



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:45 PM GMT

PDB ID : 1LWN
Title : Crystal structure of rabbit muscle glycogen phosphorylase a in complex with a potential hypoglycaemic drug at 2.0 Å resolution
Authors : Oikonomakos, N.G.; Chrysina, E.D.; Kosmopoulou, M.; Leonidas, D.D.
Deposited on : 2002-06-01
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
<http://wwpdb.org/validation/2016/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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

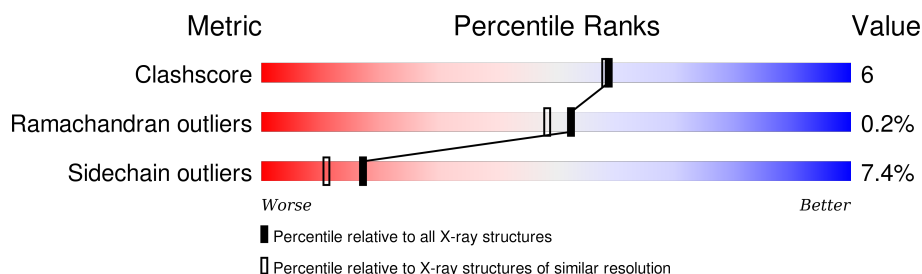
1 Overall quality at a glance

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))
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	842	 81% 14% • •

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6989 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 glycogen phosphorylase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	815	6635	4222	1170	1213	1	29	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	14	SEP	SER	MODIFIED RESIDUE	UNP P00489

- Molecule 2 is SUGAR (ALPHA-D-GLUCOSE) (three-letter code: GLC) (formula: C₆H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	12	6	6	0	0

- Molecule 3 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: C₈H₁₀NO₆P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	A	1	15	8	1	5	1	0	0

- Molecule 4 is water.

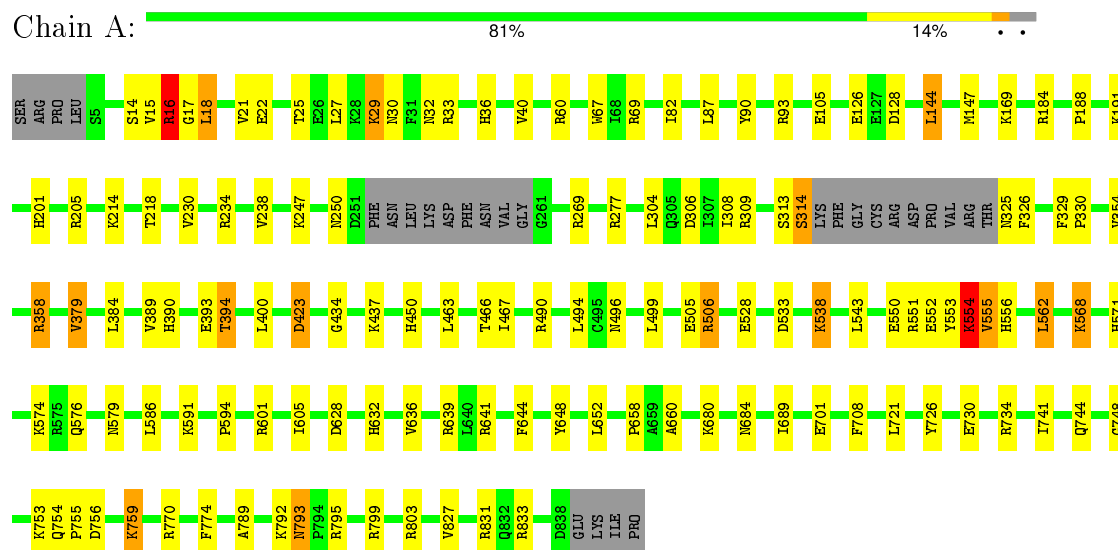
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	327	Total	O	0	0
			327	327		

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 errors 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.

Note EDS was not executed.

- Molecule 1: glycogen phosphorylase



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	128.28Å 128.28Å 116.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	14.81 – 2.00	Depositor
% Data completeness (in resolution range)	99.3 (14.81-2.00)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.179 , 0.218	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6989	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GLC, PLP, SEP

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	0.36	0/6771	0.61	5/9159 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	16	ARG	N-CA-C	6.95	129.76	111.00
1	A	17	GLY	N-CA-C	-6.88	95.90	113.10
1	A	554	LYS	N-CA-C	6.38	128.23	111.00
1	A	434	GLY	N-CA-C	-6.06	97.95	113.10
1	A	562	LEU	CA-CB-CG	5.20	127.27	115.30

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	6635	0	6571	77	0
2	A	12	0	12	0	0
3	A	15	0	7	1	0
4	A	327	0	0	6	0
All	All	6989	0	6590	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 6.

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)
1:A:555:VAL:HG12	1:A:556:HIS:H	1.19	1.01
1:A:250:ASN:HD22	1:A:269:ARG:NH1	1.62	0.97
1:A:313:SER:O	1:A:314:SER:HB2	1.68	0.93
1:A:250:ASN:HA	1:A:269:ARG:NH1	1.87	0.89
1:A:250:ASN:ND2	1:A:269:ARG:HH12	1.74	0.85
1:A:756:ASP:HB2	1:A:759:LYS:HG3	1.59	0.85
1:A:390:HIS:O	1:A:394:THR:HG22	1.77	0.84
1:A:250:ASN:HA	1:A:269:ARG:HH11	1.45	0.79
1:A:555:VAL:HG12	1:A:556:HIS:N	1.97	0.78
1:A:250:ASN:HD22	1:A:269:ARG:HH12	1.31	0.77
1:A:554:LYS:O	1:A:554:LYS:HG2	1.91	0.70
1:A:30:ASN:ND2	1:A:33:ARG:NH1	2.40	0.70
1:A:105:GLU:HG2	4:A:1034:HOH:O	1.91	0.70
1:A:250:ASN:ND2	1:A:269:ARG:NH1	2.32	0.67
1:A:304:LEU:O	1:A:308:ILE:HG12	1.97	0.65
1:A:329:PHE:HB3	1:A:330:PRO:HD3	1.79	0.65
1:A:506:ARG:NH1	1:A:533:ASP:OD1	2.31	0.61
1:A:14:SEP:OG	1:A:16:ARG:HB2	2.00	0.61
1:A:30:ASN:HD22	1:A:33:ARG:NH1	1.99	0.60
1:A:795:ARG:HG2	1:A:795:ARG:HH21	1.66	0.60
1:A:554:LYS:O	1:A:555:VAL:HG23	2.05	0.56
1:A:144:LEU:HD12	1:A:147:MET:CE	2.34	0.56
1:A:490:ARG:HA	1:A:494:LEU:HB2	1.88	0.56
1:A:734:ARG:HD2	4:A:1247:HOH:O	2.05	0.55
1:A:393:GLU:HB3	1:A:400:LEU:CD2	2.37	0.54
1:A:555:VAL:CG1	1:A:556:HIS:H	2.05	0.54
1:A:16:ARG:HD3	1:A:69:ARG:NH2	2.22	0.54
1:A:789:ALA:HA	1:A:792:LYS:HE3	1.90	0.53
1:A:16:ARG:HH11	1:A:69:ARG:HH21	1.56	0.52
1:A:393:GLU:HB3	1:A:400:LEU:HD22	1.90	0.52
1:A:67:TRP:HA	1:A:238:VAL:HB	1.92	0.52
1:A:550:GLU:HG3	1:A:551:ARG:N	2.25	0.52
1:A:793:ASN:C	1:A:793:ASN:HD22	2.13	0.52
1:A:16:ARG:HH11	1:A:69:ARG:NH2	2.07	0.52
1:A:390:HIS:O	1:A:394:THR:CG2	2.55	0.52
1:A:93:ARG:HG2	1:A:126:GLU:HG2	1.91	0.52
1:A:552:GLU:HB2	1:A:553:TYR:CD2	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:82:ILE:HD11	1:A:827:VAL:HG11	1.92	0.51
1:A:628:ASP:O	1:A:632:HIS:HD2	1.95	0.50
1:A:450:HIS:HD2	4:A:1308:HOH:O	1.95	0.49
1:A:201:HIS:HD2	1:A:218:THR:OG1	1.96	0.48
1:A:25:THR:O	1:A:29:LYS:HD3	2.12	0.48
1:A:795:ARG:O	1:A:799:ARG:HG3	2.14	0.48
1:A:15:VAL:HA	1:A:18:LEU:HD22	1.95	0.48
1:A:463:LEU:CD2	1:A:467:ILE:HD11	2.44	0.48
1:A:795:ARG:NH2	1:A:795:ARG:HG2	2.30	0.47
1:A:230:VAL:HG22	1:A:230:VAL:O	2.16	0.46
1:A:799:ARG:O	1:A:803:ARG:HG3	2.15	0.46
1:A:568:LYS:HD3	1:A:574:LYS:HD3	1.98	0.46
1:A:538:LYS:HE2	1:A:660:ALA:O	2.16	0.46
1:A:554:LYS:O	1:A:555:VAL:CG2	2.63	0.45
1:A:636:VAL:O	1:A:639:ARG:HD3	2.16	0.45
1:A:325:ASN:HB3	1:A:326:PHE:H	1.63	0.45
1:A:594:PRO:O	1:A:639:ARG:NH1	2.48	0.45
1:A:16:ARG:HD2	1:A:16:ARG:HA	1.48	0.45
1:A:21:VAL:HG12	1:A:22:GLU:N	2.31	0.45
1:A:354:VAL:O	1:A:358:ARG:HA	2.17	0.44
1:A:230:VAL:CG2	1:A:230:VAL:O	2.66	0.44
1:A:538:LYS:HE3	1:A:658:PRO:O	2.16	0.44
1:A:748:GLY:HA3	1:A:755:PRO:HA	1.99	0.44
1:A:16:ARG:HD3	1:A:69:ARG:HH21	1.83	0.43
1:A:538:LYS:NZ	1:A:684:ASN:O	2.51	0.43
1:A:648:TYR:HA	1:A:652:LEU:HD23	2.00	0.43
1:A:466:THR:OG1	1:A:467:ILE:N	2.52	0.42
1:A:423:ASP:HB2	4:A:1248:HOH:O	2.18	0.42
1:A:770:ARG:HD3	4:A:1324:HOH:O	2.18	0.42
1:A:247:LYS:HD3	1:A:247:LYS:HA	1.91	0.42
1:A:379:VAL:HG13	4:A:1104:HOH:O	2.19	0.42
1:A:730:GLU:O	1:A:734:ARG:HD3	2.20	0.42
1:A:741:ILE:HA	1:A:744:GLN:HE21	1.83	0.42
1:A:726:TYR:OH	1:A:774:PHE:HB2	2.20	0.41
1:A:605:ILE:O	1:A:644:PHE:HA	2.20	0.41
1:A:60:ARG:HD2	1:A:188:PRO:O	2.21	0.41
1:A:36:HIS:O	1:A:40:VAL:HA	2.20	0.41
1:A:689:ILE:O	1:A:689:ILE:HG23	2.21	0.41
1:A:16:ARG:O	1:A:16:ARG:HD2	2.21	0.41
1:A:680:LYS:NZ	3:A:999:PLP:O3	2.54	0.41

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	808/842 (96%)	779 (96%)	27 (3%)	2 (0%)	52	48

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	554	LYS
1	A	555	VAL

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	705/730 (97%)	653 (93%)	52 (7%)	17	11

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	ARG
1	A	18	LEU
1	A	27	LEU
1	A	29	LYS
1	A	32	ASN
1	A	87	LEU
1	A	90	TYR
1	A	128	ASP
1	A	144	LEU

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Mol	Chain	Res	Type
1	A	169	LYS
1	A	184	ARG
1	A	191	LYS
1	A	205	ARG
1	A	214	LYS
1	A	234	ARG
1	A	277	ARG
1	A	306	ASP
1	A	309	ARG
1	A	314	SER
1	A	358	ARG
1	A	379	VAL
1	A	384	LEU
1	A	389	VAL
1	A	394	THR
1	A	423	ASP
1	A	437	LYS
1	A	496	ASN
1	A	499	LEU
1	A	505	GLU
1	A	506	ARG
1	A	528	GLU
1	A	538	LYS
1	A	543	LEU
1	A	554	LYS
1	A	562	LEU
1	A	568	LYS
1	A	571	HIS
1	A	576	GLN
1	A	579	ASN
1	A	586	LEU
1	A	591	LYS
1	A	601	ARG
1	A	641	ARG
1	A	701	GLU
1	A	708	PHE
1	A	721	LEU
1	A	753	LYS
1	A	754	GLN
1	A	759	LYS
1	A	793	ASN
1	A	831	ARG

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Mol	Chain	Res	Type
1	A	833	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	ASN
1	A	36	HIS
1	A	106	ASN
1	A	201	HIS
1	A	250	ASN
1	A	408	GLN
1	A	412	ASN
1	A	450	HIS
1	A	484	ASN
1	A	496	ASN
1	A	517	GLN
1	A	541	ASN
1	A	566	GLN
1	A	576	GLN
1	A	579	ASN
1	A	588	ASN
1	A	632	HIS
1	A	684	ASN
1	A	744	GLN
1	A	793	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	SEP	A	14	1	8,9,10	1.16	0	8,12,14	6.62	2 (25%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	SEP	A	14	1	-	0/6/8/10	0/0/0/0

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	14	SEP	O3P-P-O1P	2.72	119.35	110.58
1	A	14	SEP	OG-CB-CA	18.39	123.97	108.27

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	14	SEP	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	GLC	A	998	-	12,12,12	1.37	2 (16%)	17,17,17	0.83	0
3	PLP	A	999	1	15,15,16	1.28	2 (13%)	21,22,23	1.08	1 (4%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GLC	A	998	-	-	0/2/22/22	0/1/1/1
3	PLP	A	999	1	-	0/6/6/8	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	999	PLP	C3-C2	-3.18	1.38	1.40
3	A	999	PLP	P-O3P	-2.21	1.46	1.54
2	A	998	GLC	C1-C2	2.34	1.57	1.52
2	A	998	GLC	C3-C2	2.41	1.58	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	999	PLP	O3P-P-O1P	2.86	119.79	110.58

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	999	PLP	1	0

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](#)

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.