



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 8, 2021 – 12:07 PM JST

PDB ID : 7DG5
Title : Crystal structure of mouse Smc1-Smc3 hinge domain containing a D574Y mutation
Authors : Seo, H.; Noh, H.; Oh, B.-H.
Deposited on : 2020-11-11
Resolution : 2.00 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 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	:	2.23.2
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)	:	2.23.2

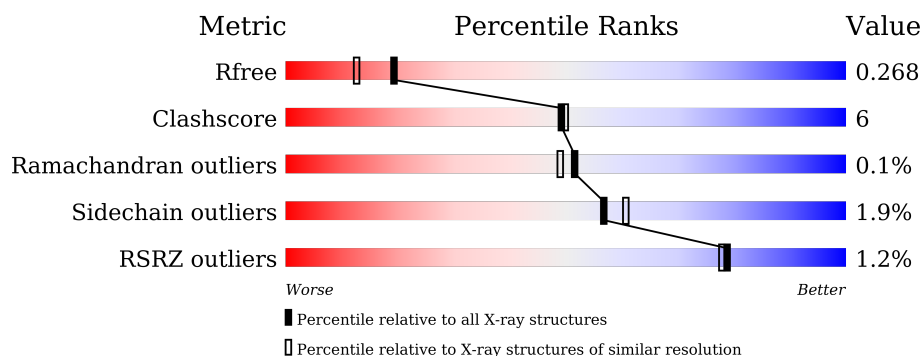
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	215	<div> <div></div> <div>72%</div> <div>11%</div> <div>•</div> <div>16%</div> </div>
1	C	215	<div> <div></div> <div>74%</div> <div>9%</div> <div></div> <div>17%</div> </div>
2	B	213	<div> <div></div> <div>75%</div> <div>14%</div> <div>•</div> <div>10%</div> </div>
2	D	213	<div> <div></div> <div>77%</div> <div>10%</div> <div></div> <div>12%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6169 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 Structural maintenance of chromosomes protein 1A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	181	Total	C	N	O	S	0	0	0
			1411	891	253	261	6			
1	C	179	Total	C	N	O	S	0	0	0
			1401	888	248	259	6			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	574	TYR	ASP	engineered mutation	UNP Q9CU62
C	574	TYR	ASP	engineered mutation	UNP Q9CU62

- Molecule 2 is a protein called Structural maintenance of chromosomes protein 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	191	Total	C	N	O	S	0	0	0
			1522	961	272	279	10			
2	D	187	Total	C	N	O	S	0	0	0
			1481	939	265	267	10			

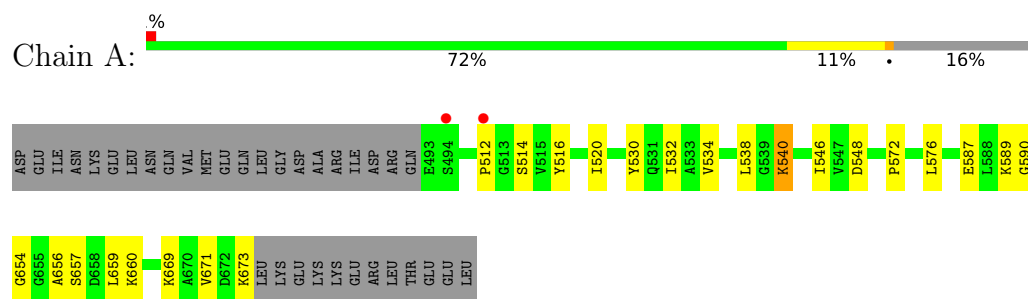
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	82	Total	O	0	0
			82	82		
3	B	103	Total	O	0	0
			103	103		
3	C	76	Total	O	0	0
			76	76		
3	D	93	Total	O	0	0
			93	93		

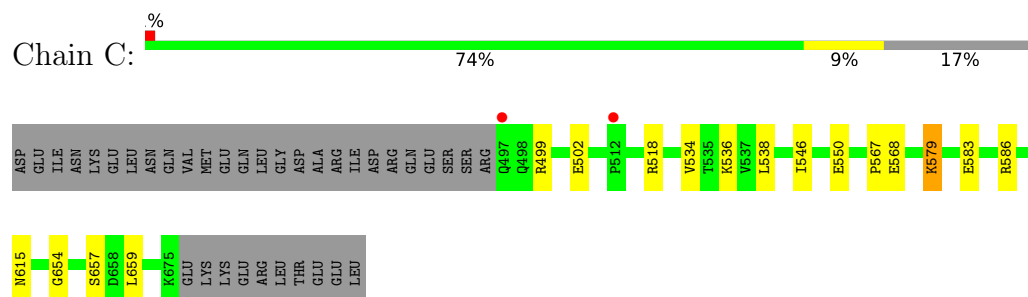
3 Residue-property plots [i](#)

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.

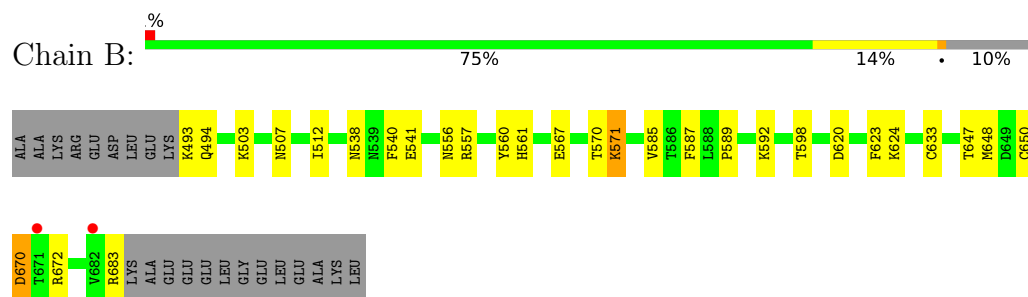
- Molecule 1: Structural maintenance of chromosomes protein 1A



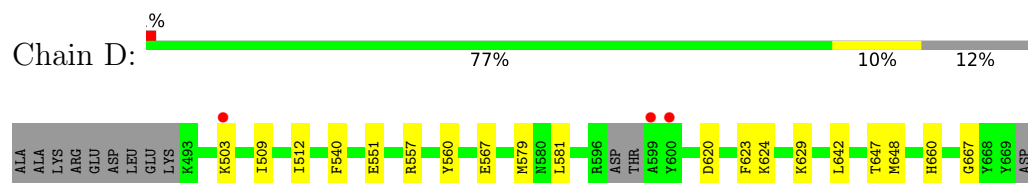
- Molecule 1: Structural maintenance of chromosomes protein 1A



- Molecule 2: Structural maintenance of chromosomes protein 3



- Molecule 2: Structural maintenance of chromosomes protein 3



R683
LYS
ALA
GLU
GLU
GLU
LEU
GLY
GLU
LEU
GLU
ALA
LYS
LEU

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	50.08Å 60.85Å 77.76Å 72.66° 88.43° 89.99°	Depositor
Resolution (Å)	42.06 – 2.00 42.06 – 2.00	Depositor EDS
% Data completeness (in resolution range)	88.4 (42.06-2.00) 88.4 (42.06-2.00)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.71 (at 2.00Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.219 , 0.269 0.219 , 0.268	Depositor DCC
R_{free} test set	2002 reflections (3.81%)	wwPDB-VP
Wilson B-factor (Å ²)	17.3	Xtriage
Anisotropy	0.270	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 46.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.035 for h,-k,-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	6169	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.42% 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	0.55	1/1433 (0.1%)	0.62	0/1929
1	C	0.51	2/1423 (0.1%)	0.59	0/1913
2	B	0.38	0/1550	0.53	0/2089
2	D	0.37	0/1507	0.53	0/2028
All	All	0.46	3/5913 (0.1%)	0.57	0/7959

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	654	GLY	C-O	-5.89	1.14	1.23
1	C	654	GLY	C-O	-5.62	1.14	1.23
1	C	657	SER	CB-OG	-5.42	1.35	1.42

There are no bond angle outliers.

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	A	1411	0	1428	17	0
1	C	1401	0	1435	12	0
2	B	1522	0	1518	26	0
2	D	1481	0	1471	16	0
3	A	82	0	0	0	0
3	B	103	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	76	0	0	0	0
3	D	93	0	0	1	0
All	All	6169	0	5852	69	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 6.

All (69) 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:B:493:LYS:HG3	2:B:494:GLN:H	1.34	0.92
2:B:647:THR:O	2:B:648:MET:HE3	1.77	0.84
2:D:629:LYS:HZ1	2:D:647:THR:HG22	1.44	0.80
2:B:567:GLU:O	2:B:571:LYS:HE2	1.81	0.80
2:D:509:ILE:O	2:D:512:ILE:HG22	1.87	0.74
2:B:648:MET:HA	2:B:648:MET:HE2	1.76	0.67
1:C:550:GLU:HG3	3:D:720:HOH:O	1.96	0.66
2:B:570:THR:OG1	2:B:571:LYS:NZ	2.17	0.65
2:B:493:LYS:CG	2:B:494:GLN:H	2.06	0.65
2:B:647:THR:O	2:B:648:MET:CE	2.46	0.63
1:A:530:TYR:CD2	1:A:597:VAL:HG11	2.34	0.63
1:A:530:TYR:CG	1:A:597:VAL:HG11	2.34	0.63
1:C:518:ARG:NH2	1:C:568:GLU:OE1	2.32	0.62
1:A:657:SER:HA	1:A:660:LYS:HE2	1.82	0.62
1:A:589:LYS:HD2	1:A:590:GLY:H	1.65	0.61
1:A:597:VAL:HG12	1:A:597:VAL:O	2.00	0.61
2:B:598:THR:HG21	2:B:647:THR:HB	1.83	0.61
1:A:656:ALA:O	1:A:660:LYS:HG3	1.99	0.60
2:B:556:ASN:ND2	3:B:702:HOH:O	2.33	0.60
1:C:601:GLU:HB3	1:C:602:PRO:HD3	1.84	0.59
1:C:536:LYS:HD3	1:C:659:LEU:HD11	1.87	0.56
2:D:648:MET:HE2	2:D:648:MET:HA	1.88	0.56
1:A:540:LYS:H	1:A:540:LYS:HD3	1.71	0.56
2:B:567:GLU:O	2:B:571:LYS:CE	2.53	0.53
1:A:520:ILE:HG12	1:A:669:LYS:HG3	1.90	0.53
2:D:629:LYS:NZ	2:D:647:THR:HG22	2.18	0.53
2:D:647:THR:O	2:D:648:MET:HE3	2.11	0.51
2:D:551:GLU:OE1	2:D:675:ARG:HD2	2.12	0.50
2:B:659:SER:HB3	2:B:663:ALA:HB3	1.92	0.50
2:B:571:LYS:HE2	2:B:571:LYS:H	1.75	0.50
2:D:620:ASP:OD1	2:D:624:LYS:HE2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:557:ARG:HG2	2:D:560:TYR:CZ	2.48	0.49
1:A:634:GLN:H	1:A:634:GLN:CD	2.16	0.48
1:C:499:ARG:HA	1:C:502:GLU:HG3	1.95	0.48
1:A:671:VAL:O	1:A:673:LYS:HG2	2.15	0.47
1:C:583:GLU:HG2	1:C:586:ARG:CZ	2.45	0.47
2:B:493:LYS:CG	2:B:494:GLN:N	2.76	0.47
1:A:516:TYR:HD2	1:A:546:ILE:HG22	1.81	0.46
1:A:534:VAL:HG12	1:A:538:LEU:HD22	1.96	0.46
2:B:571:LYS:HE2	2:B:571:LYS:N	2.30	0.46
1:A:587:GLU:OE2	1:A:587:GLU:HA	2.17	0.45
2:B:585:VAL:HG22	3:B:719:HOH:O	2.16	0.45
2:B:670:ASP:OD2	2:B:672:ARG:NH2	2.38	0.45
2:D:579:MET:HB2	2:D:581:LEU:HG	1.99	0.44
2:B:541:GLU:OE1	2:B:683:ARG:NH2	2.50	0.44
2:B:557:ARG:HG2	2:B:560:TYR:CZ	2.52	0.44
2:B:512:ILE:HD12	2:B:561:HIS:CE1	2.54	0.43
1:A:589:LYS:HD2	1:A:590:GLY:N	2.32	0.43
1:A:532:ILE:HG23	1:A:659:LEU:HB3	2.00	0.43
1:C:567:PRO:HA	2:D:667:GLY:HA3	2.01	0.43
2:D:629:LYS:HZ2	2:D:660:HIS:CD2	2.36	0.42
2:D:540:PHE:HB3	2:D:623:PHE:CE2	2.55	0.42
2:B:540:PHE:HB3	2:B:623:PHE:CE2	2.55	0.42
2:D:629:LYS:HG3	2:D:648:MET:HE2	2.02	0.42
2:B:633:CYS:SG	2:B:650:CYS:SG	3.14	0.42
2:D:642:LEU:HD23	2:D:642:LEU:HA	1.89	0.41
2:B:587:PHE:O	2:B:589:PRO:HD3	2.20	0.41
2:B:647:THR:OG1	2:D:567:GLU:HG2	2.20	0.41
1:A:514:SER:OG	1:A:548:ASP:OD2	2.31	0.41
2:B:620:ASP:OD2	2:B:624:LYS:NZ	2.41	0.41
1:C:546:ILE:HD12	1:C:546:ILE:N	2.35	0.41
2:B:493:LYS:HG3	2:B:494:GLN:N	2.17	0.41
2:D:647:THR:O	2:D:648:MET:CE	2.69	0.41
1:A:572:PRO:O	1:A:576:LEU:HG	2.21	0.41
1:C:579:LYS:NZ	1:C:615:ASN:HD21	2.18	0.41
1:C:534:VAL:HG13	1:C:538:LEU:HD23	2.03	0.40
2:B:507:ASN:HD22	2:B:507:ASN:HA	1.63	0.40
1:C:583:GLU:HG2	1:C:586:ARG:NH1	2.35	0.40
1:C:609:LEU:HD23	1:C:609: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	179/215 (83%)	174 (97%)	4 (2%)	1 (1%)	25	19
1	C	177/215 (82%)	171 (97%)	6 (3%)	0	100	100
2	B	189/213 (89%)	185 (98%)	4 (2%)	0	100	100
2	D	181/213 (85%)	178 (98%)	3 (2%)	0	100	100
All	All	726/856 (85%)	708 (98%)	17 (2%)	1 (0%)	51	49

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	512	PRO

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	146/186 (78%)	144 (99%)	2 (1%)	67	72
1	C	147/186 (79%)	146 (99%)	1 (1%)	84	88
2	B	165/185 (89%)	159 (96%)	6 (4%)	35	34
2	D	158/185 (85%)	155 (98%)	3 (2%)	57	61
All	All	616/742 (83%)	604 (98%)	12 (2%)	57	61

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	540	LYS
1	A	634	GLN
2	B	503	LYS
2	B	538	ASN
2	B	571	LYS
2	B	592	LYS
2	B	659	SER
2	B	670	ASP
1	C	579	LYS
2	D	503	LYS
2	D	672	ARG
2	D	683	ARG

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

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 [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	181/215 (84%)	-0.20	2 (1%) 80 79	9, 17, 31, 49	0
1	C	179/215 (83%)	-0.17	2 (1%) 80 79	9, 18, 32, 49	0
2	B	191/213 (89%)	0.02	2 (1%) 82 81	9, 18, 40, 50	0
2	D	187/213 (87%)	-0.07	3 (1%) 72 70	9, 18, 36, 48	0
All	All	738/856 (86%)	-0.11	9 (1%) 79 78	9, 18, 36, 50	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	599	ALA	4.6
1	A	512	PRO	3.1
1	A	494	SER	3.0
2	B	682	VAL	2.5
1	C	512	PRO	2.4
2	B	671	THR	2.2
2	D	503	LYS	2.2
1	C	497	GLN	2.1
2	D	600	TYR	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 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.