



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 9VS2 / pdb_00009vs2
Title : Crystal structure of FOXC2/NFAT1 complex bound to ARRE3-P DNA
Authors : Chen, X.J.; Chen, Y.H.
Deposited on : 2025-07-08
Resolution : 2.65 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	:	9.0.015 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.50

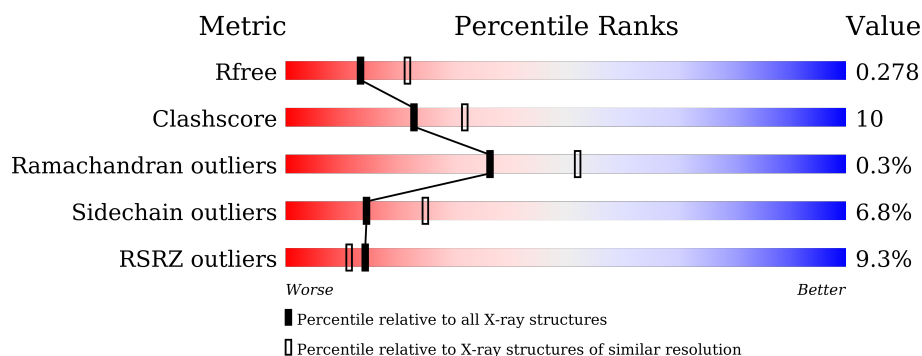
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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	1110 (2.66-2.66)
Clashscore	190562	1141 (2.66-2.66)
Ramachandran outliers	187476	1126 (2.66-2.66)
Sidechain outliers	187428	1126 (2.66-2.66)
RSRZ outliers	180081	1110 (2.66-2.66)

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	C	21	
2	D	21	
3	N	287	
4	A	103	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 3964 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 DNA chain called ARRE3-P-S.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	C	21	Total	C	N	O	P	0	0	0
			431	209	76	126	20			

- Molecule 2 is a DNA chain called ARRE3-P-AS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	21	Total	C	N	O	P	0	0	0
			424	206	76	122	20			

- Molecule 3 is a protein called Nuclear factor of activated T-cells, cytoplasmic 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	N	287	Total	C	N	O	S	0	0	0
			2281	1429	416	427	9			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
N	394	SER	LEU	conflict	UNP Q13469
N	395	VAL	PRO	conflict	UNP Q13469
N	501	VAL	ILE	conflict	UNP Q13469
N	562	ALA	THR	conflict	UNP Q13469

- Molecule 4 is a protein called Forkhead box protein C2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	A	91	Total	C	N	O	S	0	0	0
			769	497	136	132	4			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	70	GLY	-	expression tag	UNP Q99958
A	71	PRO	-	expression tag	UNP Q99958

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	12	Total 12	O 12	0	0
5	D	10	Total 10	O 10	0	0
5	N	33	Total 33	O 33	0	0
5	A	4	Total 4	O 4	0	0

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.

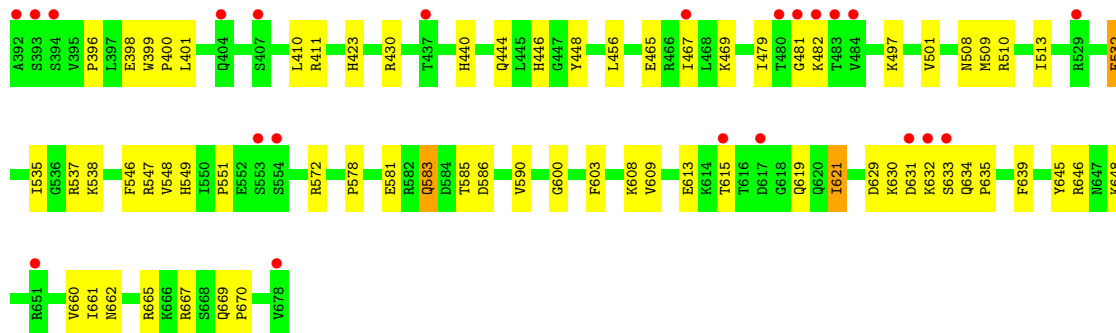
- Molecule 1: ARRE3-P-S



- Molecule 2: ARRE3-P-AS



- Molecule 3: Nuclear factor of activated T-cells, cytoplasmic 2



- Molecule 4: Forkhead box protein C2





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	67.71Å 79.51Å 120.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.40 – 2.65 47.40 – 2.65	Depositor EDS
% Data completeness (in resolution range)	95.5 (47.40-2.65) 95.4 (47.40-2.65)	Depositor EDS
R_{merge}	0.30	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.39 (at 2.65Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.228 , 0.278 0.234 , 0.278	Depositor DCC
R_{free} test set	942 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å ²)	45.3	Xtriage
Anisotropy	0.063	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 41.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	3964	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.60% 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	C	0.52	0/483	0.57	0/745
2	D	0.64	1/475 (0.2%)	0.56	0/730
3	N	0.54	0/2331	0.81	0/3155
4	A	0.92	2/791 (0.3%)	1.05	2/1067 (0.2%)
All	All	0.64	3/4080 (0.1%)	0.81	2/5697 (0.0%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	5010	DA	O3'-P	-6.54	1.51	1.61
4	A	159	GLY	C-O	-5.18	1.20	1.24
4	A	106	PHE	C-O	-5.07	1.21	1.25

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	88	ALA	CA-C-N	11.25	133.90	119.84
4	A	88	ALA	C-N-CA	11.25	133.90	119.84

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	C	431	0	242	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	424	0	240	10	0
3	N	2281	0	2278	41	0
4	A	769	0	743	27	0
5	A	4	0	0	0	0
5	C	12	0	0	0	0
5	D	10	0	0	1	0
5	N	33	0	0	0	0
All	All	3964	0	3503	77	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 (77) 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)
4:A:118:ASN:O	4:A:122:HIS:CD2	2.26	0.89
4:A:135:ARG:HD2	4:A:144:SER:HA	1.61	0.82
2:D:5008:DA:OP1	5:D:5101:HOH:O	1.96	0.81
3:N:590:VAL:HG11	3:N:648:LYS:HA	1.66	0.78
4:A:99:TYR:CE1	4:A:117:GLN:HG2	2.21	0.75
2:D:5004:DT:H2''	2:D:5005:DA:H5'	1.67	0.75
3:N:583:GLN:HE21	3:N:586:ASP:HB3	1.55	0.72
1:C:4004:DG:N7	3:N:430:ARG:NH2	2.38	0.71
3:N:630:LYS:NZ	3:N:634:GLN:O	2.25	0.70
1:C:4018:DC:H5	2:D:5006:DG:H1	1.37	0.69
3:N:398:GLU:O	4:A:105:ARG:NH2	2.26	0.69
4:A:113:LYS:O	4:A:117:GLN:HB2	1.94	0.67
2:D:5020:DC:H2''	2:D:5021:DT:H5'	1.79	0.65
3:N:423:HIS:HB3	3:N:430:ARG:HG3	1.79	0.63
3:N:532:GLU:OE1	3:N:532:GLU:HA	1.98	0.62
3:N:590:VAL:HG13	3:N:645:TYR:HB3	1.80	0.61
3:N:396:PRO:HD2	3:N:399:TRP:CE3	2.37	0.60
1:C:4003:DA:H2''	1:C:4004:DG:H5'	1.83	0.60
3:N:631:ASP:OD1	3:N:632:LYS:N	2.36	0.59
2:D:5015:DT:OP2	3:N:572:ARG:NH2	2.35	0.59
3:N:608:LYS:HB2	3:N:661:ILE:HG22	1.85	0.58
4:A:88:ALA:HB1	4:A:89:PRO:HD2	1.84	0.58
3:N:661:ILE:HG13	3:N:667:ARG:HG2	1.84	0.57
4:A:88:ALA:CB	4:A:89:PRO:HD2	2.33	0.57
3:N:398:GLU:H	3:N:398:GLU:CD	2.12	0.56
3:N:482:LYS:N	3:N:482:LYS:HD3	2.21	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:396:PRO:HB3	3:N:398:GLU:OE2	2.08	0.54
4:A:157:GLU:O	4:A:165:ARG:NH2	2.42	0.52
4:A:108:PHE:C	4:A:108:PHE:CD2	2.88	0.50
3:N:669:GLN:HG3	3:N:670:PRO:HD2	1.93	0.50
4:A:113:LYS:HA	4:A:116:TRP:NE1	2.27	0.49
3:N:583:GLN:HG3	3:N:585:THR:O	2.12	0.49
4:A:166:ARG:HH11	4:A:166:ARG:HG2	1.78	0.49
3:N:613:GLU:OE1	3:N:646:ARG:NH2	2.44	0.48
3:N:603:PHE:O	3:N:630:LYS:HE2	2.11	0.48
4:A:75:TYR:CD1	4:A:83:MET:HE1	2.48	0.48
3:N:440:HIS:HB3	3:N:513:ILE:O	2.14	0.48
2:D:5008:DA:H5''	2:D:5008:DA:C8	2.49	0.48
4:A:99:TYR:CZ	4:A:117:GLN:HG2	2.49	0.48
3:N:629:ASP:HB2	3:N:639:PHE:HB2	1.96	0.47
3:N:444:GLN:HG3	3:N:510:ARG:HG2	1.96	0.47
3:N:456:LEU:HD11	3:N:546:PHE:HB3	1.97	0.47
3:N:609:VAL:HG22	3:N:660:VAL:HG22	1.97	0.46
2:D:5016:DT:OP1	3:N:537:ARG:O	2.33	0.46
2:D:5018:DT:H1'	2:D:5019:DC:H5''	1.96	0.46
4:A:101:PHE:CD2	4:A:101:PHE:C	2.93	0.46
3:N:400:PRO:HG2	4:A:83:MET:SD	2.56	0.45
4:A:85:ILE:HG21	4:A:148:LEU:HG	1.99	0.45
1:C:4019:DT:H4'	1:C:4020:DA:OP1	2.16	0.45
3:N:633:SER:O	3:N:635:PRO:HD3	2.17	0.45
4:A:108:PHE:CD2	4:A:108:PHE:O	2.70	0.45
3:N:396:PRO:HD2	3:N:399:TRP:CD2	2.52	0.44
3:N:615:THR:HG23	3:N:621:ILE:HG21	1.99	0.44
4:A:85:ILE:HG12	4:A:93:ILE:HG22	1.98	0.44
4:A:110:ARG:HD2	4:A:110:ARG:HA	1.78	0.44
3:N:411:ARG:HD2	3:N:446:HIS:CD2	2.53	0.44
4:A:113:LYS:H	4:A:113:LYS:HG3	1.69	0.43
1:C:4019:DT:H2''	1:C:4020:DA:O5'	2.19	0.43
4:A:78:ILE:HD12	4:A:78:ILE:H	1.83	0.43
4:A:93:ILE:O	4:A:146:TRP:N	2.35	0.43
2:D:5014:DA:H5''	3:N:665:ARG:HD2	2.01	0.43
3:N:581:GLU:HG3	3:N:600:GLY:HA2	2.01	0.42
4:A:118:ASN:CG	4:A:122:HIS:HE2	2.27	0.42
2:D:5006:DG:H8	2:D:5006:DG:H5''	1.84	0.42
3:N:578:PRO:HG3	3:N:662:ASN:CG	2.44	0.41
4:A:133:VAL:HB	4:A:134:PRO:HD2	2.02	0.41
3:N:396:PRO:O	3:N:547:ARG:NH2	2.45	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:N:634:GLN:HA	3:N:634:GLN:OE1	2.21	0.41
4:A:72:LYS:N	4:A:108:PHE:CD1	2.88	0.41
1:C:4015:DT:H2'	1:C:4016:DT:H72	2.02	0.41
3:N:410:LEU:HD22	3:N:548:VAL:HG12	2.03	0.41
4:A:118:ASN:OD1	4:A:122:HIS:NE2	2.54	0.41
3:N:448:TYR:HD2	3:N:509:MET:HE3	1.86	0.41
3:N:481:GLY:C	3:N:482:LYS:HD3	2.46	0.41
3:N:630:LYS:HZ1	3:N:635:PRO:C	2.28	0.40
4:A:91:LYS:CD	4:A:91:LYS:N	2.84	0.40
3:N:549:HIS:O	3:N:551:PRO:HD3	2.21	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	
3	N	285/287 (99%)	277 (97%)	8 (3%)	0	100	100
4	A	87/103 (84%)	86 (99%)	0	1 (1%)	11	19
All	All	372/390 (95%)	363 (98%)	8 (2%)	1 (0%)	36	52

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	89	PRO

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	
3	N	254/255 (100%)	240 (94%)	14 (6%)	19	33
4	A	82/94 (87%)	73 (89%)	9 (11%)	6	9
All	All	336/349 (96%)	313 (93%)	23 (7%)	14	25

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	N	401	LEU
3	N	465	GLU
3	N	467	ILE
3	N	469	LYS
3	N	479	ILE
3	N	497	LYS
3	N	501	VAL
3	N	508	ASN
3	N	532	GLU
3	N	535	ILE
3	N	538	LYS
3	N	583	GLN
3	N	619	GLN
3	N	621	ILE
4	A	90	GLU
4	A	104	ASP
4	A	110	ARG
4	A	111	GLU
4	A	113	LYS
4	A	117	GLN
4	A	125	SER
4	A	126	LEU
4	A	128	GLU

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

Mol	Chain	Res	Type
3	N	446	HIS
3	N	583	GLN
4	A	114	GLN
4	A	117	GLN
4	A	158	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

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	C	21/21 (100%)	0.58	1 (4%) 35 28	38, 44, 58, 66	0
2	D	21/21 (100%)	0.57	1 (4%) 35 28	30, 44, 69, 70	0
3	N	287/287 (100%)	0.55	22 (7%) 19 14	20, 43, 77, 89	0
4	A	91/103 (88%)	1.04	15 (16%) 4 3	33, 61, 91, 111	0
All	All	420/432 (97%)	0.66	39 (9%) 14 11	20, 47, 79, 111	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	N	392	ALA	5.1
4	A	144	SER	4.6
4	A	126	LEU	3.7
3	N	393	SER	3.4
3	N	407	SER	3.2
4	A	118	ASN	3.1
3	N	554	SER	3.1
3	N	394	SER	3.1
3	N	480	THR	3.0
2	D	5006	DG	3.0
3	N	404	GLN	3.0
3	N	651	ARG	2.9
4	A	135	ARG	2.9
3	N	481	GLY	2.9
3	N	631	ASP	2.8
4	A	165	ARG	2.8
3	N	632	LYS	2.7
4	A	153	TYR	2.7
3	N	633	SER	2.7
4	A	112	ASN	2.6
4	A	115	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
3	N	553	SER	2.5
3	N	678	VAL	2.4
3	N	437	THR	2.4
4	A	133	VAL	2.4
3	N	617	ASP	2.4
3	N	484	VAL	2.4
4	A	113	LYS	2.3
4	A	134	PRO	2.3
4	A	125	SER	2.2
3	N	529	ARG	2.2
4	A	96	ASN	2.1
3	N	482	LYS	2.1
1	C	4020	DA	2.1
4	A	104	ASP	2.1
3	N	483	THR	2.0
4	A	107	PRO	2.0
3	N	615	THR	2.0
3	N	467	ILE	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.