



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 11:59 PM UTC

PDB ID : 5K7B / pdb_00005k7b
Title : Beclin 2 CCD homodimer
Authors : Su, M.; Sinha, S.
Deposited on : 2016-05-25
Resolution : 2.30 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

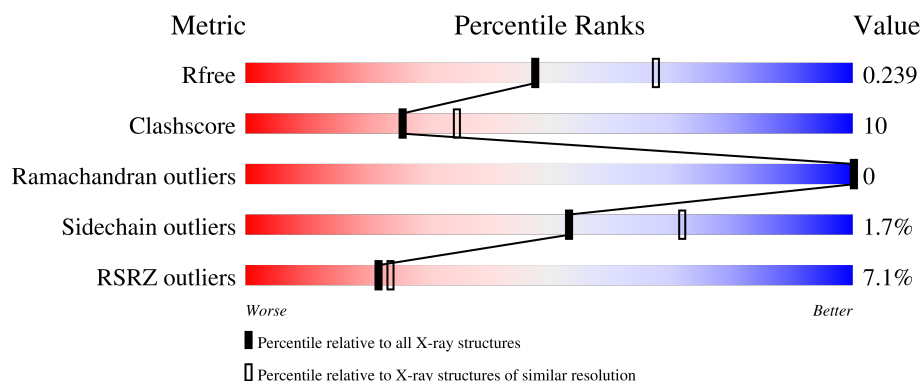
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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))
R_{free}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	98	 6% 61% 27% 11%
1	B	98	 6% 69% 23% 7%
1	C	98	 8% 57% 31% 12%
1	D	98	 5% 67% 21% 10%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3015 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 Beclin-2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	87	Total	C	N	O	0	0	0
			712	428	139	145			
1	B	91	Total	C	N	O	0	0	0
			742	447	144	151			
1	C	86	Total	C	N	O	0	0	0
			694	418	131	145			
1	D	88	Total	C	N	O	0	0	0
			728	439	141	148			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	GLY	-	expression tag	UNP A8MW95
A	-4	ALA	-	expression tag	UNP A8MW95
A	-3	MET	-	expression tag	UNP A8MW95
A	-2	ASP	-	expression tag	UNP A8MW95
A	-1	PRO	-	expression tag	UNP A8MW95
B	-5	GLY	-	expression tag	UNP A8MW95
B	-4	ALA	-	expression tag	UNP A8MW95
B	-3	MET	-	expression tag	UNP A8MW95
B	-2	ASP	-	expression tag	UNP A8MW95
B	-1	PRO	-	expression tag	UNP A8MW95
C	-5	GLY	-	expression tag	UNP A8MW95
C	-4	ALA	-	expression tag	UNP A8MW95
C	-3	MET	-	expression tag	UNP A8MW95
C	-2	ASP	-	expression tag	UNP A8MW95
C	-1	PRO	-	expression tag	UNP A8MW95
D	-5	GLY	-	expression tag	UNP A8MW95
D	-4	ALA	-	expression tag	UNP A8MW95
D	-3	MET	-	expression tag	UNP A8MW95
D	-2	ASP	-	expression tag	UNP A8MW95
D	-1	PRO	-	expression tag	UNP A8MW95

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	22	Total 22	O 22	0	0
2	B	44	Total 44	O 44	0	0
2	C	32	Total 32	O 32	0	0
2	D	41	Total 41	O 41	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 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: Beclin-2

Chain A: 



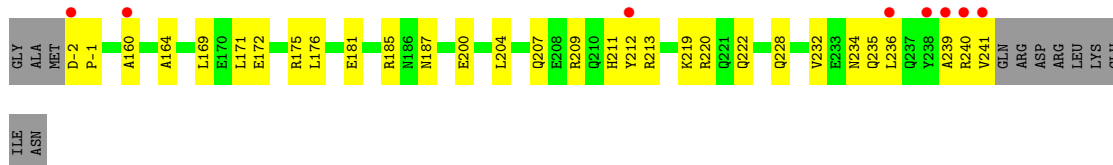
• Molecule 1: Beclin-2

Chain B: 



• Molecule 1: Beclin-2

Chain C: 



• Molecule 1: Beclin-2

Chain D: 



4 Data and refinement statistics

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	95.46Å 44.32Å 97.96Å 90.00° 96.77° 90.00°	Depositor
Resolution (Å)	40.33 – 2.30 40.33 – 2.30	Depositor EDS
% Data completeness (in resolution range)	83.5 (40.33-2.30) 83.6 (40.33-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.95 (at 2.18Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.221 , 0.236 (Not available) , 0.239	Depositor DCC
R_{free} test set	923 reflections (4.33%)	wwPDB-VP
Wilson B-factor (Å ²)	28.1	Xtriage
Anisotropy	0.469	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 51.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.000 for l,-k,h	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3015	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.59% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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

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	1.63	11/715 (1.5%)	1.07	1/962 (0.1%)
1	B	1.62	8/746 (1.1%)	1.10	1/1003 (0.1%)
1	C	1.57	8/698 (1.1%)	1.16	3/942 (0.3%)
1	D	1.66	10/731 (1.4%)	1.08	0/982
All	All	1.62	37/2890 (1.3%)	1.10	5/3889 (0.1%)

All (37) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	211	HIS	CD2-NE2	-7.58	1.29	1.37
1	A	211	HIS	CG-ND1	-6.91	1.30	1.38
1	D	218	LEU	C-O	-6.55	1.16	1.24
1	C	211	HIS	CG-ND1	-6.50	1.31	1.38
1	D	234	ASN	C-O	-6.36	1.16	1.24
1	B	188	ALA	C-O	-6.32	1.16	1.24
1	A	217	ALA	C-O	-6.13	1.17	1.24
1	B	211	HIS	CG-ND1	-6.05	1.31	1.38
1	D	233	GLU	C-O	-5.74	1.17	1.24
1	A	213	ARG	C-O	-5.73	1.17	1.24
1	A	165	GLU	C-O	-5.67	1.17	1.24
1	B	194	LEU	C-O	-5.57	1.17	1.24
1	A	222	GLN	C-O	-5.56	1.17	1.24
1	D	225	LEU	C-O	-5.54	1.17	1.24
1	A	162	LEU	C-O	-5.49	1.17	1.24
1	B	199	ALA	C-O	-5.44	1.17	1.24
1	B	238	TYR	C-O	-5.40	1.17	1.24
1	C	172	GLU	C-O	-5.40	1.17	1.24
1	B	211	HIS	CD2-NE2	-5.40	1.31	1.37
1	D	212	TYR	C-O	-5.36	1.17	1.24
1	A	220	ARG	C-O	-5.34	1.17	1.24
1	C	176	LEU	C-O	-5.27	1.17	1.24
1	D	172	GLU	C-O	-5.27	1.18	1.24
1	C	164	ALA	C-O	-5.26	1.17	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	181	GLU	C-O	-5.24	1.18	1.24
1	D	241	VAL	C-O	-5.24	1.18	1.24
1	A	202	ALA	C-O	-5.23	1.18	1.24
1	C	169	LEU	C-O	-5.23	1.17	1.24
1	C	219	LYS	C-O	-5.21	1.18	1.24
1	D	193	ASP	C-O	-5.17	1.17	1.24
1	B	181	GLU	C-O	-5.16	1.17	1.24
1	D	182	ASP	C-O	-5.16	1.18	1.24
1	D	223	LEU	C-O	-5.14	1.18	1.24
1	C	160	ALA	C-O	-5.06	1.18	1.24
1	A	215	TYR	C-O	-5.03	1.18	1.24
1	A	204	LEU	C-O	-5.02	1.18	1.24
1	B	240	ARG	C-O	-5.02	1.18	1.24

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	158	GLU	N-CA-C	-9.09	101.33	111.14
1	A	161	ALA	N-CA-C	-5.44	106.15	112.89
1	C	-1	PRO	N-CA-C	-5.25	106.88	114.18
1	C	-2	ASP	CA-C-N	-5.15	114.44	119.64
1	C	-2	ASP	C-N-CA	-5.15	114.44	119.64

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	712	0	691	20	0
1	B	742	0	725	19	0
1	C	694	0	667	23	1
1	D	728	0	711	12	0
2	A	22	0	0	0	0
2	B	44	0	0	0	0
2	C	32	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	41	0	0	1	0
All	All	3015	0	2794	54	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 10.

All (54) 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:C:240:ARG:O	1:C:241:VAL:HG23	1.37	1.18
1:A:181:GLU:CD	1:C:220:ARG:HH21	1.71	0.98
1:C:240:ARG:O	1:C:241:VAL:CG2	2.13	0.95
1:A:205:ASP:OD1	1:D:215:TYR:OH	1.86	0.93
1:B:-1:PRO:HA	1:B:160:ALA:HB2	1.63	0.80
1:A:181:GLU:OE2	1:C:220:ARG:NH2	2.13	0.79
1:D:189:ARG:HD2	2:D:319:HOH:O	1.83	0.78
1:B:-1:PRO:O	1:B:160:ALA:HB3	1.84	0.77
1:C:240:ARG:C	1:C:241:VAL:HG23	2.11	0.76
1:C:185:ARG:HH11	1:C:185:ARG:HG3	1.52	0.74
1:A:181:GLU:CD	1:C:220:ARG:NH2	2.45	0.73
1:C:185:ARG:HG3	1:C:185:ARG:NH1	2.04	0.70
1:B:-1:PRO:HA	1:B:160:ALA:CB	2.24	0.67
1:C:171:LEU:HD21	1:C:175:ARG:NH2	2.10	0.65
1:C:239:ALA:C	1:C:241:VAL:H	2.07	0.63
1:A:244:ASP:C	1:A:246:LEU:H	2.07	0.63
1:A:209:ARG:NH2	1:C:187:ASN:HB3	2.15	0.62
1:A:236:LEU:CD2	1:B:169:LEU:HB3	2.36	0.55
1:B:241:VAL:O	1:B:245:ARG:HG2	2.07	0.55
1:A:236:LEU:HD21	1:B:169:LEU:HB3	1.91	0.52
1:A:209:ARG:HH22	1:C:187:ASN:HB3	1.74	0.52
1:B:222:GLN:HG3	1:B:223:LEU:N	2.26	0.51
1:A:245:ARG:O	1:A:246:LEU:HB2	2.12	0.50
1:C:236:LEU:HD13	1:D:169:LEU:CD1	2.41	0.49
1:A:236:LEU:O	1:A:240:ARG:HG3	2.13	0.48
1:B:245:ARG:HG3	1:B:245:ARG:HH11	1.78	0.48
1:C:222:GLN:NE2	1:D:184:ASP:OD1	2.46	0.47
1:C:236:LEU:HD13	1:D:169:LEU:HD11	1.96	0.47
1:C:209:ARG:O	1:C:213:ARG:HG2	2.15	0.47
1:A:238:TYR:O	1:A:242:GLN:HG2	2.16	0.46
1:A:244:ASP:C	1:A:246:LEU:N	2.70	0.45
1:B:219:LYS:O	1:B:222:GLN:HG2	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:166:LEU:HD12	1:D:169:LEU:HD11	1.98	0.45
1:D:175:ARG:NH1	1:D:179:GLU:OE2	2.48	0.45
1:A:172:GLU:HG2	1:B:232:VAL:HG21	1.98	0.45
1:D:169:LEU:C	1:D:169:LEU:HD12	2.41	0.45
1:C:200:GLU:HB3	1:D:204:LEU:HD21	1.99	0.45
1:A:232:VAL:HG11	1:B:173:GLU:HB3	1.98	0.45
1:D:229:LEU:O	1:D:233:GLU:HG3	2.16	0.44
1:A:180:LEU:HA	1:A:183:VAL:HG22	1.99	0.44
1:A:163:ARG:NH1	1:C:234:ASN:HD22	2.16	0.44
1:B:-1:PRO:C	1:B:160:ALA:H	2.26	0.44
1:B:166:LEU:HD23	1:B:166:LEU:HA	1.79	0.44
1:B:245:ARG:HG3	1:B:245:ARG:NH1	2.32	0.43
1:B:226:LEU:HD12	1:B:226:LEU:HA	1.86	0.43
1:A:204:LEU:HD12	1:B:204:LEU:HD22	2.00	0.43
1:C:204:LEU:HD22	1:D:204:LEU:HD23	2.00	0.42
1:B:245:ARG:C	1:B:247:LYS:N	2.77	0.42
1:C:185:ARG:HH11	1:C:185:ARG:CG	2.22	0.42
1:B:245:ARG:C	1:B:247:LYS:H	2.28	0.41
1:B:226:LEU:HD21	1:D:194:LEU:HD21	2.02	0.41
1:A:163:ARG:CZ	1:C:234:ASN:HD22	2.34	0.40
1:A:181:GLU:HG2	1:C:212:TYR:OH	2.21	0.40
1:C:228:GLN:O	1:C:232:VAL:HG23	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:C:207:GLN:NE2	1:C:207:GLN:NE2[2_555]	2.05	0.15

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	85/98 (87%)	83 (98%)	2 (2%)	0	100	100
1	B	89/98 (91%)	87 (98%)	2 (2%)	0	100	100
1	C	84/98 (86%)	83 (99%)	1 (1%)	0	100	100
1	D	86/98 (88%)	86 (100%)	0	0	100	100
All	All	344/392 (88%)	339 (98%)	5 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	71/79 (90%)	70 (99%)	1 (1%)	59	76
1	B	74/79 (94%)	73 (99%)	1 (1%)	59	76
1	C	69/79 (87%)	68 (99%)	1 (1%)	59	76
1	D	74/79 (94%)	72 (97%)	2 (3%)	39	58
All	All	288/316 (91%)	283 (98%)	5 (2%)	53	72

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	185	ARG
1	B	175	ARG
1	C	235	GLN
1	D	170	GLU
1	D	245	ARG

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	198	GLN
1	B	210	GLN

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Mol	Chain	Res	Type
1	B	221	GLN
1	B	222	GLN
1	C	234	ASN
1	D	198	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](#)

There are no ligands in this entry.

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

6.1 Protein, DNA and RNA chains

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	87/98 (88%)	0.44	6 (6%) 23 25	21, 36, 65, 74	0
1	B	91/98 (92%)	0.53	6 (6%) 24 26	20, 40, 74, 99	0
1	C	86/98 (87%)	0.58	8 (9%) 14 16	20, 40, 75, 118	0
1	D	88/98 (89%)	0.53	5 (5%) 29 31	19, 40, 67, 75	0
All	All	352/392 (89%)	0.52	25 (7%) 22 24	19, 39, 69, 118	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	236	LEU	5.4
1	C	241	VAL	4.6
1	A	160	ALA	4.2
1	D	162	LEU	4.0
1	C	-2	ASP	3.9
1	C	240	ARG	3.4
1	A	246	LEU	3.2
1	B	159	ALA	3.0
1	D	168	ASP	3.0
1	C	239	ALA	2.8
1	D	164	ALA	2.7
1	B	167	ARG	2.7
1	C	238	TYR	2.6
1	A	237	GLN	2.6
1	C	212	TYR	2.4
1	B	163	ARG	2.4
1	B	247	LYS	2.3
1	A	181	GLU	2.2
1	B	-1	PRO	2.1
1	C	160	ALA	2.1
1	D	169	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	244	ASP	2.1
1	B	172	GLU	2.0
1	D	166	LEU	2.0
1	A	243	ARG	2.0

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.