Full wwPDB X-ray Structure Validation Report (i)

Feb 18, 2024 – 01:38 AM EST

PDB ID	:	4CA2
Title	:	ENGINEERING THE HYDROPHOBIC POCKET OF CARBONIC ANHYDRASE II
Authors	:	Alexander, R.S.; Christianson, D.W.
Deposited on	:	1991-06-08
Resolution	:	2.10 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 (i) 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 (i)) were used in the production of this report:

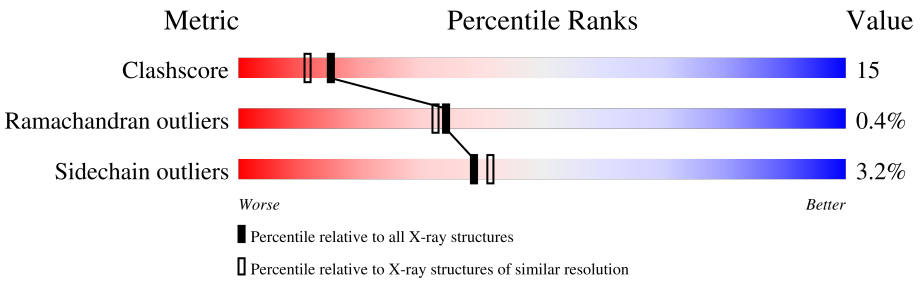
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)

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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	260	53% 35% 8% • •

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2133 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
			Total	C	N	O	S			
1	A	255	2029	1303	347	377	2	0	0	0

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 3 is MERCURY (II) ION (three-letter code: HG) (formula: Hg).

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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	102	102	102	0	0

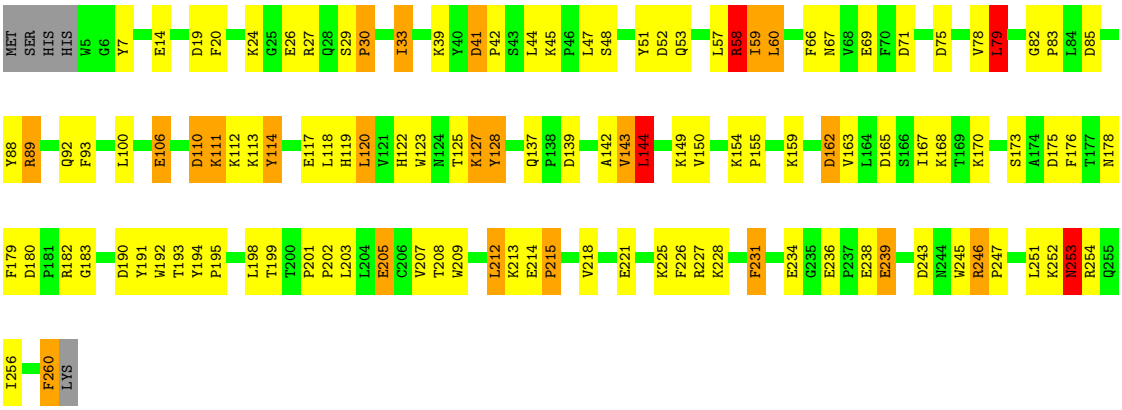
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

- Molecule 1: CARBONIC ANHYDRASE II

Chain A: 53% 35% 8%



4 Data and refinement statistics (i)

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	42.70Å 41.70Å 73.00Å 90.00° 104.60° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.10	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.10)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.180 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2133	wwPDB-VP
Average B, all atoms ($Å^2$)	12.0	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: HG, ZN

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	1.76	24/2088 (1.1%)	2.33	91/2833 (3.2%)

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	236	GLU	CD-OE2	12.29	1.39	1.25
1	A	238	GLU	CD-OE1	10.44	1.37	1.25
1	A	234	GLU	CD-OE1	10.05	1.36	1.25
1	A	173	SER	CB-OG	-9.89	1.29	1.42
1	A	221	GLU	CD-OE2	-7.70	1.17	1.25
1	A	245	TRP	NE1-CE2	7.42	1.47	1.37
1	A	58	ARG	CZ-NH1	-7.25	1.23	1.33
1	A	202	PRO	N-CD	7.09	1.57	1.47
1	A	24	LYS	N-CA	7.04	1.60	1.46
1	A	48	SER	CB-OG	6.64	1.50	1.42
1	A	260	PHE	C-O	6.50	1.35	1.23
1	A	111	LYS	C-O	6.18	1.35	1.23
1	A	234	GLU	CB-CG	6.00	1.63	1.52
1	A	26	GLU	CD-OE2	5.97	1.32	1.25
1	A	106	GLU	CD-OE2	5.86	1.32	1.25
1	A	117	GLU	C-O	-5.85	1.12	1.23
1	A	238	GLU	CG-CD	-5.62	1.43	1.51
1	A	205	GLU	CD-OE1	-5.62	1.19	1.25
1	A	165	ASP	N-CA	5.56	1.57	1.46
1	A	198	LEU	C-O	5.33	1.33	1.23
1	A	215	PRO	N-CD	5.25	1.55	1.47
1	A	92	GLN	CG-CD	-5.20	1.39	1.51
1	A	227	ARG	NE-CZ	5.20	1.39	1.33
1	A	14	GLU	CD-OE1	5.08	1.31	1.25

All (91) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	58	ARG	CB-CG-CD	18.88	160.68	111.60
1	A	89	ARG	NE-CZ-NH2	-17.45	111.58	120.30
1	A	175	ASP	CB-CG-OD1	13.45	130.41	118.30
1	A	182	ARG	NE-CZ-NH2	13.18	126.89	120.30
1	A	51	TYR	CA-CB-CG	12.72	137.57	113.40
1	A	24	LYS	CA-CB-CG	12.68	141.29	113.40
1	A	51	TYR	CB-CG-CD2	12.56	128.54	121.00
1	A	71	ASP	CB-CG-OD1	12.49	129.54	118.30
1	A	221	GLU	CA-CB-CG	11.46	138.61	113.40
1	A	89	ARG	NE-CZ-NH1	11.24	125.92	120.30
1	A	92	GLN	CB-CG-CD	11.03	140.28	111.60
1	A	58	ARG	NE-CZ-NH2	-10.58	115.01	120.30
1	A	51	TYR	CB-CG-CD1	-10.47	114.72	121.00
1	A	243	ASP	CB-CG-OD1	-9.70	109.57	118.30
1	A	165	ASP	CA-CB-CG	9.47	134.23	113.40
1	A	246	ARG	NE-CZ-NH2	-9.15	115.73	120.30
1	A	75	ASP	CB-CG-OD1	9.14	126.53	118.30
1	A	85	ASP	CB-CG-OD1	-8.86	110.33	118.30
1	A	106	GLU	CG-CD-OE2	-8.76	100.78	118.30
1	A	24	LYS	CB-CA-C	8.62	127.64	110.40
1	A	85	ASP	CB-CG-OD2	8.42	125.88	118.30
1	A	243	ASP	CB-CG-OD2	8.33	125.80	118.30
1	A	52	ASP	CB-CG-OD1	8.30	125.77	118.30
1	A	100	LEU	CA-CB-CG	8.20	134.15	115.30
1	A	93	PHE	N-CA-CB	8.08	125.14	110.60
1	A	231	PHE	CB-CG-CD1	-7.71	115.40	120.80
1	A	106	GLU	CG-CD-OE1	7.45	133.19	118.30
1	A	39	LYS	CB-CG-CD	7.40	130.83	111.60
1	A	114	TYR	CB-CG-CD2	-7.37	116.58	121.00
1	A	236	GLU	CG-CD-OE1	7.26	132.82	118.30
1	A	41	ASP	CB-CG-OD1	7.25	124.83	118.30
1	A	246	ARG	NE-CZ-NH1	7.05	123.83	120.30
1	A	191	TYR	CB-CG-CD2	-6.92	116.85	121.00
1	A	26	GLU	CG-CD-OE1	6.80	131.90	118.30
1	A	78	VAL	CA-CB-CG1	6.77	121.05	110.90
1	A	207	VAL	C-N-CA	6.76	138.59	121.70
1	A	139	ASP	CB-CG-OD2	-6.69	112.28	118.30
1	A	182	ARG	NH1-CZ-NH2	-6.65	112.08	119.40
1	A	227	ARG	O-C-N	6.58	133.23	122.70
1	A	53	GLN	CB-CA-C	6.46	123.32	110.40
1	A	58	ARG	NE-CZ-NH1	6.40	123.50	120.30
1	A	120	LEU	N-CA-CB	6.39	123.18	110.40
1	A	60	LEU	CA-C-N	-6.37	103.18	117.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	180	ASP	CB-CG-OD1	6.31	123.98	118.30
1	A	190	ASP	CB-CG-OD2	6.30	123.97	118.30
1	A	227	ARG	NE-CZ-NH2	6.28	123.44	120.30
1	A	194	TYR	CB-CG-CD2	-6.25	117.25	121.00
1	A	20	PHE	CB-CG-CD2	-6.22	116.45	120.80
1	A	24	LYS	N-CA-CB	-6.05	99.72	110.60
1	A	127	LYS	CB-CG-CD	6.03	127.28	111.60
1	A	14	GLU	CA-CB-CG	5.95	126.49	113.40
1	A	221	GLU	OE1-CD-OE2	-5.93	116.18	123.30
1	A	149	LYS	N-CA-CB	5.92	121.26	110.60
1	A	194	TYR	CB-CG-CD1	5.92	124.55	121.00
1	A	239	GLU	CA-CB-CG	5.89	126.37	113.40
1	A	39	LYS	N-CA-CB	-5.76	100.24	110.60
1	A	89	ARG	CB-CA-C	-5.75	98.90	110.40
1	A	92	GLN	CA-CB-CG	5.74	126.02	113.40
1	A	192	TRP	CA-CB-CG	5.74	124.60	113.70
1	A	236	GLU	OE1-CD-OE2	-5.74	116.42	123.30
1	A	226	PHE	CA-CB-CG	5.69	127.56	113.90
1	A	71	ASP	CB-CG-OD2	-5.68	113.18	118.30
1	A	178	ASN	CB-CG-ND2	5.67	130.32	116.70
1	A	118	LEU	O-C-N	5.67	131.77	122.70
1	A	33	ILE	O-C-N	5.58	131.62	122.70
1	A	251	LEU	CB-CA-C	5.55	120.75	110.20
1	A	142	ALA	CA-C-O	-5.53	108.48	120.10
1	A	58	ARG	CD-NE-CZ	-5.44	115.99	123.60
1	A	59	ILE	C-N-CA	5.44	135.29	121.70
1	A	111	LYS	CD-CE-NZ	5.39	124.09	111.70
1	A	110	ASP	CB-CG-OD2	5.36	123.13	118.30
1	A	52	ASP	CB-CG-OD2	-5.36	113.47	118.30
1	A	7	TYR	CB-CG-CD2	-5.35	117.79	121.00
1	A	179	PHE	CB-CG-CD1	-5.32	117.08	120.80
1	A	58	ARG	N-CA-CB	-5.32	101.03	110.60
1	A	58	ARG	CA-CB-CG	5.31	125.08	113.40
1	A	128	TYR	CB-CG-CD2	5.29	124.17	121.00
1	A	33	ILE	CA-C-N	-5.28	105.59	117.20
1	A	260	PHE	CA-C-O	-5.25	109.06	120.10
1	A	208	THR	O-C-N	5.25	131.10	122.70
1	A	79	LEU	CA-CB-CG	5.23	127.32	115.30
1	A	58	ARG	CA-C-N	-5.22	105.71	117.20
1	A	19	ASP	CB-CG-OD1	-5.19	113.63	118.30
1	A	14	GLU	CB-CG-CD	5.17	128.15	114.20
1	A	228	LYS	CB-CG-CD	-5.13	98.27	111.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	143	VAL	O-C-N	5.08	130.83	122.70
1	A	7	TYR	CB-CG-CD1	5.07	124.04	121.00
1	A	175	ASP	CB-CG-OD2	-5.06	113.75	118.30
1	A	162	ASP	CA-C-N	5.06	128.32	117.20
1	A	144	LEU	N-CA-C	-5.03	97.42	111.00
1	A	231	PHE	N-CA-CB	5.01	119.61	110.60

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	2029	0	1978	60	1
2	A	1	0	0	0	0
3	A	1	0	0	0	0
4	A	102	0	0	3	1
All	All	2133	0	1978	60	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 15.

All (60) 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:125:THR:C	1:A:127:LYS:N	2.07	1.07
1:A:144:LEU:CD2	1:A:212:LEU:HD21	1.96	0.95
1:A:144:LEU:HD21	1:A:212:LEU:HD21	1.57	0.87
1:A:110:ASP:O	1:A:111:LYS:HB2	1.91	0.70
1:A:60:LEU:O	1:A:66:PHE:HA	1.92	0.69
1:A:213:LYS:HD3	1:A:260:PHE:CZ	2.29	0.67
1:A:58:ARG:CD	1:A:69:GLU:OE1	2.43	0.67
1:A:144:LEU:HD22	1:A:212:LEU:HD21	1.78	0.66
1:A:58:ARG:HD3	1:A:69:GLU:OE1	1.97	0.64
1:A:144:LEU:CD2	1:A:212:LEU:CD2	2.75	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:60:LEU:HD21	1:A:69:GLU:OE2	2.00	0.62
1:A:125:THR:C	1:A:127:LYS:CA	2.70	0.60
1:A:60:LEU:CD2	1:A:69:GLU:OE2	2.50	0.60
1:A:253:ASN:HD22	1:A:254:ARG:N	2.00	0.59
1:A:144:LEU:HD22	1:A:212:LEU:CD2	2.32	0.59
1:A:225:LYS:HE3	4:A:345:HOH:O	2.03	0.58
1:A:213:LYS:HD3	1:A:260:PHE:CE2	2.40	0.57
1:A:89:ARG:HG3	1:A:125:THR:CG2	2.36	0.56
1:A:253:ASN:ND2	1:A:254:ARG:N	2.54	0.55
1:A:58:ARG:HD2	1:A:69:GLU:OE1	2.08	0.53
1:A:59:ILE:HA	1:A:67:ASN:O	2.08	0.53
1:A:231:PHE:HD2	1:A:239:GLU:HG2	1.73	0.53
1:A:113:LYS:NZ	4:A:360:HOH:O	2.41	0.53
1:A:33:ILE:HG12	1:A:256:ILE:HD13	1.93	0.51
1:A:212:LEU:CD2	1:A:212:LEU:N	2.72	0.51
1:A:29:SER:HB3	1:A:30:PRO:HA	1.93	0.50
1:A:112:LYS:HE3	1:A:114:TYR:CE2	2.47	0.50
1:A:88:TYR:HA	1:A:123:TRP:O	2.11	0.49
1:A:252:LYS:O	1:A:253:ASN:CG	2.50	0.49
1:A:45:LYS:O	1:A:82:GLY:HA2	2.14	0.48
1:A:88:TYR:HB3	1:A:122:HIS:HB3	1.96	0.48
1:A:128:TYR:CE1	1:A:137:GLN:HG3	2.49	0.48
1:A:106:GLU:OE1	1:A:199:THR:OG1	2.23	0.47
1:A:119:HIS:HB3	1:A:143:VAL:CG1	2.44	0.47
1:A:154:LYS:HE3	1:A:183:GLY:O	2.15	0.47
1:A:246:ARG:HA	1:A:247:PRO:HD3	1.74	0.47
1:A:58:ARG:HA	1:A:176:PHE:HB3	1.98	0.46
1:A:59:ILE:HG12	1:A:167:ILE:HD13	1.96	0.46
1:A:193:THR:HA	1:A:209:TRP:O	2.15	0.46
1:A:170:LYS:HB2	1:A:231:PHE:O	2.16	0.46
1:A:214:GLU:HA	1:A:215:PRO:HD3	1.75	0.45
1:A:168:LYS:NZ	4:A:343:HOH:O	2.41	0.45
1:A:41:ASP:HA	1:A:42:PRO:HD2	1.89	0.45
1:A:167:ILE:HG13	1:A:167:ILE:O	2.16	0.45
1:A:201:PRO:HA	1:A:203:LEU:HG	1.99	0.45
1:A:41:ASP:OD2	1:A:44:LEU:CD1	2.65	0.45
1:A:154:LYS:HA	1:A:155:PRO:HD2	1.83	0.44
1:A:57:LEU:O	1:A:58:ARG:HB3	2.18	0.43
1:A:45:LYS:H	1:A:45:LYS:HG3	1.64	0.42
1:A:159:LYS:HE2	1:A:159:LYS:HB3	1.75	0.42
1:A:252:LYS:O	1:A:253:ASN:CB	2.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:47:LEU:HD22	1:A:79:LEU:HD21	2.01	0.42
1:A:27:ARG:HG3	1:A:205:GLU:HB3	2.01	0.42
1:A:89:ARG:HG3	1:A:125:THR:HG22	2.02	0.42
1:A:163:VAL:HG11	1:A:176:PHE:CE1	2.55	0.41
1:A:212:LEU:N	1:A:212:LEU:HD22	2.36	0.40
1:A:195:PRO:O	1:A:254:ARG:NH1	2.47	0.40
1:A:89:ARG:O	1:A:122:HIS:HA	2.22	0.40
1:A:120:LEU:N	1:A:120:LEU:HD12	2.36	0.40
1:A:150:VAL:HA	1:A:218:VAL:O	2.22	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:162:ASP:OD2	4:A:330:HOH:O[2_445]	1.80	0.40

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	251/260 (96%)	239 (95%)	11 (4%)	1 (0%)	34 32

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	253	ASN

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	220/225 (98%)	213 (97%)	7 (3%)	39 41

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	PRO
1	A	58	ARG
1	A	79	LEU
1	A	83	PRO
1	A	144	LEU
1	A	212	LEU
1	A	253	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	67	ASN
1	A	136	GLN
1	A	137	GLN
1	A	253	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2 ligands modelled in this entry, 2 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)

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	2.07

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.