wwPDB X-ray Structure Validation Summary Report (i)

Jan 14, 2024 – 02:55 am GMT

PDB ID	:	6QX4
Title	:	Structure of the Bacillus anthracis Sap S-layer assembly domain
Authors	:	Remaut, H.; Fioravanti, A.
Deposited on	:	2019-03-07
Resolution	:	3.27 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 (i) 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 (i)) were used in the production of this report:

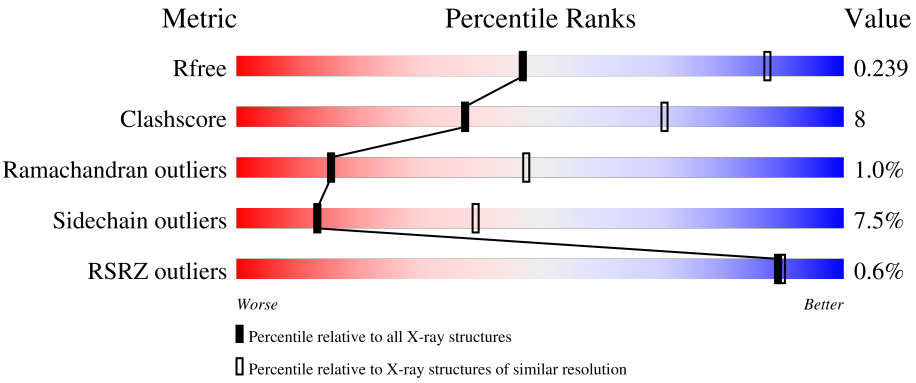
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.27 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	1177 (3.32-3.24)
Clashscore	141614	1044 (3.30-3.26)
Ramachandran outliers	138981	1026 (3.30-3.26)
Sidechain outliers	138945	1025 (3.30-3.26)
RSRZ outliers	127900	1141 (3.32-3.24)

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 <=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	606	77% 18%
1	B	606	77% 19%
2	C	129	2% 68% 22% 8%
2	E	129	% 66% 25% 8%
3	D	134	68% 22% 8%

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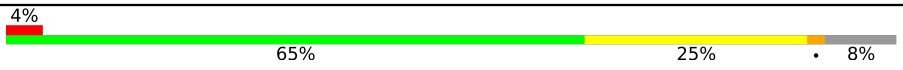
Mol	Chain	Length	Quality of chain
3	H	134	

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 12567 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 S-layer protein sap.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	585	Total	C	N	O	S	0	0	0
			4379	2757	719	900	3			
1	B	593	Total	C	N	O	S	0	0	0
			4438	2792	729	914	3			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	215	MET	-	initiating methionine	UNP P49051
A	815	HIS	-	expression tag	UNP P49051
A	816	HIS	-	expression tag	UNP P49051
A	817	HIS	-	expression tag	UNP P49051
A	818	HIS	-	expression tag	UNP P49051
A	819	HIS	-	expression tag	UNP P49051
A	820	HIS	-	expression tag	UNP P49051
B	215	MET	-	initiating methionine	UNP P49051
B	815	HIS	-	expression tag	UNP P49051
B	816	HIS	-	expression tag	UNP P49051
B	817	HIS	-	expression tag	UNP P49051
B	818	HIS	-	expression tag	UNP P49051
B	819	HIS	-	expression tag	UNP P49051
B	820	HIS	-	expression tag	UNP P49051

- Molecule 2 is a protein called Nanobody NbAF683.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	119	Total	C	N	O	S	0	0	0
			905	565	159	176	5			
2	E	119	Total	C	N	O	S	0	0	0
			905	565	159	176	5			

- Molecule 3 is a protein called Nanobody NbAF694.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	123	Total 956	C 604	N 161	O 187	S 4	0	0	0
3	H	123	Total 956	C 604	N 161	O 187	S 4	0	0	0

- Molecule 4 is water.

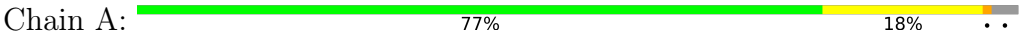
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	9	Total 9	O 9	0	0
4	B	12	Total 12	O 12	0	0
4	C	1	Total 1	O 1	0	0
4	D	3	Total 3	O 3	0	0
4	E	3	Total 3	O 3	0	0

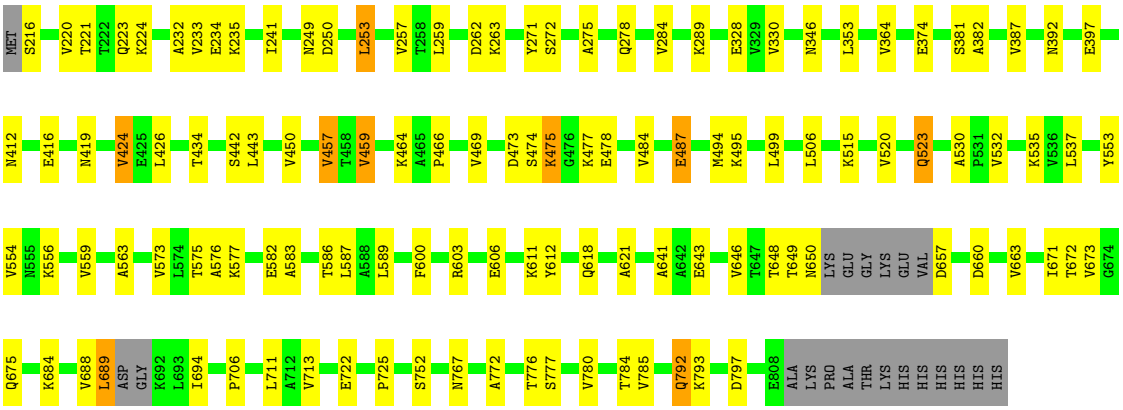
3 Residue-property plots (i)

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: S-layer protein sap

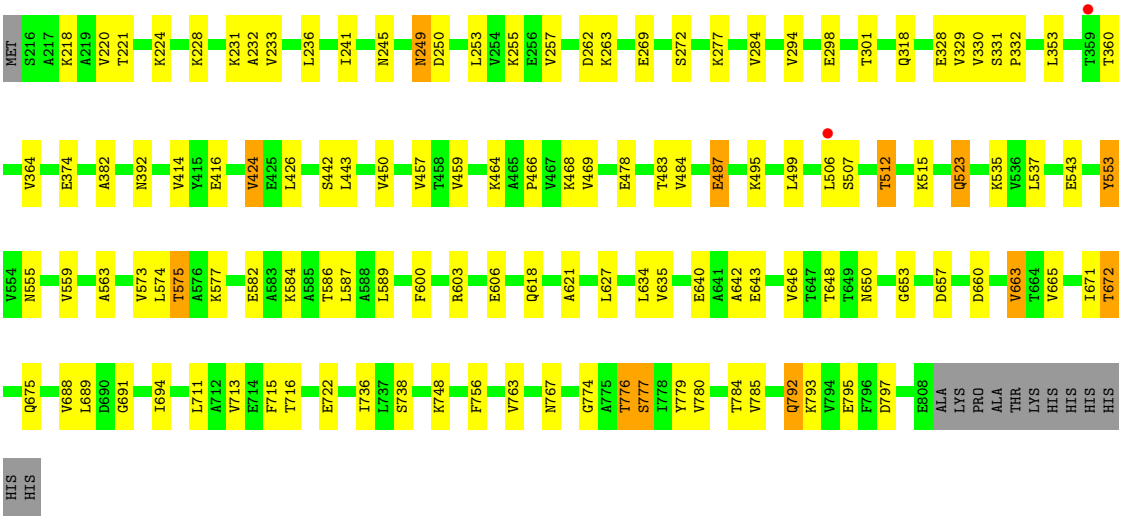
Chain A:





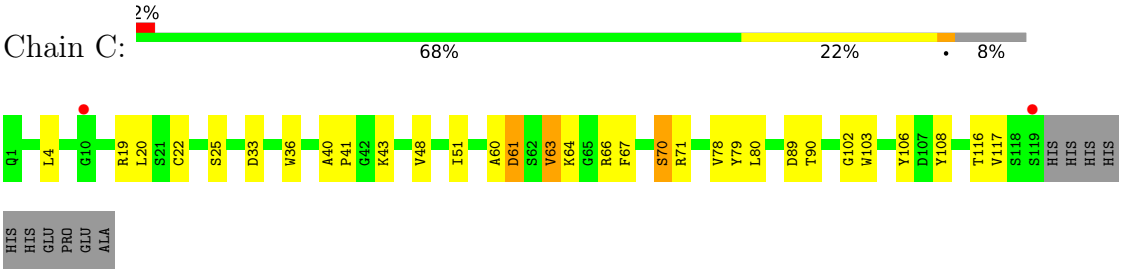
• Molecule 1: S-layer protein sap

Chain B:



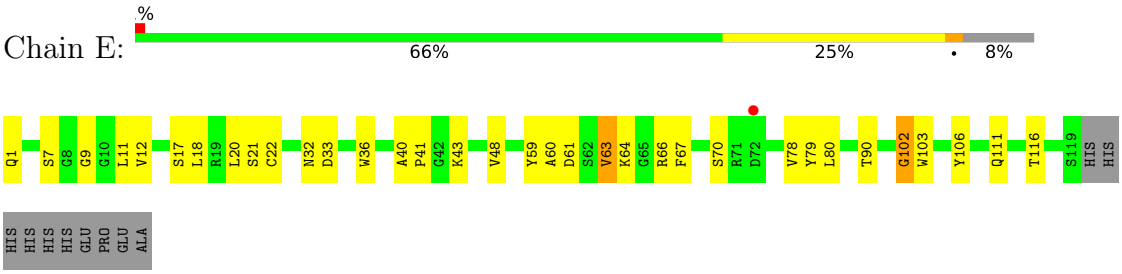
• Molecule 2: Nanobody NbAF683

Chain C:



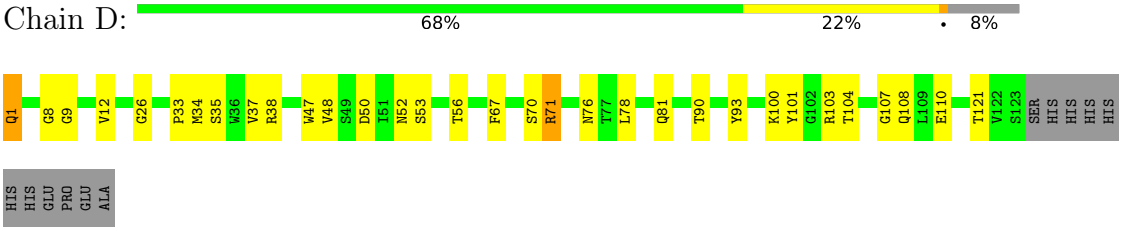
• Molecule 2: Nanobody NbAF683

Chain E:



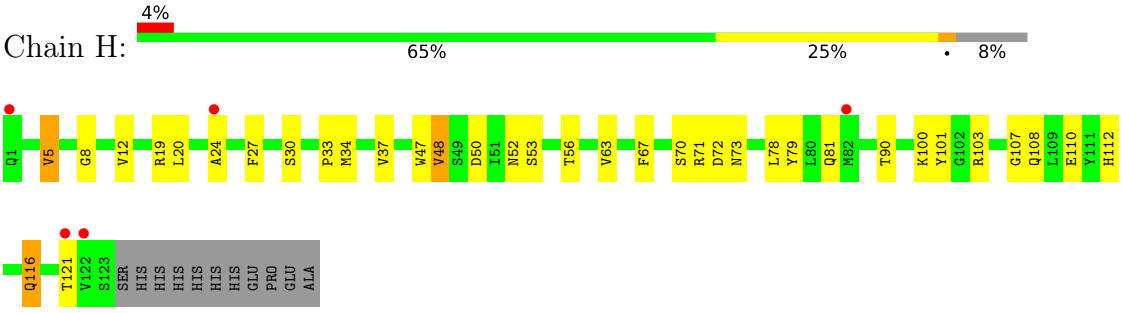
• Molecule 3: Nanobody NbAF694

Chain D:



• Molecule 3: Nanobody NbAF694

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	74.23Å 79.91Å 81.23Å 88.66° 82.00° 85.59°	Depositor
Resolution (Å)	35.00 – 3.27 80.43 – 3.27	Depositor EDS
% Data completeness (in resolution range)	93.6 (35.00-3.27) 93.5 (80.43-3.27)	Depositor EDS
R_{merge}	0.21	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.08 (at 3.26Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.173 , 0.218 0.179 , 0.239	Depositor DCC
R_{free} test set	1316 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å^2)	67.2	Xtriage
Anisotropy	0.029	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 83.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	0.036 for -h,-l,-k	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	12567	wwPDB-VP
Average B, all atoms (Å^2)	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.60% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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	0.49	0/4416	0.78	0/5973
1	B	0.50	0/4477	0.78	0/6056
2	C	0.52	0/924	0.75	0/1250
2	E	0.52	0/924	0.75	0/1250
3	D	0.52	0/981	0.73	0/1332
3	H	0.48	0/981	0.71	0/1332
All	All	0.50	0/12703	0.77	0/17193

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	4379	0	4546	69	0
1	B	4438	0	4605	57	0
2	C	905	0	871	17	0
2	E	905	0	871	13	0
3	D	956	0	906	19	0
3	H	956	0	906	27	0
4	A	9	0	0	0	0
4	B	12	0	0	0	0
4	C	1	0	0	0	0
4	D	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	E	3	0	0	0	0
All	All	12567	0	12705	194	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 8.

The worst 5 of 194 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)
3:H:5:VAL:HG13	3:H:116:GLN:NE2	1.61	1.16
1:A:473:ASP:OD1	1:A:477:LYS:HB3	1.51	1.08
1:A:711:LEU:HB2	1:A:792:GLN:NE2	1.87	0.88
3:H:5:VAL:CG1	3:H:116:GLN:NE2	2.39	0.86
1:A:474:SER:O	1:A:475:LYS:HB2	1.74	0.85

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	579/606 (96%)	532 (92%)	43 (7%)	4 (1%)	22 56
1	B	591/606 (98%)	528 (89%)	60 (10%)	3 (0%)	29 62
2	C	117/129 (91%)	110 (94%)	4 (3%)	3 (3%)	5 28
2	E	117/129 (91%)	110 (94%)	3 (3%)	4 (3%)	3 22
3	D	121/134 (90%)	115 (95%)	4 (3%)	2 (2%)	9 37
3	H	121/134 (90%)	115 (95%)	6 (5%)	0	100 100
All	All	1646/1738 (95%)	1510 (92%)	120 (7%)	16 (1%)	15 48

5 of 16 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	475	LYS
1	B	722	GLU
2	C	103	TRP
2	E	103	TRP
1	A	722	GLU

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	483/500 (97%)	451 (93%)	32 (7%)	16	46
1	B	489/500 (98%)	454 (93%)	35 (7%)	14	41
2	C	94/103 (91%)	86 (92%)	8 (8%)	10	35
2	E	94/103 (91%)	82 (87%)	12 (13%)	4	18
3	D	101/111 (91%)	94 (93%)	7 (7%)	15	44
3	H	101/111 (91%)	93 (92%)	8 (8%)	12	37
All	All	1362/1428 (95%)	1260 (92%)	102 (8%)	13	39

5 of 102 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	663	VAL
2	C	63	VAL
3	H	70	SER
1	B	675	GLN
1	B	795	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	792	GLN
3	D	73	ASN
3	H	108	GLN
2	C	3	GLN

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Mol	Chain	Res	Type
3	D	108	GLN

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 monosaccharides 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

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, 95^{th} 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	585/606 (96%)	-0.13	0 100 100	33, 79, 116, 144	0
1	B	593/606 (97%)	-0.11	2 (0%) 94 94	33, 77, 124, 165	0
2	C	119/129 (92%)	0.06	2 (1%) 70 67	31, 71, 126, 176	0
2	E	119/129 (92%)	-0.07	1 (0%) 86 86	34, 62, 93, 138	0
3	D	123/134 (91%)	-0.08	0 100 100	29, 52, 80, 113	0
3	H	123/134 (91%)	0.24	5 (4%) 37 35	47, 80, 128, 164	0
All	All	1662/1738 (95%)	-0.08	10 (0%) 89 90	29, 74, 120, 176	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	359	THR	3.8
2	C	10	GLY	2.7
1	B	506	LEU	2.5
2	E	72	ASP	2.3
3	H	122	VAL	2.2

6.2 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.