



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 07:20 PM UTC

PDB ID : 1HUH / pdb_00001huh
Title : DIFFERENCES IN ANIONIC INHIBITION OF HUMAN CARBONIC ANHYDRASE I REVEALED FROM THE STRUCTURES OF IODIDE AND GOLD CYANIDE INHIBITOR COMPLEXES
Authors : Kumar, V.; Kannan, K.K.
Deposited on : 1993-10-28
Resolution : 2.20 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
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

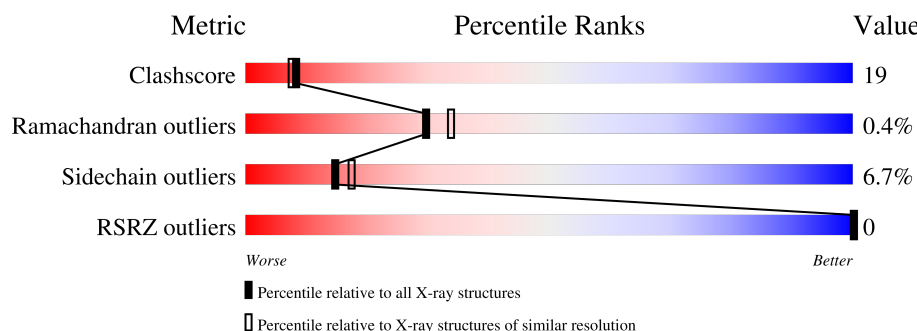
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	260	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2275 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 I.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	257	Total	C	N	O	S	0	0	0
			2016	1274	350	389	3			

- 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 IODIDE ION (CCD ID: IOD) (formula: I).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	5	Total	I	0	0
			5	5		

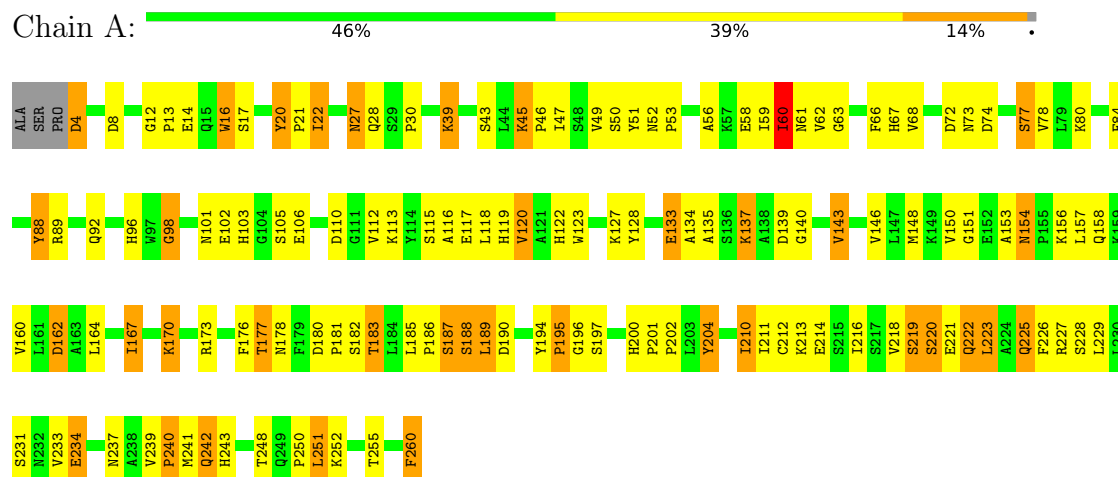
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	253	Total	O	0	0
			253	253		

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 and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: CARBONIC ANHYDRASE I



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	81.80Å 75.20Å 37.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.20 8.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (8.00-2.20) 80.5 (8.00-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtriage
Refinement program	PROLSQ	Depositor
R, R_{free}	0.166 , (Not available) 0.166 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	14.2	Xtriage
Anisotropy	0.272	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 88.4	EDS
L-test for twinning ¹	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2275	wwPDB-VP
Average B, all atoms (Å ²)	12.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.24% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, IOD

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	1.20	1/2073 (0.0%)	2.17	86/2819 (3.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	88	TYR	N-CA	5.07	1.52	1.46

All (86) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	180	ASP	CB-CA-C	9.21	120.40	110.17
1	A	120	VAL	O-C-N	9.19	132.82	122.99
1	A	73	ASN	CA-CB-CG	9.15	121.75	112.60
1	A	162	ASP	CA-CB-CG	8.99	121.59	112.60
1	A	4	ASP	CA-CB-CG	8.48	121.08	112.60
1	A	20	TYR	O-C-N	8.48	129.35	121.04
1	A	180	ASP	CA-C-O	7.84	126.81	119.59
1	A	220	SER	CA-C-O	-7.80	112.55	120.90
1	A	189	LEU	CB-CA-C	7.54	124.35	111.46
1	A	4	ASP	CA-C-N	7.51	135.59	121.69
1	A	4	ASP	C-N-CA	7.51	135.59	121.69
1	A	58	GLU	CA-C-N	7.36	132.89	123.10
1	A	58	GLU	C-N-CA	7.36	132.89	123.10
1	A	98	GLY	CA-C-O	-7.18	114.93	121.47
1	A	251	LEU	CB-CA-C	7.11	124.88	110.38
1	A	110	ASP	CA-CB-CG	6.90	119.50	112.60
1	A	45	LYS	O-C-N	6.87	127.38	121.20
1	A	226	PHE	O-C-N	6.62	128.89	122.07
1	A	39	LYS	CA-C-O	6.52	127.37	120.33
1	A	251	LEU	N-CA-CB	-6.46	100.36	110.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	60	ILE	N-CA-C	6.43	118.04	108.46
1	A	16	TRP	CA-CB-CG	6.41	125.77	113.60
1	A	177	THR	N-CA-C	6.35	119.36	109.52
1	A	190	ASP	CA-CB-CG	6.29	118.89	112.60
1	A	167	ILE	CA-C-N	6.25	128.57	120.44
1	A	167	ILE	C-N-CA	6.25	128.57	120.44
1	A	176	PHE	CA-CB-CG	6.24	120.04	113.80
1	A	27	ASN	CA-C-O	-6.22	113.87	121.89
1	A	120	VAL	N-CA-CB	6.05	119.52	111.90
1	A	27	ASN	O-C-N	6.01	129.83	121.83
1	A	133	GLU	CA-C-N	5.92	128.53	120.54
1	A	133	GLU	C-N-CA	5.92	128.53	120.54
1	A	49	VAL	O-C-N	5.91	129.13	122.98
1	A	117	GLU	CB-CG-CD	5.89	122.62	112.60
1	A	187	SER	N-CA-C	5.86	117.46	111.14
1	A	220	SER	O-C-N	5.79	128.11	122.09
1	A	43	SER	N-CA-CB	5.77	119.44	110.44
1	A	222	GLN	CA-C-N	5.75	127.92	120.44
1	A	222	GLN	C-N-CA	5.75	127.92	120.44
1	A	196	GLY	O-C-N	5.71	130.12	122.70
1	A	251	LEU	CA-C-N	5.61	130.92	122.68
1	A	251	LEU	C-N-CA	5.61	130.92	122.68
1	A	74	ASP	CB-CA-C	-5.60	98.18	110.67
1	A	220	SER	CA-CB-OG	-5.55	100.00	111.10
1	A	233	VAL	CB-CA-C	5.55	118.94	111.28
1	A	195	PRO	O-C-N	-5.51	117.19	123.03
1	A	210	ILE	CA-C-N	-5.47	116.03	122.93
1	A	210	ILE	C-N-CA	-5.47	116.03	122.93
1	A	112	VAL	CA-C-N	5.46	129.67	122.30
1	A	112	VAL	C-N-CA	5.46	129.67	122.30
1	A	237	ASN	CA-C-N	5.43	129.06	121.02
1	A	237	ASN	C-N-CA	5.43	129.06	121.02
1	A	240	PRO	CB-CA-C	5.43	118.40	110.63
1	A	214	GLU	CB-CG-CD	5.43	121.82	112.60
1	A	248	THR	N-CA-CB	5.41	118.67	110.45
1	A	73	ASN	CB-CA-C	5.41	119.31	110.17
1	A	260	PHE	CA-CB-CG	-5.39	108.41	113.80
1	A	204	TYR	N-CA-CB	5.38	118.24	109.69
1	A	188	SER	CA-C-N	-5.38	114.16	123.25
1	A	188	SER	C-N-CA	-5.38	114.16	123.25
1	A	68	VAL	CA-C-O	-5.36	114.59	120.97
1	A	225	GLN	CA-C-N	5.36	127.40	120.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	225	GLN	C-N-CA	5.36	127.40	120.44
1	A	77	SER	CA-C-O	5.31	126.07	120.33
1	A	117	GLU	CG-CD-OE2	5.30	130.59	118.40
1	A	74	ASP	O-C-N	5.29	129.63	122.96
1	A	234	GLU	CA-CB-CG	5.26	124.63	114.10
1	A	143	VAL	CA-C-N	-5.24	114.12	122.50
1	A	143	VAL	C-N-CA	-5.24	114.12	122.50
1	A	154	ASN	CB-CA-C	5.23	115.98	110.17
1	A	241	MET	CA-C-N	5.20	127.20	120.44
1	A	241	MET	C-N-CA	5.20	127.20	120.44
1	A	162	ASP	CA-C-N	5.20	128.22	120.31
1	A	162	ASP	C-N-CA	5.20	128.22	120.31
1	A	229	LEU	O-C-N	5.18	128.79	122.68
1	A	183	THR	N-CA-C	-5.17	106.48	112.89
1	A	231	SER	O-C-N	5.17	129.19	122.42
1	A	52	ASN	O-C-N	5.16	127.68	121.29
1	A	211	ILE	CB-CA-C	5.09	117.76	110.84
1	A	194	TYR	CA-C-N	5.08	126.47	120.23
1	A	194	TYR	C-N-CA	5.08	126.47	120.23
1	A	170	LYS	CA-C-O	5.07	126.70	120.92
1	A	219	SER	CA-C-O	5.05	128.31	121.89
1	A	103	HIS	CA-CB-CG	-5.04	108.76	113.80
1	A	223	LEU	O-C-N	5.02	127.24	122.07
1	A	88	TYR	CA-C-O	-5.02	115.39	120.71

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	2016	0	1938	75	1
2	A	1	0	0	0	0
3	A	5	0	0	2	0
4	A	253	0	0	15	1
All	All	2275	0	1938	76	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 19.

All (76) 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)
3:A:520:IOD:I	4:A:271:HOH:O	2.46	1.03
1:A:188:SER:O	1:A:189:LEU:HD23	1.79	0.80
1:A:39:LYS:HD3	1:A:255:THR:HG21	1.64	0.79
1:A:63:GLY:HA3	1:A:170:LYS:HD2	1.65	0.79
1:A:250:PRO:HG2	1:A:252:LYS:HE2	1.68	0.76
1:A:158:GLN:NE2	1:A:162:ASP:OD1	2.18	0.75
1:A:133:GLU:O	1:A:137:LYS:HE2	1.87	0.72
1:A:260:PHE:OXT	4:A:349:HOH:O	2.11	0.69
1:A:139:ASP:OD2	4:A:270:HOH:O	2.11	0.69
1:A:8:ASP:HB3	4:A:476:HOH:O	1.91	0.68
1:A:59:ILE:HG12	1:A:167:ILE:HD13	1.76	0.68
1:A:101:ASN:OD1	1:A:227:ARG:NH2	2.27	0.63
1:A:154:ASN:HB3	1:A:157:LEU:HD12	1.82	0.62
1:A:105:SER:O	1:A:113:LYS:HE3	2.02	0.60
1:A:14:GLU:OE2	3:A:521:IOD:I	2.90	0.60
1:A:101:ASN:O	1:A:115:SER:HB3	2.01	0.59
1:A:128:TYR:CE1	1:A:137:LYS:HG3	2.38	0.58
1:A:195:PRO:HB3	4:A:279:HOH:O	2.03	0.58
1:A:197:SER:HB2	1:A:204:TYR:O	2.04	0.58
1:A:63:GLY:CA	1:A:170:LYS:HD2	2.33	0.57
1:A:84:PHE:HB3	4:A:321:HOH:O	2.03	0.57
1:A:60:ILE:HG13	1:A:61:ASN:N	2.19	0.56
1:A:47:ILE:O	1:A:47:ILE:HG13	2.06	0.55
1:A:51:TYR:CD2	1:A:181:PRO:HG2	2.43	0.54
1:A:225:GLN:HG2	4:A:409:HOH:O	2.07	0.53
1:A:102:GLU:OE1	4:A:296:HOH:O	2.19	0.53
1:A:222:GLN:O	1:A:225:GLN:HB2	2.09	0.52
1:A:39:LYS:CD	1:A:255:THR:HG21	2.39	0.50
1:A:88:TYR:HB3	1:A:122:HIS:HB3	1.93	0.50
1:A:39:LYS:HD3	1:A:255:THR:CG2	2.38	0.50
1:A:30:PRO:HG3	1:A:106:GLU:HB3	1.95	0.49
1:A:128:TYR:CZ	1:A:137:LYS:HG3	2.48	0.49
1:A:242:GLN:HG3	4:A:359:HOH:O	2.12	0.49
1:A:151:GLY:O	4:A:285:HOH:O	2.19	0.49
1:A:78:VAL:HG23	4:A:503:HOH:O	2.11	0.48
1:A:45:LYS:HB3	1:A:46:PRO:HD2	1.94	0.48
1:A:59:ILE:HA	1:A:67:HIS:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:TYR:HB3	1:A:122:HIS:CB	2.42	0.48
1:A:21:PRO:HD2	4:A:461:HOH:O	2.12	0.47
1:A:50:SER:O	1:A:77:SER:HA	2.15	0.47
1:A:62:VAL:O	1:A:62:VAL:HG23	2.13	0.47
1:A:146:VAL:HG22	1:A:212:CYS:SG	2.54	0.47
1:A:213:LYS:HE2	1:A:260:PHE:CE1	2.50	0.47
1:A:72:ASP:HB2	1:A:89:ARG:CD	2.44	0.47
1:A:202:PRO:HB2	1:A:204:TYR:CZ	2.50	0.47
1:A:234:GLU:HA	4:A:306:HOH:O	2.13	0.47
1:A:200:HIS:HB2	1:A:201:PRO:HD2	1.96	0.47
1:A:223:LEU:HD23	1:A:223:LEU:HA	1.70	0.47
1:A:96:HIS:CD2	1:A:119:HIS:CE1	3.03	0.46
1:A:185:LEU:O	4:A:500:HOH:O	2.20	0.46
1:A:250:PRO:HB2	1:A:252:LYS:CG	2.46	0.46
1:A:56:ALA:HB3	1:A:177:THR:HA	1.98	0.46
1:A:22:ILE:O	1:A:28:GLN:NE2	2.49	0.45
1:A:8:ASP:O	1:A:12:GLY:N	2.50	0.45
1:A:98:GLY:HA2	1:A:243:HIS:CB	2.48	0.44
1:A:53:PRO:O	1:A:178:ASN:HA	2.17	0.44
1:A:158:GLN:HE21	1:A:162:ASP:CG	2.22	0.43
1:A:116:ALA:HB3	1:A:148:MET:HB2	2.01	0.43
1:A:160:VAL:O	1:A:164:LEU:HG	2.18	0.42
1:A:153:ALA:HB2	4:A:357:HOH:O	2.18	0.42
1:A:186:PRO:O	1:A:189:LEU:HD21	2.18	0.42
1:A:51:TYR:CD2	1:A:182:SER:HB3	2.54	0.42
1:A:67:HIS:ND1	1:A:92:GLN:NE2	2.66	0.42
1:A:13:PRO:HA	1:A:16:TRP:CD2	2.55	0.42
1:A:123:TRP:HA	1:A:140:GLY:O	2.19	0.42
1:A:148:MET:HA	1:A:216:ILE:O	2.20	0.41
1:A:181:PRO:C	1:A:183:THR:H	2.28	0.41
1:A:66:PHE:O	1:A:67:HIS:HD2	2.04	0.41
1:A:17:SER:HA	1:A:20:TYR:O	2.21	0.41
1:A:120:VAL:O	1:A:143:VAL:HA	2.20	0.41
1:A:119:HIS:HB3	1:A:143:VAL:CG1	2.50	0.41
1:A:219:SER:O	1:A:220:SER:C	2.62	0.41
1:A:134:ALA:O	1:A:140:GLY:HA3	2.21	0.40
1:A:200:HIS:O	1:A:201:PRO:C	2.63	0.40
1:A:150:VAL:HA	1:A:218:VAL:O	2.21	0.40
1:A:239:VAL:HA	1:A:240:PRO:HD3	1.92	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:221:GLU:OE2	4:A:339:HOH:O[4_555]	2.16	0.04

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	255/260 (98%)	243 (95%)	11 (4%)	1 (0%)	30 34

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	135	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	223/225 (99%)	208 (93%)	15 (7%)	15 17

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

Mol	Chain	Res	Type
1	A	4	ASP
1	A	22	ILE
1	A	27	ASN
1	A	60	ILE
1	A	80	LYS

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Mol	Chain	Res	Type
1	A	118	LEU
1	A	127	LYS
1	A	137	LYS
1	A	156	LYS
1	A	173	ARG
1	A	187	SER
1	A	210	ILE
1	A	228	SER
1	A	242	GLN
1	A	251	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	26	ASN
1	A	69	ASN
1	A	92	GLN
1	A	103	HIS
1	A	225	GLN
1	A	242	GLN
1	A	243	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

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.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

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

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	257/260 (98%)	-0.76	0 100 100	2, 10, 24, 41	0

There are no RSRZ outliers to report.

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	IOD	A	523	1/1	0.89	0.05	42,42,42,42	1
3	IOD	A	521	1/1	0.96	0.03	25,25,25,25	1
3	IOD	A	522	1/1	0.99	0.03	11,11,11,11	1
2	ZN	A	261	1/1	0.99	0.04	7,7,7,7	0
3	IOD	A	524	1/1	0.99	0.04	21,21,21,21	1
3	IOD	A	520	1/1	1.00	0.04	14,14,14,14	1

6.5 Other polymers [i](#)

There are no such residues in this entry.