



wwPDB X-ray Structure Validation Summary Report ⓘ

May 26, 2020 – 06:23 pm BST

PDB ID : 6ECN
Title : HIV-1 CA 1/2-hexamer-EE
Authors : Summers, B.J.; Xiong, Y.
Deposited on : 2018-08-08
Resolution : 3.40 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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	:	2.11
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)	:	2.11

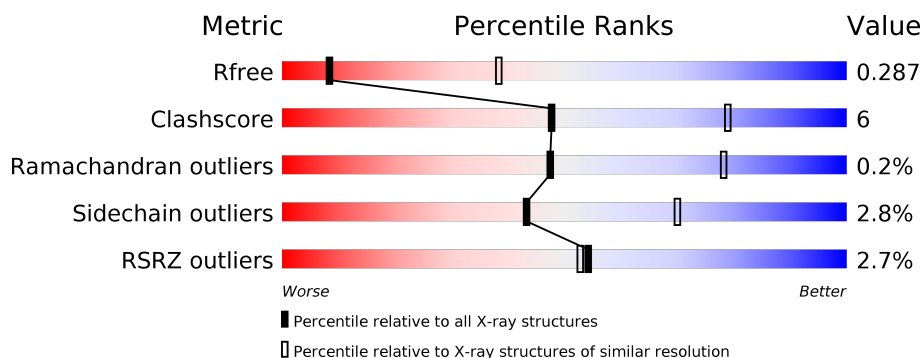
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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	1026 (3.48-3.32)
Clashscore	141614	1055 (3.48-3.32)
Ramachandran outliers	138981	1038 (3.48-3.32)
Sidechain outliers	138945	1038 (3.48-3.32)
RSRZ outliers	127900	2173 (3.50-3.30)

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 on 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	231	<div> <div>%</div> <div> <div></div> <div>71%</div> <div>14%</div> <div>•</div> <div>13%</div> </div> </div>
1	D	231	<div> <div>2%</div> <div> <div></div> <div>80%</div> <div>10%</div> <div>10%</div> </div> </div>
2	B	231	<div> <div>6%</div> <div> <div></div> <div>77%</div> <div>13%</div> <div>10%</div> </div> </div>
2	E	231	<div> <div>3%</div> <div> <div></div> <div>66%</div> <div>19%</div> <div>14%</div> </div> </div>
3	C	149	<div> <div>%</div> <div> <div></div> <div>86%</div> <div>11%</div> <div>• •</div> </div> </div>
3	F	149	<div> <div></div> <div> <div></div> <div>80%</div> <div>14%</div> <div>• •</div> <div>5%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8369 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 HIV-1 CA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	201	Total	C	N	O	S	0	0	0
			1539	971	268	288	12			
1	D	207	Total	C	N	O	S	0	0	0
			1560	986	268	293	13			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	6	LEU	ILE	conflict	UNP P04591
A	45	CYS	GLU	engineered mutation	UNP P04591
A	54	CYS	THR	engineered mutation	UNP P04591
A	83	LEU	VAL	conflict	UNP P04591
A	120	HIS	ASN	conflict	UNP P04591
A	184	ALA	TRP	engineered mutation	UNP P04591
A	185	ALA	MET	engineered mutation	UNP P04591
A	208	GLY	ALA	conflict	UNP P04591
D	6	LEU	ILE	conflict	UNP P04591
D	45	CYS	GLU	engineered mutation	UNP P04591
D	54	CYS	THR	engineered mutation	UNP P04591
D	83	LEU	VAL	conflict	UNP P04591
D	120	HIS	ASN	conflict	UNP P04591
D	184	ALA	TRP	engineered mutation	UNP P04591
D	185	ALA	MET	engineered mutation	UNP P04591
D	208	GLY	ALA	conflict	UNP P04591

- Molecule 2 is a protein called HIV-1 CA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	207	Total	C	N	O	S	0	0	0
			1535	965	260	298	12			
2	E	199	Total	C	N	O	S	0	0	0
			1533	969	263	289	12			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	6	LEU	ILE	conflict	UNP P04591
B	42	CYS	ALA	engineered mutation	UNP P04591
B	54	GLU	THR	engineered mutation	UNP P04591
B	83	LEU	VAL	conflict	UNP P04591
B	120	HIS	ASN	conflict	UNP P04591
B	184	ALA	TRP	engineered mutation	UNP P04591
B	185	ALA	MET	engineered mutation	UNP P04591
B	208	GLY	ALA	conflict	UNP P04591
E	6	LEU	ILE	conflict	UNP P04591
E	42	CYS	ALA	engineered mutation	UNP P04591
E	54	GLU	THR	engineered mutation	UNP P04591
E	83	LEU	VAL	conflict	UNP P04591
E	120	HIS	ASN	conflict	UNP P04591
E	184	ALA	TRP	engineered mutation	UNP P04591
E	185	ALA	MET	engineered mutation	UNP P04591
E	208	GLY	ALA	conflict	UNP P04591

- Molecule 3 is a protein called HIV-1 CA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	145	Total	C	N	O	S	0	0	0
			1113	703	193	208	9			
3	F	142	Total	C	N	O	S	0	0	0
			1089	689	188	204	8			

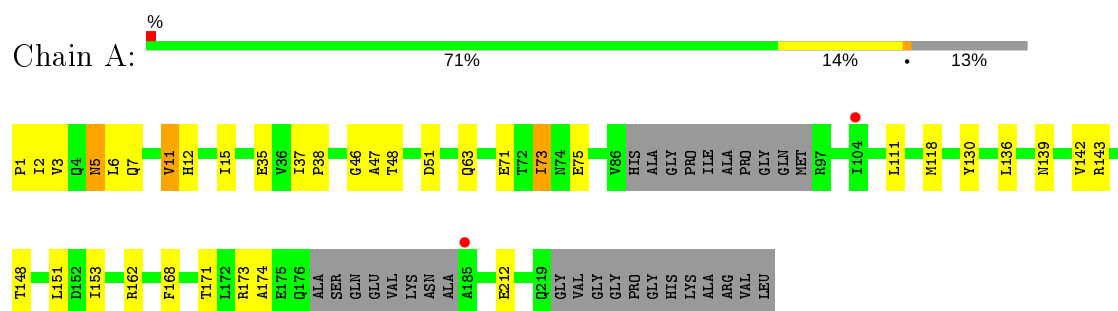
There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	14	CYS	ALA	engineered mutation	UNP A0A248SME6
C	42	GLU	ALA	engineered mutation	UNP A0A248SME6
C	147	LYS	-	expression tag	UNP A0A248SME6
C	148	LEU	-	expression tag	UNP A0A248SME6
C	149	GLN	-	expression tag	UNP A0A248SME6
F	14	CYS	ALA	engineered mutation	UNP A0A248SME6
F	42	GLU	ALA	engineered mutation	UNP A0A248SME6
F	147	LYS	-	expression tag	UNP A0A248SME6
F	148	LEU	-	expression tag	UNP A0A248SME6
F	149	GLN	-	expression tag	UNP A0A248SME6

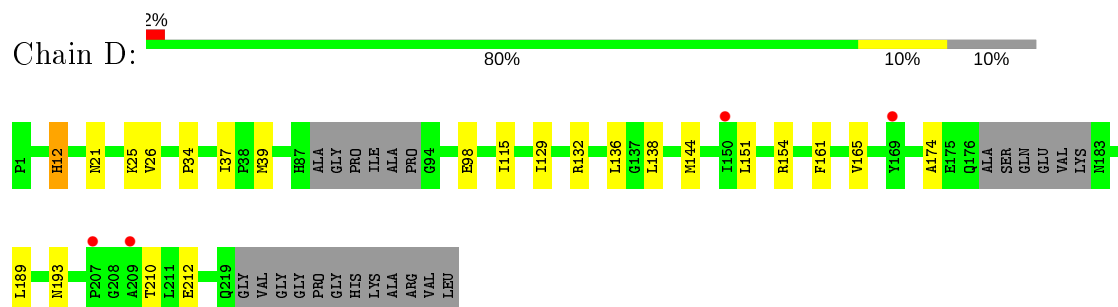
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

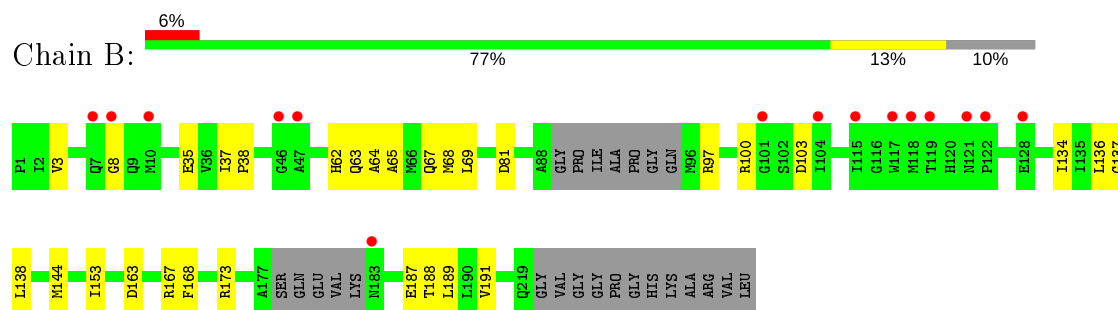
• Molecule 1: HIV-1 CA



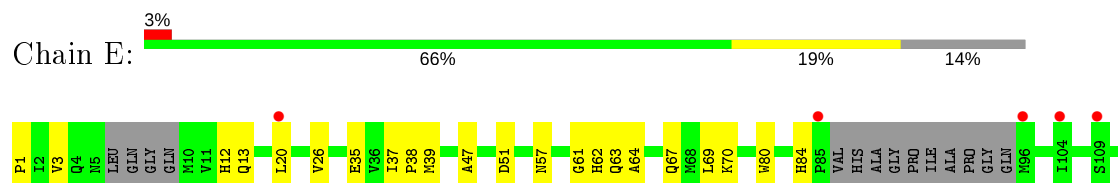
• Molecule 1: HIV-1 CA

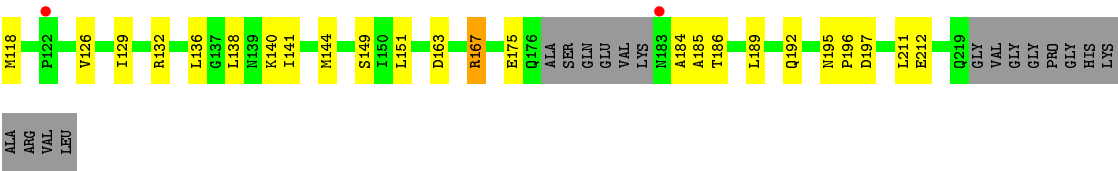


• Molecule 2: HIV-1 CA

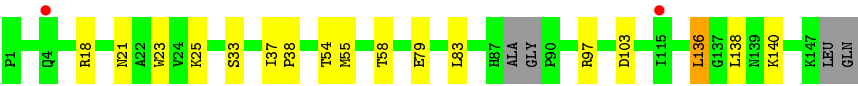
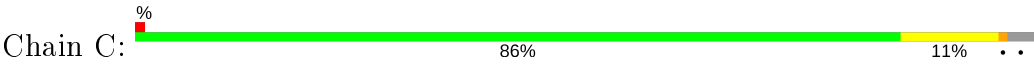


• Molecule 2: HIV-1 CA

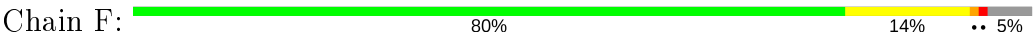




● Molecule 3: HIV-1 CA



● Molecule 3: HIV-1 CA



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	65.60Å 84.10Å 248.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.01 – 3.40 49.98 – 3.40	Depositor EDS
% Data completeness (in resolution range)	99.7 (50.01-3.40) 99.8 (49.98-3.40)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.70 (at 3.40Å)	Xtriage
Refinement program	REFMAC 5.8.0103, PHENIX 1.12-2829	Depositor
R, R_{free}	0.225 , 0.275 0.237 , 0.287	Depositor DCC
R_{free} test set	955 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å ²)	115.1	Xtriage
Anisotropy	0.226	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 82.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8369	wwPDB-VP
Average B, all atoms (Å ²)	147.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.08% 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	0.58	0/1571	0.77	1/2137 (0.0%)
1	D	0.60	0/1592	0.79	0/2166
2	B	0.59	0/1563	0.77	0/2131
2	E	0.60	0/1564	0.84	3/2125 (0.1%)
3	C	0.66	0/1139	0.79	1/1548 (0.1%)
3	F	0.62	0/1115	0.80	1/1516 (0.1%)
All	All	0.61	0/8544	0.79	6/11623 (0.1%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	197	ASP	CB-CG-OD2	6.33	124.00	118.30
3	C	136	LEU	CA-CB-CG	-6.28	100.86	115.30
2	E	211	LEU	CB-CG-CD2	-6.04	100.72	111.00
2	E	167	ARG	NE-CZ-NH2	-5.99	117.31	120.30
1	A	173	ARG	NE-CZ-NH1	-5.79	117.41	120.30

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	1539	0	1506	21	0
1	D	1560	0	1508	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1535	0	1466	28	0
2	E	1533	0	1501	28	0
3	C	1113	0	1087	10	0
3	F	1089	0	1056	15	0
All	All	8369	0	8124	100	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.

The worst 5 of 100 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:69:LEU:HD13	2:B:137:GLY:HA3	1.55	0.87
1:A:3:VAL:HB	1:A:5:ASN:OD1	1.78	0.84
1:D:212:GLU:HG3	3:F:144:MET:HE1	1.64	0.78
1:A:63:GLN:NE2	2:B:173:ARG:HH11	1.83	0.76
2:B:64:ALA:HB2	2:E:63:GLN:CD	2.07	0.75

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	195/231 (84%)	188 (96%)	6 (3%)	1 (0%)	29	61
1	D	201/231 (87%)	196 (98%)	5 (2%)	0	100	100
2	B	201/231 (87%)	196 (98%)	4 (2%)	1 (0%)	29	61
2	E	191/231 (83%)	182 (95%)	9 (5%)	0	100	100
3	C	141/149 (95%)	140 (99%)	1 (1%)	0	100	100
3	F	138/149 (93%)	135 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1067/1222 (87%)	1037 (97%)	28 (3%)	2 (0%)	47 78

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	7	GLN
2	B	8	GLY

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	163/192 (85%)	156 (96%)	7 (4%)	29 59
1	D	161/192 (84%)	158 (98%)	3 (2%)	57 78
2	B	157/193 (81%)	155 (99%)	2 (1%)	69 84
2	E	163/193 (84%)	158 (97%)	5 (3%)	40 68
3	C	119/128 (93%)	117 (98%)	2 (2%)	60 80
3	F	116/128 (91%)	110 (95%)	6 (5%)	23 53
All	All	879/1026 (86%)	854 (97%)	25 (3%)	43 70

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	12	HIS
1	D	136	LEU
3	F	125	PRO
1	D	98	GLU
2	E	12	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	63	GLN
2	B	63	GLN

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 carbohydrates 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	201/231 (87%)	-0.04	2 (0%) 82 81	94, 140, 223, 277	0
1	D	207/231 (89%)	-0.14	4 (1%) 66 65	77, 130, 183, 214	0
2	B	207/231 (89%)	0.39	15 (7%) 15 17	90, 181, 251, 297	0
2	E	199/231 (86%)	0.16	7 (3%) 44 43	86, 149, 239, 273	0
3	C	145/149 (97%)	0.00	2 (1%) 75 74	82, 117, 176, 226	0
3	F	142/149 (95%)	-0.15	0 100 100	93, 133, 197, 230	0
All	All	1101/1222 (90%)	0.05	30 (2%) 54 53	77, 139, 228, 297	0

The worst 5 of 30 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	104	ILE	5.4
2	E	85	PRO	4.8
2	E	183	ASN	4.6
2	B	47	ALA	4.3
2	B	101	GLY	4.1

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 carbohydrates 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.