



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 11:58 AM UTC

PDB ID : 1PVU / pdb_00001pvu
Title : THE CRYSTAL STRUCTURE OF PVUII ENDONUCLEASE REVEALS
EXTENSIVE STRUCTURAL HOMOLOGIES TO ECORV
Authors : Vlassi, M.; Athanasiadis, A.
Deposited on : 1995-03-09
Resolution : 2.40 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)	:	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

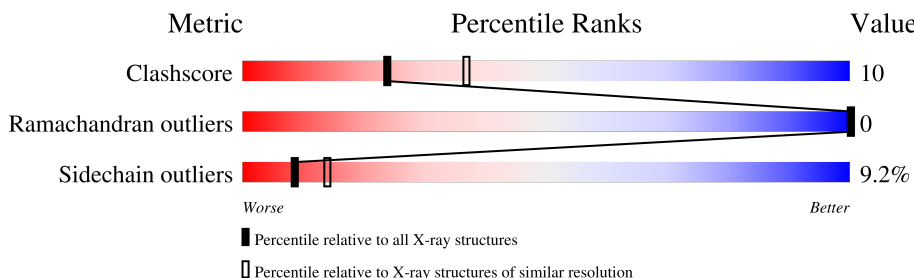
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)

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	156	 62% 27% 9% ..
1	B	156	 60% 29% 10% ..

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2623 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 Pvu II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	154	Total	C	N	O	S	0	0	0
			1272	827	214	229	2			
1	B	154	Total	C	N	O	S	0	0	0
			1272	827	214	229	2			

- Molecule 2 is water.

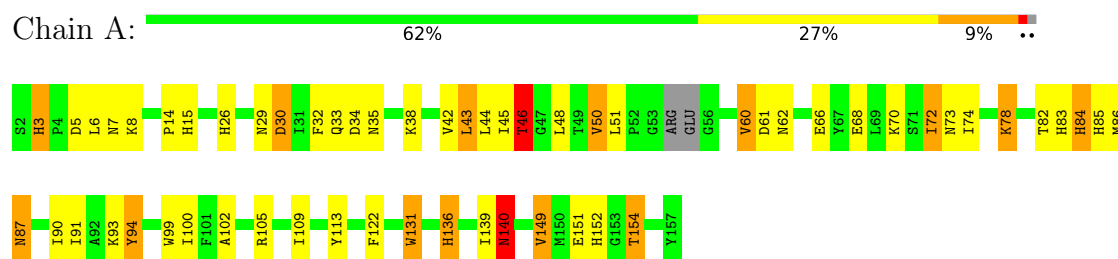
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	49	Total	O	0	0
			49	49		
2	B	30	Total	O	0	0
			30	30		

3 Residue-property plots [i](#)

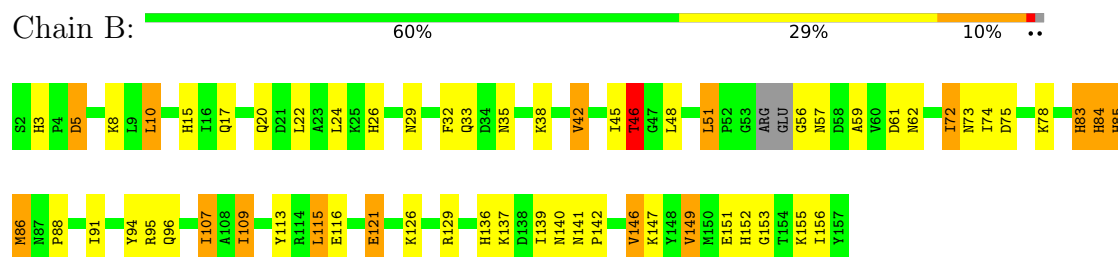
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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: Pvu II



• Molecule 1: Pvu II



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 2	Depositor
Cell constants a, b, c, α , β , γ	84.65Å 106.46Å 47.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	6.00 – 2.40	Depositor
% Data completeness (in resolution range)	(Not available) (6.00-2.40)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.184 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2623	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

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	1.26	12/1308 (0.9%)	1.97	45/1773 (2.5%)
1	B	1.30	10/1308 (0.8%)	2.01	43/1773 (2.4%)
All	All	1.28	22/2616 (0.8%)	1.99	88/3546 (2.5%)

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	149	VAL	CA-CB	10.36	1.67	1.54
1	A	84	HIS	CD2-NE2	-7.52	1.29	1.37
1	A	3	HIS	CD2-NE2	-7.03	1.30	1.37
1	A	152	HIS	CD2-NE2	-7.02	1.30	1.37
1	A	72	ILE	CA-CB	6.93	1.65	1.54
1	B	83	HIS	CD2-NE2	-6.64	1.30	1.37
1	A	149	VAL	CA-CB	6.60	1.63	1.54
1	B	152	HIS	CD2-NE2	-6.54	1.30	1.37
1	A	83	HIS	CD2-NE2	-6.48	1.30	1.37
1	B	136	HIS	CD2-NE2	-6.41	1.30	1.37
1	A	85	HIS	CD2-NE2	-6.35	1.30	1.37
1	B	85	HIS	CD2-NE2	-5.95	1.31	1.37
1	B	107	ILE	CA-CB	5.91	1.62	1.54
1	B	84	HIS	CD2-NE2	-5.80	1.31	1.37
1	B	15	HIS	CD2-NE2	-5.76	1.31	1.37
1	A	136	HIS	CD2-NE2	-5.58	1.31	1.37
1	A	26	HIS	CD2-NE2	-5.50	1.31	1.37
1	B	3	HIS	CD2-NE2	-5.46	1.31	1.37
1	A	83	HIS	CG-ND1	-5.36	1.32	1.38
1	B	83	HIS	CG-ND1	-5.24	1.32	1.38
1	A	152	HIS	CG-ND1	-5.23	1.32	1.38
1	A	15	HIS	CD2-NE2	-5.16	1.32	1.37

All (88) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	140	ASN	CA-CB-CG	10.30	122.90	112.60
1	A	46	THR	N-CA-CB	-9.46	95.62	110.28
1	B	109	ILE	N-CA-CB	9.36	123.09	110.26
1	B	46	THR	N-CA-CB	-8.82	96.72	110.30
1	A	29	ASN	CA-CB-CG	-8.49	104.11	112.60
1	B	17	GLN	OE1-CD-NE2	-8.28	114.32	122.60
1	B	109	ILE	CB-CA-C	-8.13	99.79	111.34
1	B	151	GLU	CA-CB-CG	7.80	129.71	114.10
1	A	33	GLN	CA-C-N	-7.33	112.32	122.87
1	A	33	GLN	C-N-CA	-7.33	112.32	122.87
1	B	96	GLN	OE1-CD-NE2	-7.31	115.29	122.60
1	B	57	ASN	CA-CB-CG	-7.28	105.33	112.60
1	A	3	HIS	CA-CB-CG	7.10	120.90	113.80
1	A	30	ASP	CA-CB-CG	7.10	119.70	112.60
1	B	149	VAL	N-CA-C	-7.00	103.66	110.72
1	A	85	HIS	CB-CG-CD2	-6.98	122.13	131.20
1	B	86	MET	CA-CB-CG	6.95	128.01	114.10
1	B	42	VAL	N-CA-C	-6.85	104.09	110.53
1	B	26	HIS	CB-CG-CD2	-6.84	122.30	131.20
1	A	7	ASN	CA-CB-CG	6.74	119.34	112.60
1	A	33	GLN	N-CA-C	6.66	121.25	112.72
1	A	152	HIS	CB-CG-CD2	-6.59	122.64	131.20
1	A	152	HIS	N-CA-C	6.55	121.27	113.28
1	B	20	GLN	OE1-CD-NE2	-6.50	116.10	122.60
1	A	140	ASN	OD1-CG-ND2	-6.44	116.16	122.60
1	A	26	HIS	CB-CG-CD2	-6.38	122.91	131.20
1	A	3	HIS	CA-C-N	6.33	125.56	118.97
1	A	3	HIS	C-N-CA	6.33	125.56	118.97
1	A	73	ASN	N-CA-C	-6.25	98.35	108.41
1	A	61	ASP	CA-CB-CG	6.21	118.81	112.60
1	A	154	THR	CA-CB-OG1	-6.14	100.38	109.60
1	A	84	HIS	CB-CG-CD2	-6.08	123.30	131.20
1	B	109	ILE	N-CA-C	-6.06	100.97	109.21
1	B	151	GLU	CB-CA-C	-6.03	101.38	110.90
1	B	45	ILE	CA-C-N	5.96	130.82	120.68
1	B	45	ILE	C-N-CA	5.96	130.82	120.68
1	B	5	ASP	CA-CB-CG	5.96	118.56	112.60
1	B	75	ASP	N-CA-C	-5.94	104.72	111.07
1	B	26	HIS	CB-CG-ND1	5.90	131.56	122.70
1	B	15	HIS	CB-CG-CD2	-5.90	123.53	131.20
1	B	83	HIS	CB-CG-CD2	-5.88	123.56	131.20
1	A	34	ASP	CA-CB-CG	5.86	118.46	112.60
1	B	73	ASN	OD1-CG-ND2	-5.85	116.75	122.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	94	TYR	N-CA-C	5.83	118.38	111.33
1	B	3	HIS	CA-C-N	5.77	125.48	119.82
1	B	3	HIS	C-N-CA	5.77	125.48	119.82
1	A	78	LYS	N-CA-CB	-5.75	101.95	111.49
1	A	46	THR	CB-CA-C	5.71	121.63	110.67
1	B	85	HIS	CB-CG-CD2	-5.70	123.79	131.20
1	A	26	HIS	CB-CG-ND1	5.68	131.22	122.70
1	A	78	LYS	CA-CB-CG	5.64	125.38	114.10
1	B	22	LEU	O-C-N	-5.62	116.16	122.12
1	B	152	HIS	CB-CG-CD2	-5.55	123.99	131.20
1	B	96	GLN	N-CA-C	5.54	119.77	112.89
1	B	84	HIS	CA-CB-CG	-5.49	108.31	113.80
1	A	93	LYS	N-CA-C	-5.49	105.22	111.14
1	B	149	VAL	N-CA-CB	5.46	118.77	110.58
1	B	29	ASN	N-CA-C	5.44	118.13	111.82
1	A	152	HIS	CA-C-N	-5.44	116.19	122.77
1	A	152	HIS	C-N-CA	-5.44	116.19	122.77
1	A	51	LEU	O-C-N	-5.42	117.24	121.14
1	B	75	ASP	CA-CB-CG	5.42	118.02	112.60
1	A	45	ILE	CA-C-N	5.41	128.53	120.31
1	A	45	ILE	C-N-CA	5.41	128.53	120.31
1	B	72	ILE	CB-CG1-CD1	-5.40	102.45	113.80
1	A	46	THR	O-C-N	-5.39	115.63	122.27
1	B	116	GLU	CA-C-O	-5.34	114.90	120.88
1	A	33	GLN	CA-CB-CG	-5.31	103.48	114.10
1	A	68	GLU	O-C-N	-5.30	117.12	123.06
1	A	62	ASN	N-CA-C	5.30	117.80	111.71
1	A	15	HIS	CB-CG-CD2	-5.25	124.37	131.20
1	A	131	TRP	CG-CD2-CE3	5.24	139.14	133.90
1	B	74	ILE	CA-CB-CG1	-5.21	101.54	110.40
1	B	3	HIS	CB-CG-CD2	-5.21	124.42	131.20
1	B	61	ASP	CA-CB-CG	5.20	117.80	112.60
1	B	121	GLU	CB-CG-CD	-5.19	103.78	112.60
1	A	100	ILE	N-CA-C	-5.18	100.28	107.80
1	B	141	ASN	N-CA-C	5.17	121.23	109.81
1	A	87	ASN	CA-C-N	5.13	124.80	119.56
1	A	87	ASN	C-N-CA	5.13	124.80	119.56
1	B	152	HIS	CA-C-N	-5.13	117.91	122.47
1	B	152	HIS	C-N-CA	-5.13	117.91	122.47
1	A	136	HIS	CB-CG-CD2	-5.09	124.58	131.20
1	B	146	VAL	CG1-CB-CG2	-5.09	99.61	110.80
1	A	43	LEU	O-C-N	-5.09	116.35	122.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	46	THR	OG1-CB-CG2	5.08	119.47	109.30
1	A	99	TRP	CG-CD2-CE3	5.07	138.97	133.90
1	A	83	HIS	CB-CG-CD2	-5.01	124.69	131.20

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	1272	0	1253	28	0
1	B	1272	0	1253	26	0
2	A	49	0	0	1	0
2	B	30	0	0	2	0
All	All	2623	0	2506	51	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 10.

All (51) 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:B:46:THR:HG23	1:B:48:LEU:HG	1.50	0.91
1:A:46:THR:HG23	1:A:48:LEU:HG	1.64	0.79
1:A:5:ASP:HA	1:A:8:LYS:HD2	1.76	0.67
1:B:84:HIS:O	1:B:140:ASN:HA	1.93	0.67
1:A:3:HIS:HD2	1:A:6:LEU:H	1.41	0.66
1:B:78:LYS:O	1:B:146:VAL:HG23	1.96	0.65
1:A:42:VAL:O	1:A:46:THR:HB	1.96	0.65
1:A:86:MET:HE1	1:A:94:TYR:CE2	2.33	0.63
1:B:42:VAL:O	1:B:46:THR:HB	2.00	0.61
1:B:91:ILE:O	1:B:95:ARG:HG3	2.02	0.59
1:A:3:HIS:CD2	1:A:6:LEU:H	2.21	0.58
1:A:84:HIS:O	1:A:140:ASN:HA	2.04	0.58
1:B:83:HIS:HB2	1:B:94:TYR:OH	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:113:TYR:CE1	1:B:155:LYS:HB2	2.41	0.56
1:A:35:ASN:ND2	1:A:38:LYS:HE3	2.21	0.54
1:A:44:LEU:HD22	1:B:5:ASP:HB2	1.92	0.52
1:B:86:MET:HE3	1:B:142:PRO:HG2	1.92	0.52
1:A:46:THR:CG2	1:A:48:LEU:HG	2.37	0.52
1:A:86:MET:HB3	1:A:139:ILE:HB	1.91	0.52
1:A:60:VAL:HG12	1:A:66:GLU:HG2	1.92	0.51
1:A:3:HIS:HB3	1:A:6:LEU:HB3	1.91	0.51
1:A:87:ASN:ND2	1:A:90:ILE:HG12	2.24	0.51
1:B:46:THR:CG2	1:B:48:LEU:HG	2.32	0.51
1:A:35:ASN:HD22	1:A:38:LYS:HE3	1.77	0.50
1:A:74:ILE:HD12	1:A:74:ILE:HA	1.67	0.48
1:B:48:LEU:HD13	1:B:59:ALA:HB1	1.98	0.46
1:B:72:ILE:HD11	1:B:146:VAL:HG21	1.97	0.46
1:B:8:LYS:HA	1:B:8:LYS:HD2	1.68	0.45
1:A:43:LEU:HD21	1:A:50:VAL:HG13	1.99	0.45
1:A:30:ASP:OD1	1:B:107:ILE:HG22	2.17	0.45
1:B:48:LEU:HD13	1:B:59:ALA:CB	2.47	0.44
1:B:24:LEU:HD23	1:B:24:LEU:HA	1.88	0.44
1:B:56:GLY:N	2:B:183:HOH:O	2.51	0.43
1:A:131:TRP:O	1:A:136:HIS:N	2.50	0.43
1:B:46:THR:HG22	1:B:48:LEU:H	1.83	0.43
1:A:86:MET:HE2	1:A:91:ILE:HG13	2.00	0.43
1:B:147:LYS:H	1:B:147:LYS:HE2	1.82	0.43
1:A:32:PHE:HA	1:B:32:PHE:HA	2.01	0.42
1:A:60:VAL:CG1	1:A:66:GLU:HG2	2.49	0.42
1:B:129:ARG:HB3	2:B:170:HOH:O	2.18	0.42
1:A:122:PHE:CD1	1:A:122:PHE:C	2.98	0.42
1:A:8:LYS:HE3	2:A:185:HOH:O	2.19	0.41
1:A:113:TYR:HA	1:A:154:THR:O	2.21	0.41
1:A:78:LYS:HE2	1:A:78:LYS:HB3	1.87	0.41
1:B:10:LEU:HD13	1:B:10:LEU:HA	1.86	0.41
1:B:95:ARG:HH21	1:B:121:GLU:HG3	1.86	0.41
1:B:115:LEU:HD22	1:B:153:GLY:CA	2.51	0.41
1:A:102:ALA:HB1	1:A:109:ILE:HD11	2.02	0.40
1:B:35:ASN:O	1:B:38:LYS:HB2	2.21	0.40
1:A:3:HIS:HB3	1:A:6:LEU:CB	2.51	0.40
1:B:51:LEU:HD12	1:B:51:LEU:HA	1.92	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	150/156 (96%)	143 (95%)	7 (5%)	0	100	100
1	B	150/156 (96%)	145 (97%)	5 (3%)	0	100	100
All	All	300/312 (96%)	288 (96%)	12 (4%)	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	136/138 (99%)	125 (92%)	11 (8%)	11	18
1	B	136/138 (99%)	122 (90%)	14 (10%)	7	11
All	All	272/276 (99%)	247 (91%)	25 (9%)	8	14

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	PRO
1	A	46	THR
1	A	50	VAL
1	A	60	VAL
1	A	70	LYS
1	A	72	ILE
1	A	82	THR
1	A	105	ARG

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Mol	Chain	Res	Type
1	A	140	ASN
1	A	149	VAL
1	A	151	GLU
1	B	10	LEU
1	B	33	GLN
1	B	46	THR
1	B	51	LEU
1	B	62	ASN
1	B	85	HIS
1	B	88	PRO
1	B	109	ILE
1	B	115	LEU
1	B	126	LYS
1	B	137	LYS
1	B	139	ILE
1	B	149	VAL
1	B	156	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3	HIS
1	A	7	ASN
1	A	15	HIS
1	A	35	ASN
1	A	65	GLN
1	A	140	ASN
1	A	152	HIS
1	B	41	GLN
1	B	62	ASN

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 [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 ⓘ

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.