



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 3, 2023 – 09:27 am GMT

PDB ID : 1H8A
Title : CRYSTAL STRUCTURE OF TERNARY PROTEIN-DNA COMPLEX3
Authors : Tahirov, T.H.; Ogata, K.
Deposited on : 2001-01-31
Resolution : 2.23 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 : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.36
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

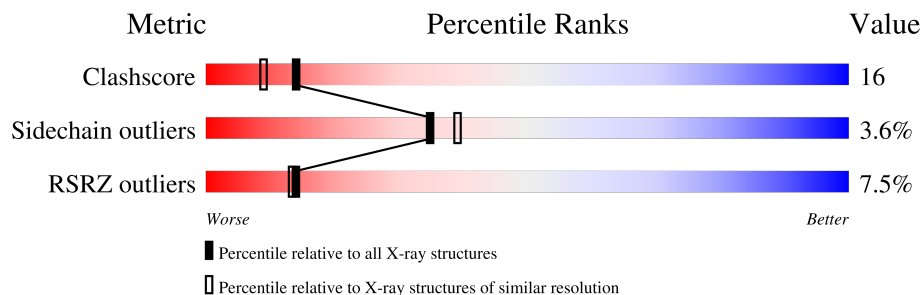
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.23 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	2539 (2.26-2.22)
Sidechain outliers	138945	2490 (2.26-2.22)
RSRZ outliers	127900	2353 (2.26-2.22)

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	78	 5% (poor fit), 73% (0 outliers), 14% (1 outlier), 13% (2+ outliers)
1	B	78	 % (poor fit), 72% (0 outliers), 12% (1 outlier), 14% (2+ outliers)
2	C	128	 13% (poor fit), 56% (0 outliers), 23% (1 outlier), 18% (2+ outliers)
3	D	26	 46% (0 outliers), 46% (1 outlier), 8% (2+ outliers)
4	E	26	 31% (0 outliers), 69% (1 outlier)

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 3276 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 CAAT/ENHANCER BINDING PROTEIN BETA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	68	Total 579	C 354	N 117	O 107	S 1	0	0	0
1	B	67	Total 572	C 349	N 116	O 106	S 1	0	0	0

- Molecule 2 is a protein called MYB TRANSFORMING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	105	Total 894	C 557	N 180	O 155	S 2	0	0	0

- Molecule 3 is a DNA chain called DNA(5'-(*GP*AP*TP*GP*TP*GP*GP*CP*GP*CP*A
P* AP*TP*CP*CP*TP*TP*AP*AP*CP*GP*GP*AP*CP*TP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	D	26	Total 533	C 254	N 100	O 154	P 25	0	0	0

- Molecule 4 is a DNA chain called DNA(5'-(*CP*CP*AP*GP*TP*CP*CP*GP*TP*TP*AP
* AP*GP*GP*AP*TP*TP*GP*CP*GP*CP*CP*AP*CP*AP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
4	E	26	Total 527	C 252	N 96	O 154	P 25	0	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	42	Total 42	O 42	0	0
5	B	46	Total 46	O 46	0	0

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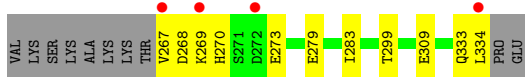
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	C	7	Total O 7 7	0	0
5	D	42	Total O 42 42	0	0
5	E	34	Total O 34 34	0	0

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.

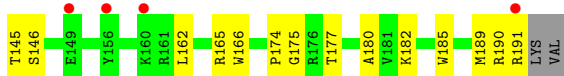
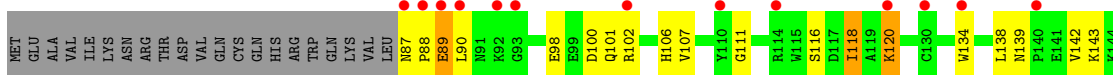
- Molecule 1: CAAT/ENHANCER BINDING PROTEIN BETA



- Molecule 1: CAAT/ENHANCER BINDING PROTEIN BETA



- Molecule 2: MYB TRANSFORMING PROTEIN



- Molecule 3: DNA(5'-(*GP*AP*TP*GP*TP*GP*GP*CP*GP*CP*AP* AP*TP*CP*CP*TP*TP*AP*AP*CP*GP*GP*AP*CP*TP*G)-3')



- Molecule 4: DNA(5'-(*CP*CP*AP*GP*TP*CP*CP*GP*TP*TP*AP* AP*GP*GP*AP*TP*TP*GP*CP*GP*CP*AP*CP*AP*T)-3')



C1	G4	T5	C6	C7	G8	T9	A15	T16	T17	G18	C19	G20	C21	C22	A23	C24	A25	T26
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4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	109.86Å 166.70Å 39.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.85 – 2.23 19.85 – 2.10	Depositor EDS
% Data completeness (in resolution range)	97.9 (19.85-2.23) 97.2 (19.85-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.33 (at 2.11Å)	Xtrriage
Refinement program	CNS 0.9	Depositor
R, R_{free}	0.245 , 0.288 0.231 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	50.6	Xtrriage
Anisotropy	0.220	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 51.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3276	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.00% 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 [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	0.37	0/582	0.52	0/772
1	B	0.37	0/575	0.52	0/762
2	C	0.27	0/918	0.49	0/1236
3	D	0.48	0/598	0.87	0/922
4	E	0.46	0/590	0.81	0/908
All	All	0.39	0/3263	0.66	0/4600

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
3	D	0	2
4	E	0	1
All	All	0	3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	D	1	DG	Sidechain
3	D	2	DA	Sidechain
4	E	1	DC	Sidechain

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	579	0	609	14	0
1	B	572	0	600	10	0
2	C	894	0	884	40	0
3	D	533	0	294	14	0
4	E	527	0	294	16	0
5	A	42	0	0	1	0
5	B	46	0	0	1	0
5	C	7	0	0	1	0
5	D	42	0	0	0	0
5	E	34	0	0	0	0
All	All	3276	0	2681	91	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 16.

All (91) 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)
2:C:87:ASN:HB3	2:C:88:PRO:HD2	1.47	0.95
2:C:98:GLU:HG3	2:C:102:ARG:HH12	1.36	0.90
4:E:8:DG:H1'	4:E:9:DT:H5'	1.60	0.83
2:C:87:ASN:HB3	2:C:88:PRO:CD	2.09	0.83
3:D:14:DC:H1'	3:D:15:DC:H5'	1.65	0.78
2:C:139:ASN:O	2:C:142:VAL:HG12	1.84	0.78
1:B:329:ASN:O	1:B:333:GLN:HG2	1.88	0.74
1:A:267:VAL:HG23	5:A:2001:HOH:O	1.90	0.72
3:D:7:DG:H2''	3:D:8:DC:H5'	1.69	0.72
2:C:118:ILE:HD13	2:C:118:ILE:O	1.90	0.71
2:C:120:LYS:HZ2	2:C:120:LYS:HA	1.57	0.69
1:A:299:THR:HG22	1:B:299:THR:HG22	1.74	0.69
2:C:143:LYS:HG3	2:C:175:GLY:HA3	1.74	0.69
2:C:116:SER:O	2:C:120:LYS:HD2	1.94	0.68
4:E:23:DA:H1'	4:E:24:DC:H5'	1.77	0.66
2:C:177:THR:HG23	2:C:180:ALA:H	1.61	0.65
1:A:267:VAL:HG12	1:A:268:ASP:N	2.11	0.65
4:E:19:DC:H2''	4:E:20:DG:H5'	1.80	0.64
4:E:21:DC:H2''	4:E:22:DC:H5'	1.79	0.63
4:E:21:DC:H2''	4:E:22:DC:C5'	2.32	0.60
2:C:89:GLU:O	2:C:90:LEU:HD23	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:7:DG:H2''	3:D:8:DC:C5'	2.33	0.59
4:E:6:DC:H2''	4:E:7:DC:H5'	1.85	0.59
4:E:19:DC:H2''	4:E:20:DG:C5'	2.33	0.59
4:E:5:DT:H1'	4:E:6:DC:H5'	1.85	0.58
1:A:309:GLU:HA	1:A:309:GLU:OE1	2.04	0.57
3:D:19:DA:H1'	3:D:20:DC:C5	2.39	0.57
2:C:142:VAL:O	2:C:142:VAL:HG13	2.03	0.57
2:C:145:THR:HG22	2:C:146:SER:N	2.20	0.57
2:C:120:LYS:HA	2:C:120:LYS:NZ	2.19	0.56
3:D:1:DG:H2''	3:D:2:DA:H8	1.71	0.56
2:C:87:ASN:CB	2:C:88:PRO:HD2	2.30	0.56
3:D:20:DC:H2''	3:D:21:DG:H5'	1.88	0.56
4:E:19:DC:H1'	4:E:20:DG:H5''	1.86	0.55
1:A:299:THR:CG2	1:B:299:THR:HG22	2.37	0.55
3:D:21:DG:H2''	3:D:22:DG:OP2	2.05	0.55
2:C:145:THR:HG22	2:C:146:SER:H	1.72	0.54
2:C:107:VAL:O	2:C:111:GLY:HA2	2.07	0.54
2:C:177:THR:CG2	2:C:180:ALA:H	2.21	0.53
1:A:267:VAL:CG1	1:A:268:ASP:N	2.72	0.53
4:E:15:DA:H1'	4:E:16:DT:H5''	1.90	0.53
3:D:7:DG:H1'	3:D:8:DC:H5''	1.91	0.53
2:C:98:GLU:HG3	2:C:102:ARG:NH1	2.15	0.52
2:C:107:VAL:HG11	2:C:134:TRP:CZ2	2.45	0.52
4:E:4:DG:H1'	4:E:5:DT:H5''	1.92	0.52
2:C:87:ASN:CB	2:C:88:PRO:CD	2.86	0.51
4:E:5:DT:H2''	4:E:6:DC:H5'	1.93	0.51
2:C:190:ARG:HG2	2:C:190:ARG:HH11	1.76	0.50
2:C:100:ASP:OD1	2:C:138:LEU:HD21	2.11	0.50
2:C:107:VAL:HG21	2:C:134:TRP:CE3	2.46	0.50
2:C:166:TRP:NE1	2:C:182:LYS:HG3	2.26	0.50
1:A:279:GLU:O	1:A:283:ILE:HG12	2.12	0.49
1:B:297:LEU:HA	1:B:300:GLN:HE21	1.77	0.49
1:B:309:GLU:HA	1:B:309:GLU:OE1	2.13	0.49
1:A:268:ASP:CG	1:A:270:HIS:H	2.16	0.49
3:D:1:DG:H2''	3:D:2:DA:C8	2.47	0.49
2:C:191:ARG:HB2	2:C:191:ARG:NH1	2.29	0.48
2:C:190:ARG:HG2	2:C:190:ARG:NH1	2.27	0.48
1:B:296:ASN:O	1:B:300:GLN:HG3	2.13	0.47
1:A:268:ASP:OD1	1:A:270:HIS:HB2	2.14	0.47
2:C:106:HIS:CG	2:C:118:ILE:HB	2.50	0.47
1:A:268:ASP:OD2	1:A:269:LYS:N	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:267:VAL:CG1	1:A:268:ASP:H	2.28	0.47
4:E:5:DT:C2'	4:E:6:DC:H5'	2.46	0.46
4:E:25:DA:H2''	4:E:26:DT:H5'	1.95	0.46
1:B:311:GLU:HA	1:B:311:GLU:OE1	2.16	0.46
1:A:334:LEU:N	1:A:334:LEU:HD23	2.31	0.45
1:B:300:GLN:NE2	5:B:2027:HOH:O	2.49	0.45
2:C:185:TRP:HA	2:C:189:MET:HB2	1.97	0.45
4:E:24:DC:H2''	4:E:25:DA:OP2	2.17	0.45
1:A:299:THR:HG22	1:B:299:THR:CG2	2.43	0.44
2:C:182:LYS:HE3	5:C:2005:HOH:O	2.18	0.44
2:C:143:LYS:HG3	2:C:175:GLY:CA	2.45	0.43
2:C:102:ARG:HH11	2:C:102:ARG:HG3	1.83	0.43
3:D:7:DG:C2'	3:D:8:DC:C5'	2.96	0.43
3:D:23:DA:H1'	3:D:24:DC:H5'	2.00	0.43
3:D:23:DA:H2''	3:D:24:DC:H5'	2.01	0.42
2:C:143:LYS:HE2	2:C:174:PRO:O	2.19	0.42
1:A:267:VAL:HG12	1:A:268:ASP:H	1.80	0.42
1:B:274:TYR:HD1	1:B:277:ARG:HH22	1.68	0.41
2:C:118:ILE:HD13	2:C:118:ILE:C	2.40	0.41
2:C:98:GLU:CG	2:C:102:ARG:HH12	2.21	0.41
2:C:134:TRP:HA	2:C:138:LEU:HB2	2.01	0.41
4:E:18:DG:H2''	4:E:19:DC:H5'	2.02	0.41
2:C:101:GLN:HE21	2:C:101:GLN:HB2	1.69	0.41
3:D:23:DA:H1'	3:D:24:DC:C5'	2.51	0.41
3:D:25:DT:H2''	3:D:26:DG:OP2	2.19	0.41
2:C:107:VAL:HG11	2:C:134:TRP:CH2	2.56	0.41
2:C:98:GLU:HA	2:C:98:GLU:OE1	2.21	0.41
2:C:120:LYS:HD2	2:C:120:LYS:N	2.37	0.40
2:C:162:LEU:HB3	2:C:165:ARG:HG3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

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	65/74 (88%)	63 (97%)	2 (3%)	40	46
1	B	64/74 (86%)	61 (95%)	3 (5%)	26	27
2	C	94/116 (81%)	91 (97%)	3 (3%)	39	44
All	All	223/264 (84%)	215 (96%)	8 (4%)	35	39

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	273	GLU
1	A	333	GLN
1	B	273	GLU
1	B	309	GLU
1	B	311	GLU
2	C	89	GLU
2	C	118	ILE
2	C	120	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	333	GLN
1	B	300	GLN
2	C	101	GLN
2	C	108	GLN
2	C	136	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](#)

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	68/78 (87%)	0.18	4 (5%) 22 21	30, 52, 102, 113	0
1	B	67/78 (85%)	0.18	1 (1%) 73 74	27, 47, 77, 96	0
2	C	105/128 (82%)	1.10	17 (16%) 1 1	54, 87, 111, 137	0
3	D	26/26 (100%)	-0.25	0 100 100	36, 55, 71, 72	0
4	E	26/26 (100%)	-0.32	0 100 100	37, 53, 71, 80	0
All	All	292/336 (86%)	0.42	22 (7%) 14 13	27, 62, 107, 137	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	87	ASN	8.4
2	C	90	LEU	7.3
2	C	88	PRO	7.0
2	C	93	GLY	6.6
2	C	110	TYR	6.4
2	C	89	GLU	4.7
2	C	156	TYR	4.5
1	A	272	ASP	4.0
2	C	149	GLU	3.6
1	A	267	VAL	3.1
2	C	130	CYS	3.1
2	C	120	LYS	2.9
2	C	92	LYS	2.8
1	A	334	LEU	2.8
2	C	140	PRO	2.7
2	C	102	ARG	2.6
1	A	269	LYS	2.6
2	C	160	LYS	2.5
2	C	114	ARG	2.5
2	C	191	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	334	LEU	2.3
2	C	134	TRP	2.1

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 monosaccharides 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.