



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:24 PM UTC

PDB ID : 1AVN / pdb_00001avn
Title : HUMAN CARBONIC ANHYDRASE II COMPLEXED WITH THE HISTAMINE ACTIVATOR
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Deposited on : 1997-09-17
Resolution : 2.00 Å(reported)

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

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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
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

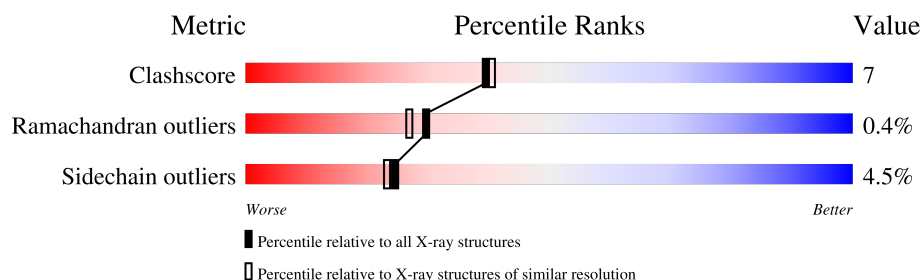
1 Overall quality at a glance

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	259	46% 46% 6% ..

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
5	HSM	A	264	-	-	X	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 2206 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 CARBONIC ANHYDRASE II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	257	Total	C	N	O	S	0	0	0
			2038	1308	350	378	2			

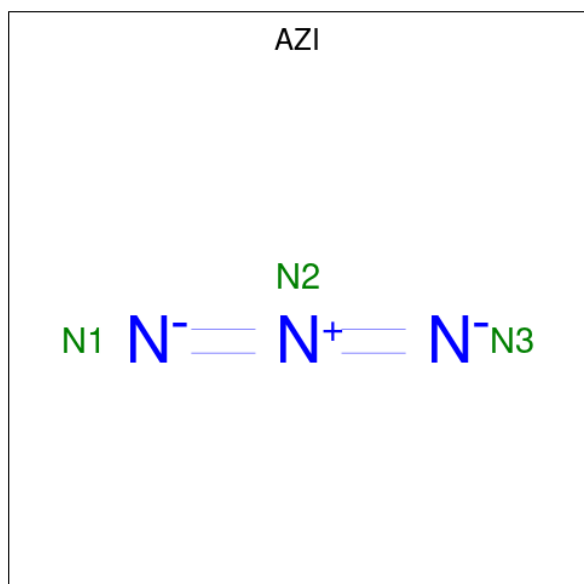
- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 3 is MERCURY (II) ION (CCD ID: HG) (formula: Hg).

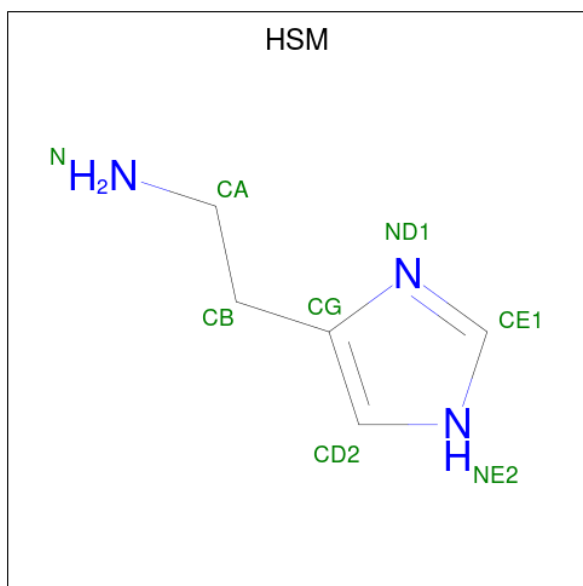
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Hg	0	0
			1	1		

- Molecule 4 is AZIDE ION (CCD ID: AZI) (formula: N₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total N 3 3	0	0

- Molecule 5 is HISTAMINE (CCD ID: HSM) (formula: $C_5H_9N_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C N 8 5 3	0	0

- Molecule 6 is water.

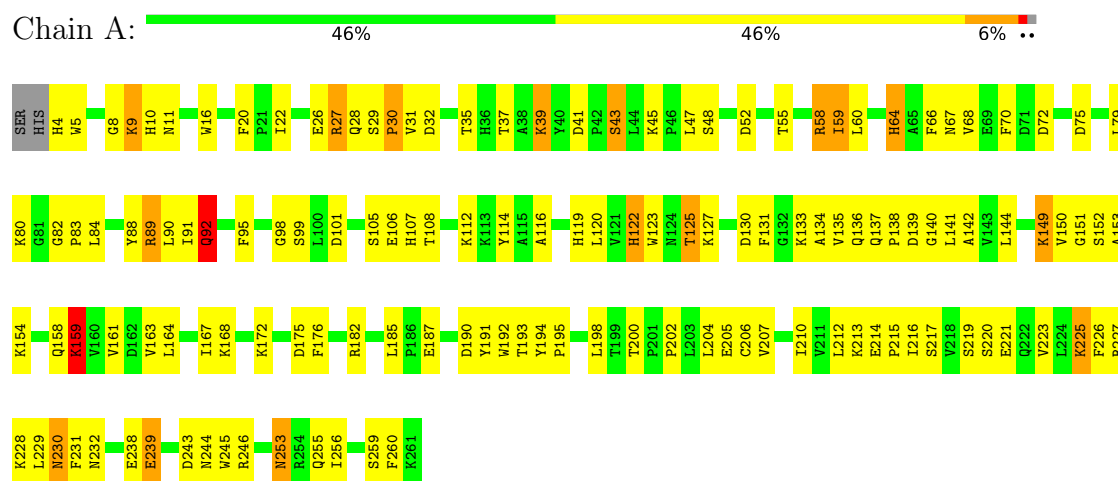
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	155	Total O 155 155	1	0

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: CARBONIC ANHYDRASE II



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	42.61Å 41.69Å 72.78Å 90.00° 104.24° 90.00°	Depositor
Resolution (Å)	15.00 – 2.00	Depositor
% Data completeness (in resolution range)	80.6 (15.00-2.00)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	0.09	Depositor
Refinement program	CCP4	Depositor
R, R_{free}	0.154 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2206	wwPDB-VP
Average B, all atoms (Å ²)	15.0	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: HSM, AZI, ZN, HG

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	1.38	10/2098 (0.5%)	3.10	191/2845 (6.7%)

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	125	THR	C-N	22.93	1.65	1.33
1	A	29	SER	CA-C	11.84	1.64	1.52
1	A	30	PRO	N-CD	9.95	1.61	1.47
1	A	30	PRO	N-CA	-7.51	1.37	1.47
1	A	29	SER	C-O	-6.90	1.17	1.24
1	A	4	HIS	N-CA	6.04	1.57	1.46
1	A	207	VAL	CA-C	-5.78	1.45	1.52
1	A	48	SER	C-O	-5.17	1.18	1.24
1	A	29	SER	N-CA	-5.15	1.41	1.45
1	A	90	LEU	C-N	-5.06	1.28	1.33

All (191) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	29	SER	O-C-N	49.88	160.45	121.55
1	A	29	SER	CA-C-N	44.06	174.92	119.84
1	A	29	SER	C-N-CA	44.06	174.92	119.84
1	A	30	PRO	N-CA-CB	23.27	127.68	103.25
1	A	30	PRO	CA-N-CD	-18.73	85.78	112.00
1	A	29	SER	CA-C-O	-15.66	105.14	120.64
1	A	58	ARG	CD-NE-CZ	12.69	142.16	124.40
1	A	75	ASP	CA-CB-CG	12.40	125.00	112.60
1	A	26	GLU	CB-CG-CD	11.44	132.04	112.60
1	A	185	LEU	CA-C-O	11.06	129.48	120.19
1	A	92	GLN	CA-C-O	-10.95	108.84	120.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	30	PRO	N-CD-CG	10.59	119.08	103.20
1	A	52	ASP	CA-CB-CG	10.32	122.92	112.60
1	A	39	LYS	CA-CB-CG	10.08	134.26	114.10
1	A	92	GLN	OE1-CD-NE2	-9.95	112.65	122.60
1	A	255	GLN	CA-CB-CG	9.82	133.74	114.10
1	A	207	VAL	N-CA-C	9.54	122.36	108.53
1	A	43	SER	CA-CB-OG	9.18	129.47	111.10
1	A	253	ASN	CA-CB-CG	-9.08	103.52	112.60
1	A	131	PHE	CA-C-N	8.99	129.96	119.98
1	A	131	PHE	C-N-CA	8.99	129.96	119.98
1	A	139	ASP	CA-CB-CG	8.92	121.52	112.60
1	A	16	TRP	O-C-N	8.90	132.63	122.22
1	A	228	LYS	CB-CG-CD	8.84	131.63	111.30
1	A	119	HIS	CA-CB-CG	8.81	122.61	113.80
1	A	29	SER	C-N-CD	-8.74	89.14	125.00
1	A	130	ASP	CA-CB-CG	8.63	121.23	112.60
1	A	187	GLU	O-C-N	-8.56	112.39	122.15
1	A	227	ARG	NE-CZ-NH2	8.55	126.89	119.20
1	A	135	VAL	CA-C-N	8.28	135.20	122.29
1	A	135	VAL	C-N-CA	8.28	135.20	122.29
1	A	9	LYS	CA-C-O	-8.01	110.76	119.97
1	A	107	HIS	CA-CB-CG	-7.98	105.82	113.80
1	A	75	ASP	CA-C-N	7.81	138.28	121.64
1	A	75	ASP	C-N-CA	7.81	138.28	121.64
1	A	226	PHE	CA-CB-CG	7.80	121.60	113.80
1	A	130	ASP	OD1-CG-OD2	-7.73	104.35	122.90
1	A	32	ASP	CA-C-O	-7.62	111.93	120.54
1	A	67	ASN	OD1-CG-ND2	-7.48	115.12	122.60
1	A	232	ASN	OD1-CG-ND2	-7.44	115.16	122.60
1	A	8	GLY	O-C-N	-7.28	116.55	122.81
1	A	138	PRO	CA-C-O	7.17	129.44	119.18
1	A	10	HIS	CA-CB-CG	-7.17	106.63	113.80
1	A	30	PRO	N-CA-C	-7.16	97.72	112.47
1	A	67	ASN	CA-C-O	-7.15	112.59	120.38
1	A	11	ASN	CA-CB-CG	7.14	119.74	112.60
1	A	255	GLN	OE1-CD-NE2	-7.12	115.48	122.60
1	A	127	LYS	CA-CB-CG	7.11	128.32	114.10
1	A	135	VAL	O-C-N	-7.11	113.69	122.57
1	A	142	ALA	CA-C-O	7.09	128.85	120.20
1	A	112	LYS	CB-CG-CD	7.06	127.54	111.30
1	A	207	VAL	O-C-N	-6.99	116.01	123.14
1	A	90	LEU	CA-C-N	6.95	130.90	122.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	90	LEU	C-N-CA	6.95	130.90	122.63
1	A	187	GLU	N-CA-CB	-6.93	99.91	110.16
1	A	107	HIS	ND1-CE1-NE2	6.87	115.27	108.40
1	A	195	PRO	N-CA-CB	6.84	109.04	103.36
1	A	92	GLN	N-CA-C	6.82	119.53	108.76
1	A	191	TYR	O-C-N	6.79	130.91	123.10
1	A	84	LEU	N-CA-C	6.79	121.12	110.32
1	A	136	GLN	CB-CG-CD	-6.73	101.17	112.60
1	A	28	GLN	CA-C-O	6.70	129.71	121.81
1	A	231	PHE	CA-CB-CG	6.65	120.45	113.80
1	A	83	PRO	N-CA-CB	-6.64	95.64	102.88
1	A	35	THR	N-CA-C	6.56	120.55	112.54
1	A	194	TYR	CA-C-N	6.55	127.53	120.13
1	A	194	TYR	C-N-CA	6.55	127.53	120.13
1	A	123	TRP	CA-C-O	6.52	127.74	120.70
1	A	138	PRO	O-C-N	-6.49	113.54	122.24
1	A	158	GLN	OE1-CD-NE2	-6.47	116.13	122.60
1	A	206	CYS	CA-C-N	-6.41	114.83	123.10
1	A	206	CYS	C-N-CA	-6.41	114.83	123.10
1	A	91	ILE	O-C-N	-6.36	113.15	121.99
1	A	58	ARG	N-CA-CB	-6.32	101.11	111.66
1	A	105	SER	O-C-N	-6.31	115.65	122.85
1	A	75	ASP	O-C-N	-6.31	114.30	122.56
1	A	68	VAL	O-C-N	-6.30	114.65	122.97
1	A	59	ILE	N-CA-CB	6.29	120.70	111.52
1	A	31	VAL	CA-C-O	6.28	127.85	121.63
1	A	70	PHE	CA-CB-CG	-6.28	107.53	113.80
1	A	141	LEU	N-CA-C	6.20	119.29	109.50
1	A	11	ASN	CA-C-N	6.19	131.58	121.87
1	A	11	ASN	C-N-CA	6.19	131.58	121.87
1	A	37	THR	CB-CA-C	6.16	119.90	109.55
1	A	137	GLN	CA-C-N	6.15	125.84	119.56
1	A	137	GLN	C-N-CA	6.15	125.84	119.56
1	A	92	GLN	CG-CD-NE2	6.15	125.62	116.40
1	A	64	HIS	N-CA-CB	6.13	120.10	111.15
1	A	116	ALA	O-C-N	6.12	129.69	123.26
1	A	256	ILE	N-CA-CB	6.11	117.38	110.72
1	A	108	THR	O-C-N	-6.10	115.22	123.15
1	A	66	PHE	N-CA-CB	6.09	121.44	110.83
1	A	207	VAL	CA-C-N	6.08	130.75	122.84
1	A	207	VAL	C-N-CA	6.08	130.75	122.84
1	A	239	GLU	CA-C-O	-6.06	114.04	120.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	216	ILE	N-CA-C	-6.04	99.87	109.17
1	A	223	VAL	CB-CA-C	-6.03	104.00	112.14
1	A	144	LEU	CA-C-O	-6.01	113.70	120.43
1	A	89	ARG	CB-CA-C	-6.00	99.39	109.48
1	A	190	ASP	CA-CB-CG	5.99	118.58	112.60
1	A	99	SER	CA-C-N	5.97	131.88	122.21
1	A	99	SER	C-N-CA	5.97	131.88	122.21
1	A	232	ASN	O-C-N	-5.95	115.33	122.65
1	A	101	ASP	CA-CB-CG	5.94	118.54	112.60
1	A	244	ASN	CB-CG-ND2	5.93	125.29	116.40
1	A	58	ARG	N-CA-C	5.91	118.05	109.07
1	A	72	ASP	O-C-N	-5.90	114.64	122.20
1	A	106	GLU	O-C-N	5.89	129.09	122.32
1	A	200	THR	CA-CB-OG1	-5.87	100.79	109.60
1	A	91	ILE	CA-CB-CG1	-5.87	100.43	110.40
1	A	176	PHE	N-CA-CB	-5.85	101.91	112.27
1	A	219	SER	O-C-N	-5.83	116.21	122.85
1	A	215	PRO	O-C-N	-5.81	116.05	123.14
1	A	149	LYS	CB-CG-CD	5.80	124.65	111.30
1	A	221	GLU	O-C-N	5.79	128.26	122.12
1	A	10	HIS	N-CA-C	5.78	120.33	113.28
1	A	210	ILE	CA-C-O	5.75	126.54	120.51
1	A	217	SER	CA-CB-OG	-5.73	99.64	111.10
1	A	210	ILE	O-C-N	-5.73	117.15	122.71
1	A	212	LEU	CA-C-O	5.70	127.54	121.16
1	A	91	ILE	CA-C-O	5.69	126.66	120.69
1	A	20	PHE	CA-CB-CG	-5.68	108.12	113.80
1	A	55	THR	CA-C-O	-5.67	113.43	120.57
1	A	83	PRO	O-C-N	-5.67	113.07	122.36
1	A	67	ASN	CA-CB-CG	5.65	118.25	112.60
1	A	230	ASN	N-CA-CB	-5.65	101.42	111.08
1	A	175	ASP	CB-CG-OD1	5.64	131.37	118.40
1	A	41	ASP	CA-C-N	5.59	125.21	119.56
1	A	41	ASP	C-N-CA	5.59	125.21	119.56
1	A	153	ALA	CA-C-O	-5.59	115.47	121.56
1	A	191	TYR	CB-CG-CD2	5.59	129.19	120.80
1	A	253	ASN	OD1-CG-ND2	5.58	128.18	122.60
1	A	244	ASN	CA-CB-CG	5.57	118.17	112.60
1	A	164	LEU	N-CA-C	5.56	118.10	111.71
1	A	11	ASN	OD1-CG-ND2	-5.55	117.05	122.60
1	A	150	VAL	O-C-N	-5.53	116.19	122.94
1	A	198	LEU	N-CA-C	-5.52	102.72	110.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	182	ARG	NE-CZ-NH1	5.51	127.01	121.50
1	A	31	VAL	CA-CB-CG2	5.50	119.76	110.40
1	A	191	TYR	N-CA-CB	-5.47	102.92	111.56
1	A	214	GLU	N-CA-CB	-5.46	103.08	110.23
1	A	220	SER	CA-C-O	5.46	126.33	120.55
1	A	187	GLU	CA-C-O	5.46	126.20	120.42
1	A	130	ASP	N-CA-CB	5.44	120.16	111.56
1	A	246	ARG	CA-C-O	5.40	125.21	120.19
1	A	149	LYS	CA-CB-CG	5.38	124.87	114.10
1	A	52	ASP	CA-C-O	-5.38	114.02	120.10
1	A	228	LYS	N-CA-CB	5.37	118.53	110.53
1	A	27	ARG	NE-CZ-NH1	5.37	126.87	121.50
1	A	192	TRP	N-CA-C	-5.35	100.69	109.40
1	A	139	ASP	CA-C-O	-5.31	114.12	120.65
1	A	194	TYR	CA-C-O	5.30	125.30	120.26
1	A	72	ASP	CA-C-O	5.28	126.94	120.55
1	A	230	ASN	CA-C-N	5.28	129.61	120.58
1	A	230	ASN	C-N-CA	5.28	129.61	120.58
1	A	39	LYS	N-CA-CB	-5.25	102.23	110.69
1	A	137	GLN	CA-C-O	-5.25	113.88	120.23
1	A	37	THR	CA-C-N	5.24	129.00	121.50
1	A	37	THR	C-N-CA	5.24	129.00	121.50
1	A	149	LYS	N-CA-CB	5.24	119.24	110.85
1	A	230	ASN	CB-CG-ND2	5.22	124.22	116.40
1	A	154	LYS	N-CA-C	-5.20	99.33	108.69
1	A	193	THR	CA-C-O	5.20	126.09	120.32
1	A	95	PHE	CA-C-N	5.20	130.74	122.74
1	A	95	PHE	C-N-CA	5.20	130.74	122.74
1	A	130	ASP	CB-CG-OD2	5.17	130.30	118.40
1	A	159	LYS	CB-CG-CD	5.17	123.20	111.30
1	A	112	LYS	O-C-N	-5.17	116.99	123.04
1	A	210	ILE	CB-CA-C	5.17	116.83	111.09
1	A	238	GLU	CB-CG-CD	5.17	121.38	112.60
1	A	225	LYS	CB-CG-CD	5.14	123.12	111.30
1	A	207	VAL	CB-CA-C	-5.13	103.01	110.81
1	A	130	ASP	CA-C-N	5.12	127.56	120.29
1	A	130	ASP	C-N-CA	5.12	127.56	120.29
1	A	120	LEU	CA-C-N	5.12	129.45	122.90
1	A	120	LEU	C-N-CA	5.12	129.45	122.90
1	A	259	SER	N-CA-C	-5.11	106.82	113.16
1	A	175	ASP	N-CA-C	-5.11	102.71	110.28
1	A	122	HIS	CA-C-O	-5.11	115.13	121.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	5	TRP	CA-C-N	5.10	127.90	121.83
1	A	5	TRP	C-N-CA	5.10	127.90	121.83
1	A	200	THR	O-C-N	-5.09	117.42	121.80
1	A	151	GLY	CA-C-N	5.08	129.81	121.39
1	A	151	GLY	C-N-CA	5.08	129.81	121.39
1	A	30	PRO	CA-C-N	5.06	129.88	122.69
1	A	30	PRO	C-N-CA	5.06	129.88	122.69
1	A	152	SER	CA-C-O	-5.06	115.65	121.47
1	A	219	SER	CA-C-O	5.03	127.74	121.81
1	A	114	TYR	CA-C-O	-5.03	115.35	121.78
1	A	98	GLY	O-C-N	5.02	129.04	123.12
1	A	246	ARG	N-CA-C	-5.00	103.41	110.31

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	2038	0	1991	26	0
2	A	1	0	0	0	0
3	A	1	0	0	0	0
4	A	3	0	0	0	0
5	A	8	0	9	4	0
6	A	155	0	0	6	0
All	All	2206	0	2000	27	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (27) 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)
5:A:264:HSM:HE1	6:A:396:HOH:O	1.57	1.05
1:A:64:HIS:HD2	6:A:391:HOH:O	1.43	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:239:GLU:OE2	6:A:312:HOH:O	2.14	0.65
1:A:92:GLN:NE2	5:A:264:HSM:HE2	1.93	0.65
1:A:89:ARG:HG3	1:A:125:THR:HG22	1.78	0.65
1:A:59:ILE:HG12	1:A:167:ILE:HD13	1.82	0.61
1:A:134:ALA:O	1:A:140:GLY:HA3	2.07	0.54
1:A:22:ILE:HD11	1:A:205:GLU:HG3	1.92	0.52
1:A:243:ASP:HA	1:A:245:TRP:CD1	2.46	0.51
1:A:92:GLN:HE22	5:A:264:HSM:HE2	1.59	0.51
1:A:168:LYS:O	1:A:230:ASN:HB2	2.12	0.49
1:A:149:LYS:HE3	6:A:348:HOH:O	2.14	0.47
1:A:9:LYS:HD2	1:A:9:LYS:O	2.14	0.46
1:A:88:TYR:HB3	1:A:122:HIS:HB3	1.97	0.46
1:A:213:LYS:HD3	1:A:260:PHE:CZ	2.51	0.46
1:A:168:LYS:HA	1:A:229:LEU:HD23	1.98	0.46
1:A:27:ARG:HG3	1:A:205:GLU:HB3	1.98	0.45
1:A:133:LYS:HD2	6:A:324:HOH:O	2.16	0.45
1:A:22:ILE:CD1	1:A:205:GLU:HG3	2.46	0.44
1:A:27:ARG:CG	1:A:205:GLU:HB3	2.48	0.44
1:A:202:PRO:HG2	1:A:204:LEU:HG	1.99	0.43
1:A:89:ARG:HG3	1:A:125:THR:CG2	2.48	0.43
1:A:47:LEU:HD22	1:A:79:LEU:HD11	1.99	0.43
1:A:45:LYS:O	1:A:82:GLY:HA2	2.18	0.43
1:A:159:LYS:HB2	6:A:304:HOH:O	2.18	0.42
1:A:92:GLN:NE2	5:A:264:HSM:NE2	2.65	0.41
1:A:161:VAL:HG13	1:A:225:LYS:HB2	2.03	0.40

There are no symmetry-related clashes.

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	255/259 (98%)	242 (95%)	12 (5%)	1 (0%)	30	27

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	30	PRO

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	220/224 (98%)	210 (96%)	10 (4%)	24	23

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

Mol	Chain	Res	Type
1	A	39	LYS
1	A	43	SER
1	A	58	ARG
1	A	60	LEU
1	A	80	LYS
1	A	92	GLN
1	A	159	LYS
1	A	163	VAL
1	A	172	LYS
1	A	253	ASN

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	64	HIS
1	A	92	GLN
1	A	178	ASN

5.3.3 RNA ⓘ

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 4 ligands modelled in this entry, 2 are 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	$\# Z > 2$
4	AZI	A	265	2	2,2,2	0.95	0	0,1,1	-	-
5	HSM	A	264	-	8,8,8	0.43	0	9,9,9	3.14	4 (44%)

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
5	HSM	A	264	-	-	2/3/3/3	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	264	HSM	CA-CB-CG	8.21	125.39	112.02
5	A	264	HSM	CE1-ND1-CG	2.68	111.89	105.80
5	A	264	HSM	CD2-CG-ND1	-2.17	104.47	108.86
5	A	264	HSM	NE2-CE1-ND1	-2.02	106.54	111.49

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	264	HSM	N-CA-CB-CG
5	A	264	HSM	CA-CB-CG-ND1

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	264	HSM	4	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	125:THR	C	127:LYS	N	1.65

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.