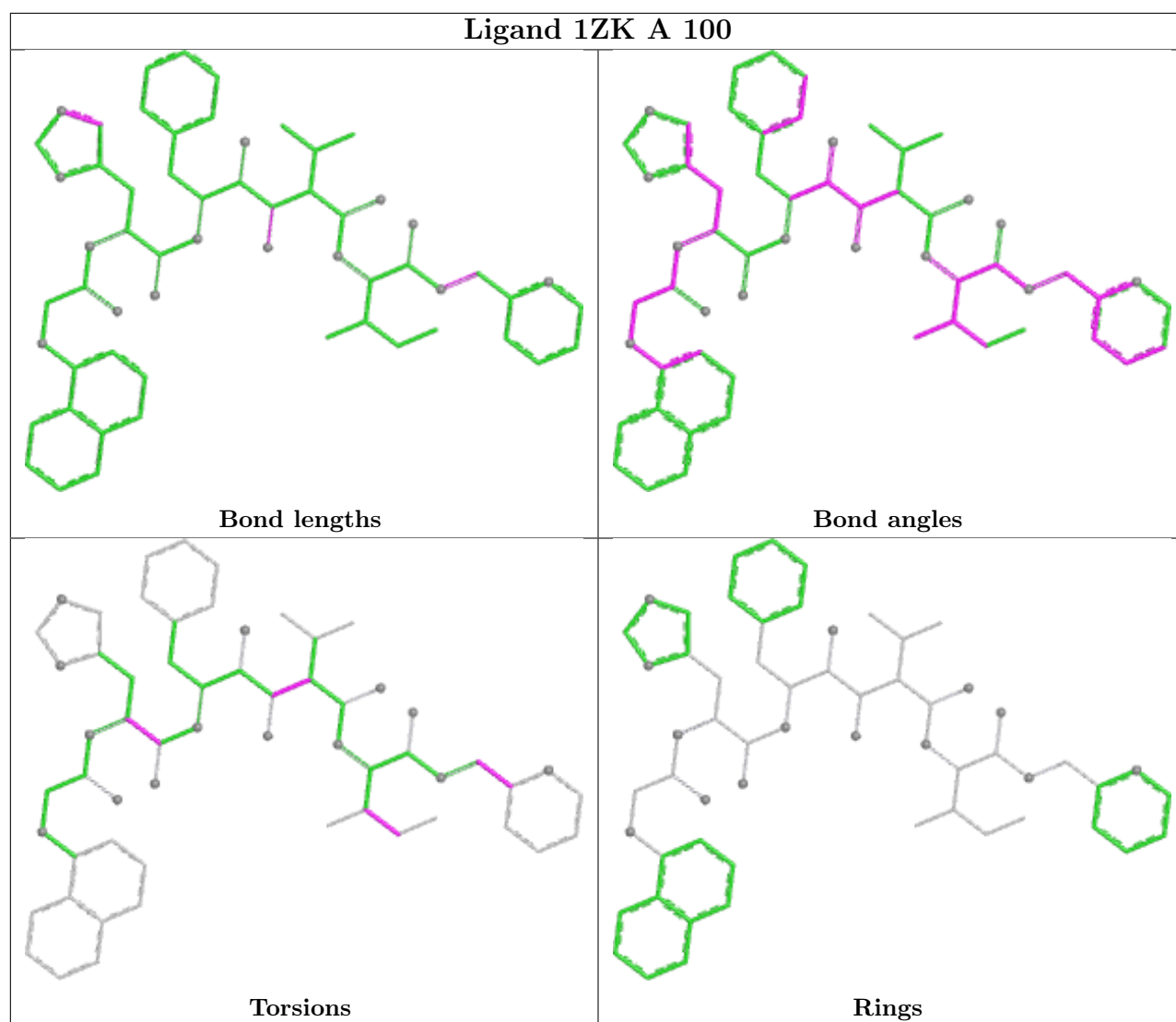
Mol	Chain	Res	Type	Atoms
2	A	100	1ZK	O2-C9-CA1-N
2	A	100	1ZK	CB'-CA'-CB11-OB1
2	A	100	1ZK	CA3-CB2-CG12-CD11
2	A	100	1ZK	C31-C21-CM-N3
2	A	100	1ZK	N11-C21-CM-N3

There are no ring outliers.

1 monomer is involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	100	1ZK	24	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [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.