



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 10, 2024 – 05:27 PM EST

PDB ID : 4N9H
Title : Crystal structure of Transcription regulation Protein CRP
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Deposited on : 2013-10-21
Resolution : 2.20 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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

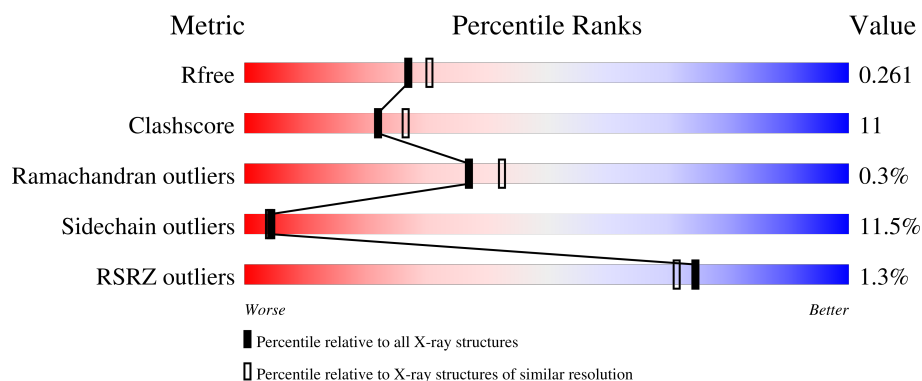
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 2.20 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}	164625	5791 (2.20-2.20)
Clashscore	180529	6634 (2.20-2.20)
Ramachandran outliers	177936	6560 (2.20-2.20)
Sidechain outliers	177891	6561 (2.20-2.20)
RSRZ outliers	164620	5791 (2.20-2.20)

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	210	 71% 20% . .
1	B	210	 2% 63% 24% 8% . .

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3269 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 Catabolite gene activator.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	201	Total	C	N	O	S	Se	0	0	0
			1578	1001	276	292	3	6			
1	B	201	Total	C	N	O	S	Se	0	0	0
			1578	1001	276	292	3	6			

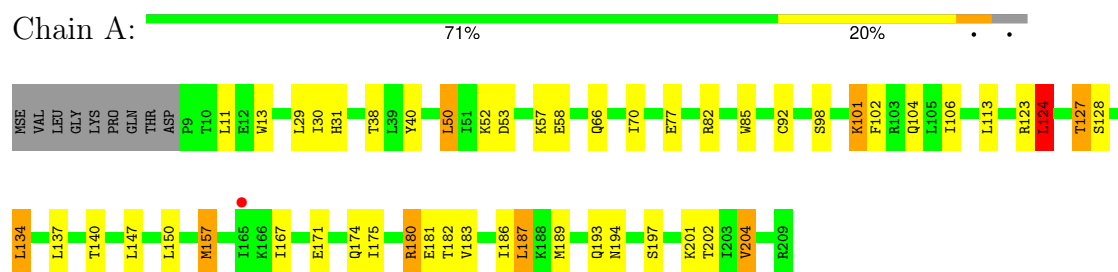
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	63	Total	O	0	0
			63	63		
2	B	50	Total	O	0	0
			50	50		

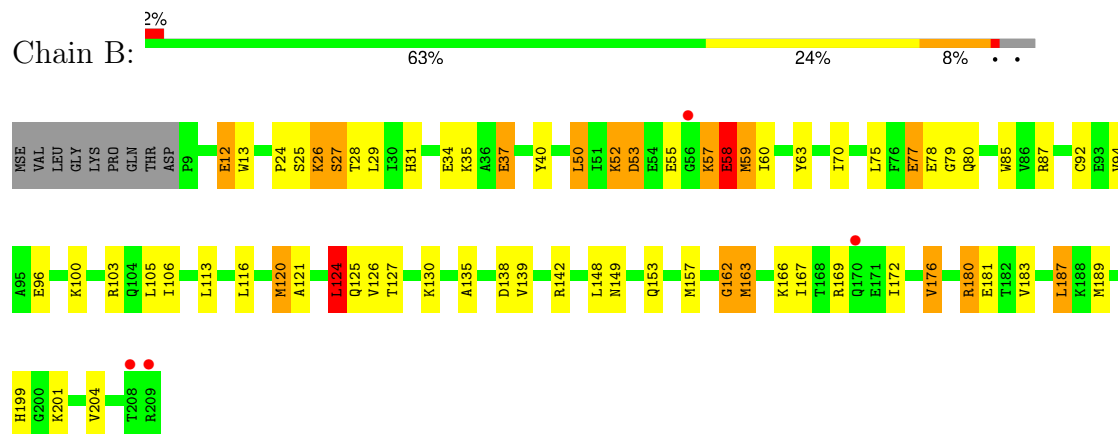
3 Residue-property plots

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 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: Catabolite gene activator



• Molecule 1: Catabolite gene activator



4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	120.62Å 120.62Å 60.35Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.20 50.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.5 (50.00-2.20) 99.6 (50.00-2.20)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	11.20 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.202 , 0.263 0.200 , 0.261	Depositor DCC
R_{free} test set	1300 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	43.0	Xtriage
Anisotropy	0.040	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 45.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.041 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3269	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.33% 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	0.97	2/1597 (0.1%)	1.02	5/2141 (0.2%)
1	B	1.05	6/1597 (0.4%)	1.20	12/2141 (0.6%)
All	All	1.01	8/3194 (0.3%)	1.11	17/4282 (0.4%)

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	B	0	2

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	162	GLY	C-O	7.70	1.35	1.23
1	B	59	MSE	N-CA	6.08	1.58	1.46
1	A	92	CYS	CB-SG	-6.05	1.72	1.82
1	B	149	ASN	CG-OD1	6.00	1.37	1.24
1	B	12	GLU	CD-OE2	5.50	1.31	1.25
1	B	13	TRP	CD2-CE2	5.50	1.48	1.41
1	B	85	TRP	CD2-CE2	5.31	1.47	1.41
1	A	13	TRP	CD2-CE2	5.04	1.47	1.41

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	163	MSE	O-C-N	-20.04	90.64	122.70
1	B	58	GLU	CA-C-O	14.20	149.91	120.10
1	B	189	MSE	CG-SE-CE	-8.62	79.93	98.90
1	B	163	MSE	CA-C-N	7.89	134.56	117.20
1	A	29	LEU	CA-CB-CG	7.62	132.82	115.30
1	B	120	MSE	CG-SE-CE	-7.29	82.87	98.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	163	MSE	CB-CA-C	-7.25	95.89	110.40
1	B	124	LEU	CB-CG-CD1	7.25	123.33	111.00
1	B	148	LEU	CA-CB-CG	6.53	130.33	115.30
1	A	134	LEU	CA-CB-CG	5.95	128.98	115.30
1	B	180	ARG	NE-CZ-NH1	5.92	123.26	120.30
1	B	120	MSE	CA-CB-CG	-5.68	103.65	113.30
1	A	134	LEU	CB-CG-CD1	5.55	120.43	111.00
1	A	123	ARG	NE-CZ-NH1	5.53	123.06	120.30
1	A	124	LEU	CA-CB-CG	5.23	127.33	115.30
1	B	12	GLU	OE1-CD-OE2	5.20	129.54	123.30
1	B	92	CYS	CA-CB-SG	-5.09	104.83	114.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	162	GLY	Mainchain
1	B	163	MSE	Mainchain

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	1578	0	1610	30	0
1	B	1578	0	1610	41	0
2	A	63	0	0	1	0
2	B	50	0	0	3	0
All	All	3269	0	3220	67	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 11.

All (67) 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:124:LEU:HD13	1:B:124:LEU:HD13	1.52	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:197:SER:OG	1:A:204:VAL:HG13	1.76	0.85
1:A:127:THR:HG21	1:B:127:THR:HG21	1.62	0.81
1:B:57:LYS:HE3	1:B:58:GLU:H	1.45	0.81
1:B:31:HIS:O	1:B:34:GLU:HG3	1.82	0.80
1:B:135:ALA:O	1:B:139:VAL:HG23	1.88	0.73
1:B:96:GLU:OE2	2:B:307:HOH:O	2.05	0.73
1:B:31:HIS:N	1:B:34:GLU:OE2	2.19	0.72
1:B:77:GLU:OE2	1:B:77:GLU:O	2.06	0.72
1:A:77:GLU:OE1	1:B:125:GLN:NE2	2.22	0.72
1:B:35:LYS:HE2	1:B:37:GLU:OE2	1.93	0.69
1:B:52:LYS:HA	1:B:57:LYS:O	1.94	0.68
1:B:78:GLU:OE1	1:B:78:GLU:HA	1.92	0.67
1:A:102:PHE:CZ	1:A:106:ILE:HD11	2.31	0.65
1:A:201:LYS:HG2	1:A:201:LYS:O	2.00	0.62
1:B:53:ASP:HB3	1:B:59:MSE:CG	2.30	0.61
1:B:106:ILE:HD12	1:B:113:LEU:HB2	1.81	0.60
1:B:138:ASP:O	1:B:142:ARG:HG3	2.02	0.59
1:B:40:TYR:HB2	1:B:70:ILE:HB	1.85	0.58
1:B:180:ARG:HH11	1:B:180:ARG:HG3	1.67	0.58
1:B:53:ASP:HB3	1:B:59:MSE:HG3	1.86	0.57
1:B:169:ARG:NE	2:B:338:HOH:O	2.36	0.57
1:B:57:LYS:CE	1:B:58:GLU:H	2.17	0.55
1:A:31:HIS:HA	1:A:85:TRP:CE3	2.42	0.54
1:B:60:ILE:O	1:B:60:ILE:HG23	2.08	0.54
1:A:180:ARG:N	1:A:180:ARG:HD3	2.23	0.54
1:B:24:PRO:O	1:B:27:SER:OG	2.23	0.54
1:A:127:THR:HG21	1:B:127:THR:CG2	2.38	0.51
1:A:197:SER:OG	1:A:204:VAL:CG1	2.54	0.51
1:A:171:GLU:O	1:A:175:ILE:HG13	2.11	0.51
1:B:172:ILE:O	1:B:176:VAL:HB	2.13	0.49
1:A:38:THR:HG22	1:A:98:SER:HA	1.95	0.49
1:B:60:ILE:HD11	1:B:63:TYR:CZ	2.49	0.48
1:A:186:ILE:O	1:A:189:MSE:HB3	2.14	0.48
1:B:50:LEU:HA	1:B:59:MSE:O	2.14	0.48
1:A:102:PHE:CE2	1:A:106:ILE:HD11	2.48	0.47
1:A:106:ILE:HG13	1:A:113:LEU:HB2	1.96	0.47
1:B:35:LYS:CE	1:B:37:GLU:OE2	2.63	0.47
1:B:53:ASP:HB3	1:B:59:MSE:HG2	1.96	0.46
1:B:28:THR:HG21	1:B:31:HIS:CD2	2.49	0.46
1:A:101:LYS:HE2	1:A:104:GLN:OE1	2.16	0.46
1:A:150:LEU:HD11	1:A:167:ILE:HD13	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:180:ARG:O	1:A:181:GLU:C	2.54	0.46
1:B:25:SER:O	1:B:26:LYS:HB2	2.14	0.46
1:B:35:LYS:HE3	1:B:79:GLY:HA2	1.98	0.46
1:A:193:GLN:O	1:A:194:ASN:HB2	2.15	0.46
1:A:50:LEU:HG	1:A:85:TRP:HB2	1.99	0.45
1:B:60:ILE:O	1:B:60:ILE:CG2	2.65	0.45
1:A:53:ASP:OD2	1:A:57:LYS:NZ	2.46	0.45
1:B:166:LYS:HB3	1:B:166:LYS:HE2	1.62	0.44
1:B:183:VAL:HG12	1:B:187:LEU:HD22	2.00	0.44
1:A:53:ASP:OD2	1:A:57:LYS:HB2	2.17	0.44
1:A:102:PHE:O	1:A:106:ILE:HD13	2.18	0.44
1:A:66:GLN:CG	2:A:349:HOH:O	2.65	0.44
1:A:30:ILE:HG23	1:A:82:ARG:HG3	2.00	0.44
1:B:29:LEU:HD21	1:B:94:VAL:HG21	2.00	0.44
1:B:166:LYS:HA	1:B:201:LYS:O	2.18	0.43
1:B:199:HIS:HB2	2:B:348:HOH:O	2.17	0.43
1:B:116:LEU:HD23	1:B:120:MSE:HE2	2.02	0.42
1:A:180:ARG:C	1:A:182:THR:N	2.74	0.41
1:A:183:VAL:HG12	1:A:187:LEU:HD22	2.01	0.41
1:A:40:TYR:HB2	1:A:70:ILE:HB	2.03	0.41
1:A:52:LYS:HG2	1:A:58:GLU:HG2	2.03	0.41
1:A:157:MSE:HE2	1:A:157:MSE:HB3	1.93	0.41
1:B:75:LEU:O	1:B:103:ARG:NH2	2.47	0.41
1:B:167:ILE:HG12	1:B:172:ILE:HG13	2.02	0.40
1:B:121:ALA:O	1:B:125:GLN:HG3	2.20	0.40

There are no symmetry-related clashes.

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	199/210 (95%)	193 (97%)	6 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	199/210 (95%)	190 (96%)	8 (4%)	1 (0%)	25	28
All	All	398/420 (95%)	383 (96%)	14 (4%)	1 (0%)	37	42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	53	ASP

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	170/174 (98%)	154 (91%)	16 (9%)	7	7
1	B	170/174 (98%)	147 (86%)	23 (14%)	3	2
All	All	340/348 (98%)	301 (88%)	39 (12%)	4	4

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	LEU
1	A	50	LEU
1	A	101	LYS
1	A	124	LEU
1	A	127	THR
1	A	128	SER
1	A	134	LEU
1	A	137	LEU
1	A	140	THR
1	A	147	LEU
1	A	157	MSE
1	A	174	GLN
1	A	180	ARG
1	A	187	LEU
1	A	202	THR

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Mol	Chain	Res	Type
1	A	204	VAL
1	B	12	GLU
1	B	26	LYS
1	B	27	SER
1	B	37	GLU
1	B	50	LEU
1	B	52	LYS
1	B	55	GLU
1	B	57	LYS
1	B	58	GLU
1	B	77	GLU
1	B	80	GLN
1	B	87	ARG
1	B	100	LYS
1	B	105	LEU
1	B	124	LEU
1	B	126	VAL
1	B	130	LYS
1	B	153	GLN
1	B	157	MSE
1	B	176	VAL
1	B	181	GLU
1	B	187	LEU
1	B	204	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	195/210 (92%)	0.07	1 (0%) 87 85	25, 46, 75, 99	0
1	B	195/210 (92%)	0.09	4 (2%) 63 59	28, 48, 80, 112	0
All	All	390/420 (92%)	0.08	5 (1%) 74 71	25, 47, 77, 112	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	208	THR	4.0
1	B	170	GLN	3.6
1	B	209	ARG	2.3
1	B	56	GLY	2.2
1	A	165	ILE	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.