



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:54 AM UTC

PDB ID : 1PTD / pdb_00001ptd
Title : PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C
Authors : Heinz, D.W.; Ryan, M.; Bullock, T.L.; Griffith, O.H.
Deposited on : 1995-05-24
Resolution : 2.60 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

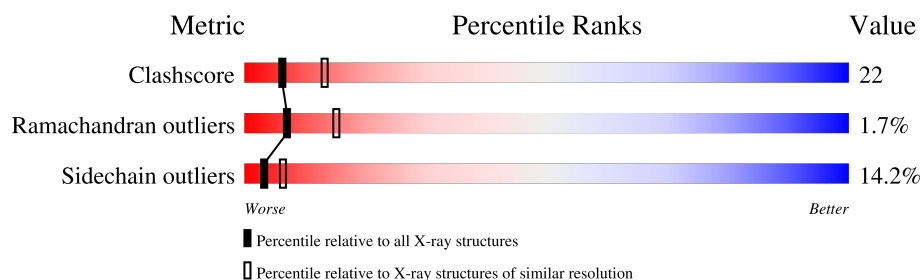
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)

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	298	49% 35% 14% ..

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2474 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 PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	296	Total	C	N	O	S	0	0	0
			2422	1548	400	467	7			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	52	Total	O	0	0
			52	52		

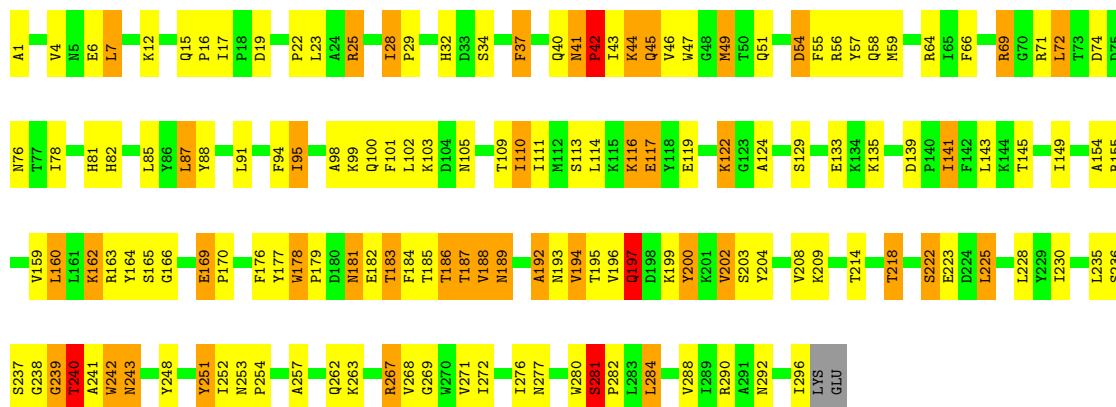
3 Residue-property plots

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: PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C

Chain A: 



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 21	Depositor
Cell constants a, b, c, α , β , γ	45.20Å 45.60Å 160.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.60	Depositor
% Data completeness (in resolution range)	86.0 (8.00-2.60)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.187 , 0.264	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2474	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	1.07	2/2486 (0.1%)	1.43	45/3373 (1.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	28	ILE	CA-CB	7.31	1.59	1.54
1	A	271	VAL	CA-CB	5.41	1.59	1.53

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	165	SER	N-CA-C	9.34	125.52	111.04
1	A	200	TYR	N-CA-C	-9.10	97.40	110.59
1	A	141	ILE	N-CA-C	-8.64	101.77	113.00
1	A	149	ILE	N-CA-C	8.60	120.19	108.84
1	A	243	ASN	N-CA-C	-8.22	101.12	112.30
1	A	183	THR	N-CA-C	-7.92	95.37	108.76
1	A	87	LEU	N-CA-C	-7.61	100.28	110.55
1	A	28	ILE	CA-C-N	-7.46	112.31	119.85
1	A	28	ILE	C-N-CA	-7.46	112.31	119.85
1	A	34	SER	N-CA-C	7.37	120.25	111.33
1	A	222	SER	N-CA-C	7.11	120.85	111.75
1	A	139	ASP	CA-C-N	-6.91	113.06	120.94
1	A	139	ASP	C-N-CA	-6.91	113.06	120.94
1	A	41	ASN	CA-C-N	6.63	128.13	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	41	ASN	C-N-CA	6.63	128.13	119.84
1	A	87	LEU	CA-C-N	-6.55	112.67	122.24
1	A	87	LEU	C-N-CA	-6.55	112.67	122.24
1	A	105	ASN	CA-C-N	6.44	126.13	119.82
1	A	105	ASN	C-N-CA	6.44	126.13	119.82
1	A	257	ALA	N-CA-C	-6.42	104.20	111.07
1	A	154	ALA	N-CA-C	6.36	121.20	113.38
1	A	57	TYR	N-CA-C	-6.34	104.37	111.28
1	A	182	GLU	N-CA-C	6.33	116.80	108.07
1	A	181	ASN	N-CA-C	6.29	120.08	111.39
1	A	197	GLN	N-CA-C	-6.26	98.21	108.41
1	A	95	ILE	N-CA-C	6.21	119.75	111.17
1	A	28	ILE	N-CA-C	6.14	120.95	107.92
1	A	54	ASP	N-CA-C	5.97	118.60	110.55
1	A	44	LYS	N-CA-C	-5.95	104.70	111.07
1	A	162	LYS	N-CA-C	5.87	117.77	108.67
1	A	37	PHE	N-CA-C	5.75	119.91	113.01
1	A	7	LEU	N-CA-C	-5.71	106.36	113.38
1	A	49	MET	N-CA-C	5.66	122.85	110.80
1	A	195	THR	N-CA-C	-5.54	99.39	108.41
1	A	281	SER	N-CA-C	5.50	121.97	109.81
1	A	178	TRP	N-CA-C	5.48	121.92	109.81
1	A	113	SER	N-CA-C	-5.43	100.39	109.24
1	A	69	ARG	CA-C-N	-5.40	117.66	122.47
1	A	69	ARG	C-N-CA	-5.40	117.66	122.47
1	A	17	ILE	N-CA-C	5.34	113.99	109.02
1	A	117	GLU	N-CA-C	5.09	118.65	112.23
1	A	169	GLU	CA-C-N	5.08	124.84	119.76
1	A	169	GLU	C-N-CA	5.08	124.84	119.76
1	A	189	ASN	N-CA-C	-5.06	102.52	110.36
1	A	45	GLN	N-CA-C	5.01	117.13	111.11

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	251	TYR	Sidechain

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	2422	0	2340	106	1
2	A	52	0	0	11	0
All	All	2474	0	2340	106	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 22.

All (106) 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:1:ALA:HB3	1:A:16:PRO:HA	1.57	0.84
1:A:238:GLY:O	1:A:243:ASN:HB3	1.80	0.80
1:A:40:GLN:HA	1:A:45:GLN:HE21	1.46	0.80
1:A:281:SER:CB	1:A:282:PRO:HD3	2.13	0.78
1:A:94:PHE:HZ	1:A:110:ILE:HD11	1.50	0.76
1:A:135:LYS:HE2	2:A:746:HOH:O	1.86	0.76
1:A:188:VAL:HG22	1:A:194:VAL:CG2	2.16	0.75
1:A:189:ASN:HB2	2:A:749:HOH:O	1.84	0.75
1:A:40:GLN:HA	1:A:45:GLN:NE2	2.02	0.74
1:A:197:GLN:NE2	1:A:199:LYS:H	1.84	0.74
1:A:254:PRO:HG3	1:A:280:TRP:HB3	1.69	0.74
1:A:49:MET:HE2	1:A:51:GLN:O	1.88	0.74
1:A:69:ARG:HB3	1:A:117:GLU:HB2	1.72	0.72
1:A:183:THR:HG23	1:A:199:LYS:HE3	1.71	0.72
1:A:281:SER:OG	1:A:282:PRO:HD3	1.90	0.71
1:A:116:LYS:HB2	2:A:707:HOH:O	1.90	0.70
1:A:242:TRP:HA	1:A:242:TRP:CE3	2.26	0.69
1:A:41:ASN:HB2	1:A:44:LYS:HD2	1.73	0.69
1:A:94:PHE:CZ	1:A:110:ILE:HD11	2.28	0.69
1:A:166:GLY:N	2:A:706:HOH:O	2.24	0.69
1:A:94:PHE:HZ	1:A:110:ILE:CD1	2.08	0.67
1:A:43:ILE:O	1:A:47:TRP:HD1	1.78	0.66
1:A:197:GLN:HE22	1:A:199:LYS:H	1.45	0.65
1:A:237:SER:N	2:A:718:HOH:O	2.31	0.63
1:A:242:TRP:HA	1:A:242:TRP:HE3	1.64	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:177:TYR:CD2	1:A:179:PRO:HD3	2.35	0.61
1:A:46:VAL:HG23	1:A:47:TRP:CD1	2.35	0.61
1:A:214:THR:O	1:A:218:THR:HG23	2.01	0.61
1:A:230:ILE:HG23	1:A:272:ILE:HD13	1.83	0.61
1:A:41:ASN:HD22	1:A:44:LYS:HD2	1.67	0.60
1:A:281:SER:HB3	1:A:282:PRO:HD3	1.84	0.59
1:A:160:LEU:HD13	1:A:162:LYS:HG2	1.84	0.59
1:A:183:THR:HG22	1:A:197:GLN:HG2	1.83	0.58
1:A:239:GLY:C	1:A:241:ALA:H	2.10	0.58
1:A:129:SER:O	1:A:133:GLU:HG3	2.02	0.58
1:A:56:ARG:NH1	1:A:101:PHE:HA	2.19	0.58
1:A:272:ILE:HD12	1:A:272:ILE:N	2.20	0.57
1:A:248:TYR:O	1:A:252:ILE:HG13	2.04	0.57
1:A:41:ASN:O	1:A:44:LYS:HB2	2.04	0.57
1:A:122:LYS:HD3	1:A:122:LYS:H	1.70	0.57
1:A:72:LEU:HD13	1:A:124:ALA:HB1	1.88	0.56
1:A:239:GLY:O	1:A:241:ALA:N	2.39	0.55
1:A:267:ARG:HD3	2:A:743:HOH:O	2.07	0.55
1:A:185:THR:HA	1:A:194:VAL:O	2.08	0.54
1:A:284:LEU:O	1:A:288:VAL:HG23	2.07	0.54
1:A:183:THR:CG2	1:A:199:LYS:HE3	2.37	0.54
1:A:19:ASP:OD1	1:A:155:ARG:NH1	2.42	0.52
1:A:204:TYR:O	1:A:208:VAL:HG23	2.10	0.52
1:A:181:ASN:OD1	1:A:199:LYS:HA	2.10	0.51
1:A:253:ASN:HB2	1:A:254:PRO:HD3	1.92	0.51
1:A:188:VAL:HG22	1:A:194:VAL:HG22	1.90	0.51
1:A:32:HIS:HB2	1:A:272:ILE:HG22	1.92	0.51
1:A:46:VAL:HB	1:A:240:THR:H	1.76	0.50
1:A:183:THR:HG23	1:A:199:LYS:CE	2.40	0.50
1:A:184:PHE:CZ	1:A:196:VAL:HB	2.45	0.50
1:A:28:ILE:HG22	1:A:29:PRO:O	2.11	0.50
1:A:176:PHE:CD2	1:A:188:VAL:HG13	2.47	0.50
1:A:202:VAL:HG13	1:A:203:SER:N	2.26	0.49
1:A:268:VAL:O	1:A:268:VAL:HG12	2.11	0.49
1:A:230:ILE:HG23	1:A:272:ILE:CD1	2.43	0.49
1:A:25:ARG:HG3	1:A:225:LEU:HD22	1.95	0.48
1:A:204:TYR:CE1	1:A:208:VAL:HG21	2.48	0.48
1:A:95:ILE:O	1:A:99:LYS:HG3	2.14	0.48
1:A:42:PRO:O	1:A:45:GLN:HB2	2.14	0.47
1:A:281:SER:CB	1:A:282:PRO:CD	2.89	0.47
1:A:74:ASP:C	1:A:76:ASN:H	2.21	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:119:GLU:HG2	2:A:736:HOH:O	2.15	0.47
1:A:239:GLY:C	1:A:241:ALA:N	2.73	0.46
1:A:204:TYR:OH	1:A:251:TYR:HB3	2.16	0.46
1:A:6:GLU:HB2	1:A:16:PRO:HG3	1.98	0.46
1:A:177:TYR:CE2	1:A:179:PRO:HD3	2.51	0.45
1:A:82:HIS:CD2	1:A:82:HIS:C	2.95	0.45
1:A:40:GLN:O	1:A:42:PRO:HD3	2.17	0.44
1:A:192:ALA:HB3	2:A:749:HOH:O	2.18	0.44
1:A:222:SER:HA	1:A:267:ARG:HG2	1.99	0.44
1:A:43:ILE:HA	1:A:46:VAL:HG22	1.99	0.44
1:A:82:HIS:HB2	1:A:87:LEU:HD21	1.99	0.44
1:A:269:GLY:HA2	2:A:743:HOH:O	2.17	0.44
1:A:95:ILE:HG22	1:A:99:LYS:HE3	2.00	0.44
1:A:200:TYR:HB2	1:A:236:SER:OG	2.18	0.44
1:A:183:THR:CG2	1:A:197:GLN:HG2	2.48	0.43
1:A:54:ASP:O	1:A:58:GLN:HG3	2.19	0.43
1:A:15:GLN:N	1:A:16:PRO:HD2	2.32	0.43
1:A:276:ILE:O	1:A:276:ILE:HG23	2.18	0.43
1:A:290:ARG:C	1:A:292:ASN:H	2.26	0.43
1:A:122:LYS:H	1:A:122:LYS:CD	2.29	0.43
1:A:7:LEU:HG	1:A:296:ILE:HD11	2.01	0.43
1:A:116:LYS:HE2	1:A:164:TYR:HA	2.01	0.42
1:A:41:ASN:ND2	1:A:44:LYS:HD2	2.33	0.42
1:A:23:LEU:HA	1:A:23:LEU:HD23	1.83	0.42
1:A:267:ARG:CD	2:A:743:HOH:O	2.67	0.42
1:A:281:SER:OG	1:A:282:PRO:CD	2.62	0.42
1:A:1:ALA:CB	1:A:16:PRO:HA	2.40	0.42
1:A:64:ARG:HD2	1:A:109:THR:O	2.19	0.42
1:A:178:TRP:HA	1:A:184:PHE:CZ	2.55	0.42
1:A:28:ILE:CG2	1:A:64:ARG:HB2	2.50	0.41
1:A:59:MET:HG3	1:A:66:PHE:CZ	2.55	0.41
1:A:169:GLU:HA	1:A:170:PRO:HD2	1.93	0.41
1:A:98:ALA:O	1:A:102:LEU:HD12	2.21	0.41
1:A:111:ILE:HA	1:A:159:VAL:O	2.20	0.41
1:A:163:ARG:HD3	2:A:741:HOH:O	2.21	0.41
1:A:186:THR:HG22	1:A:187:THR:H	1.86	0.41
1:A:37:PHE:HE1	1:A:55:PHE:CE2	2.39	0.40
1:A:277:ASN:OD1	1:A:277:ASN:C	2.63	0.40
1:A:71:ARG:NE	1:A:119:GLU:O	2.46	0.40
1:A:88:TYR:CD1	1:A:88:TYR:N	2.90	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the sym-

metry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:199:LYS:NZ	1:A:262:GLN:NE2[3_646]	2.15	0.05

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	294/298 (99%)	259 (88%)	30 (10%)	5 (2%)	7 15

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	240	THR
1	A	281	SER
1	A	42	PRO
1	A	192	ALA
1	A	239	GLY

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	268/270 (99%)	230 (86%)	38 (14%)	3 6

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	VAL
1	A	12	LYS
1	A	22	PRO
1	A	25	ARG
1	A	42	PRO
1	A	72	LEU
1	A	78	ILE
1	A	81	HIS
1	A	85	LEU
1	A	91	LEU
1	A	100	GLN
1	A	103	LYS
1	A	110	ILE
1	A	114	LEU
1	A	116	LYS
1	A	122	LYS
1	A	141	ILE
1	A	143	LEU
1	A	145	THR
1	A	160	LEU
1	A	186	THR
1	A	187	THR
1	A	188	VAL
1	A	193	ASN
1	A	194	VAL
1	A	197	GLN
1	A	202	VAL
1	A	209	LYS
1	A	218	THR
1	A	223	GLU
1	A	225	LEU
1	A	228	LEU
1	A	235	LEU
1	A	240	THR
1	A	242	TRP
1	A	263	LYS
1	A	267	ARG
1	A	284	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	ASN

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Mol	Chain	Res	Type
1	A	41	ASN
1	A	45	GLN
1	A	81	HIS
1	A	82	HIS
1	A	100	GLN
1	A	148	ASN
1	A	193	ASN
1	A	197	GLN
1	A	220	ASN
1	A	221	ASN
1	A	258	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 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.