



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 06:18 AM UTC

PDB ID : 1M0W / pdb_00001m0w
Title : Yeast Glutathione Synthase Bound to gamma-glutamyl-cysteine, AMP-PNP and 2 Magnesium Ions
Authors : Gogos, A.; Shapiro, L.; Burley, S.K.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2002-06-14
Resolution : 1.80 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 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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

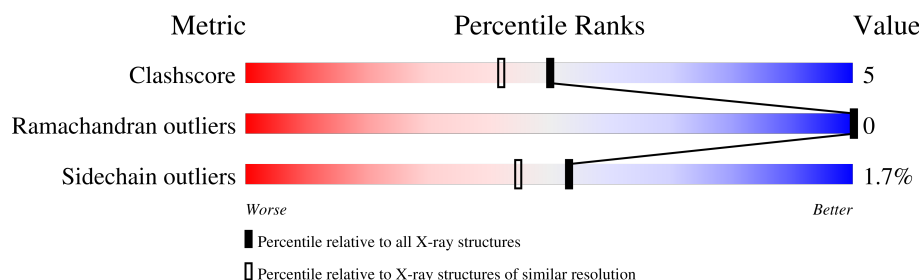
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	190562	8479 (1.80-1.80)
Ramachandran outliers	187476	8391 (1.80-1.80)
Sidechain outliers	187428	8390 (1.80-1.80)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	491	 84% 13% ..
1	B	491	 85% 12% ..

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 8810 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.

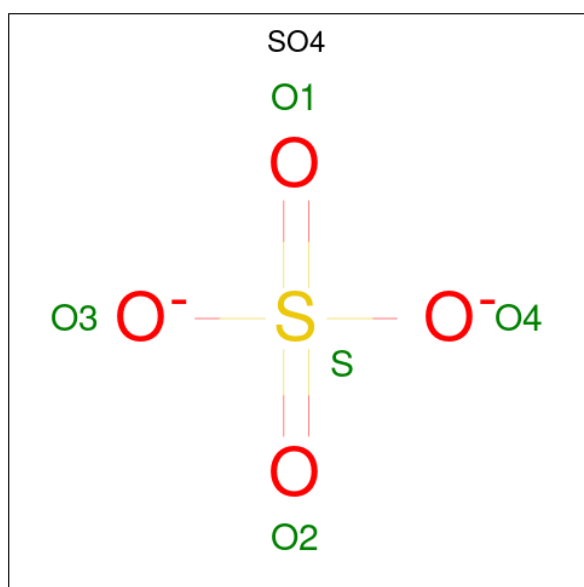
- Molecule 1 is a protein called glutathione synthetase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	481	Total	C	N	O	S	0	25	0
			3984	2541	654	780	9			
1	B	479	Total	C	N	O	S	0	10	0
			3860	2469	635	748	8			

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

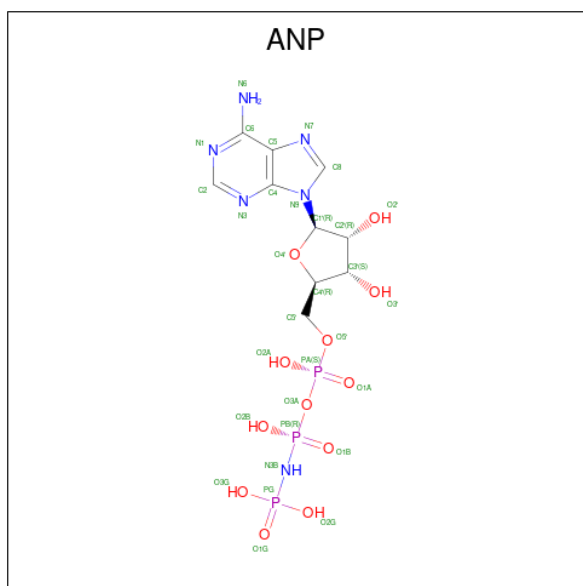
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Mg	0	0
			2	2		
2	B	2	Total	Mg	0	0
			2	2		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



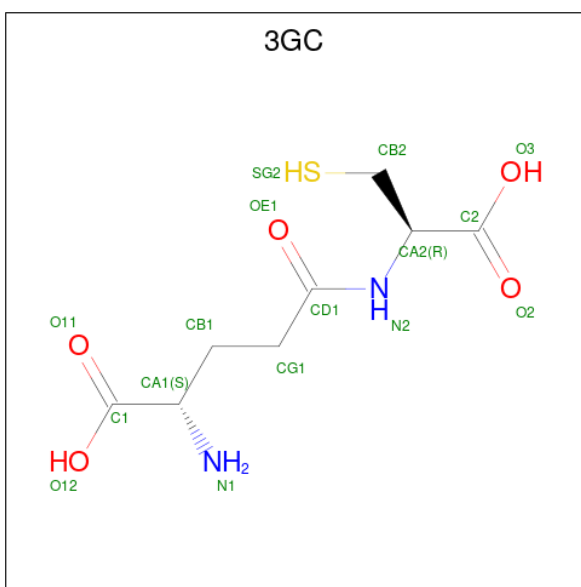
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	
			58	20	12	21	5	1
4	B	1	Total	C	N	O	P	
			58	20	12	21	5	1

- Molecule 5 is GAMMA-GLUTAMYL CYSTEINE (CCD ID: 3GC) (formula: $C_8H_{14}N_2O_5S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total 32	C 16	N 4	O 10	S 2	0	1
5	B	1	Total 32	C 16	N 4	O 10	S 2	0	1

- Molecule 6 is water.

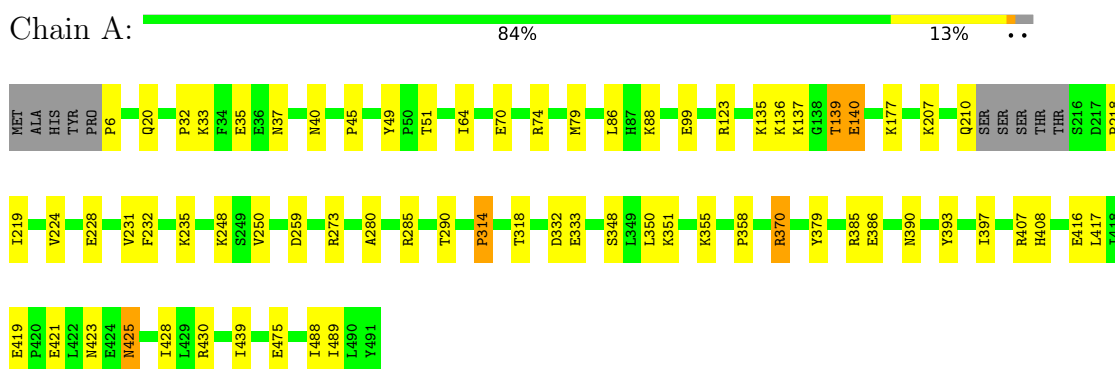
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	377	Total O 377 377	0	0
6	B	370	Total O 370 370	0	0

3 Residue-property plots [i](#)

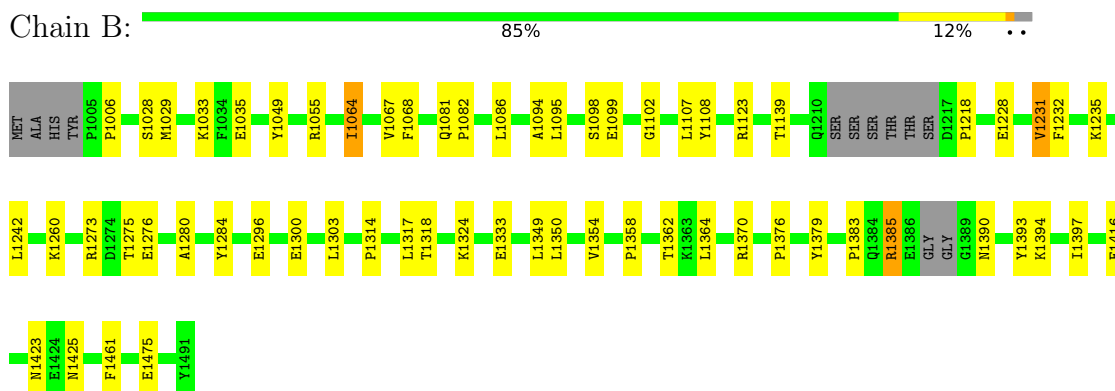
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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: glutathione synthetase



- Molecule 1: glutathione synthetase



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	51.66Å 52.01Å 100.64Å 82.08° 86.77° 77.49°	Depositor
Resolution (Å)	20.00 – 1.80	Depositor
% Data completeness (in resolution range)	94.4 (20.00-1.80)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
Refinement program	CNS 0.5	Depositor
R, R_{free}	0.172 , 0.196	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	8810	wwPDB-VP
Average B, all atoms (Å ²)	20.0	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: ANP, 3GC, SO4, MG

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	0.56	0/4059	0.97	12/5492 (0.2%)
1	B	0.59	1/3935 (0.0%)	1.00	13/5328 (0.2%)
All	All	0.58	1/7994 (0.0%)	0.99	25/10820 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1397	ILE	CA-CB	5.87	1.57	1.54

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	273	ARG	N-CA-C	7.45	120.10	111.02
1	A	386	GLU	N-CA-C	6.88	120.70	110.52
1	A	379	TYR	N-CA-C	6.56	119.39	109.41
1	B	1273	ARG	N-CA-C	6.53	118.99	111.02
1	B	1232	PHE	CA-CB-CG	-6.23	107.57	113.80

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	3984	0	3838	47	0
1	B	3860	0	3738	40	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	15	0	0	0	0
3	B	20	0	0	0	0
4	A	58	0	26	0	0
4	B	58	0	26	1	0
5	A	32	0	25	0	0
5	B	32	0	24	0	0
6	A	377	0	0	5	0
6	B	370	0	0	5	0
All	All	8810	0	7677	84	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 5.

The worst 5 of 84 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:370[A]:ARG:HG3	1:A:370[A]:ARG:HH11	1.41	0.85
1:A:136:LYS:O	1:A:139:THR:HG23	1.82	0.80
1:B:1064:ILE:HD13	1:B:1064:ILE:O	1.85	0.75
1:A:248[B]:LYS:N	1:A:248[B]:LYS:HD2	2.03	0.74
1:B:1333:GLU:HG2	1:B:1350:LEU:HD11	1.69	0.73

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	500/491 (102%)	485 (97%)	15 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	483/491 (98%)	472 (98%)	11 (2%)	0	100	100
All	All	983/982 (100%)	957 (97%)	26 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	426/440 (97%)	417 (98%)	9 (2%)	47	36
1	B	412/440 (94%)	406 (98%)	6 (2%)	57	49
All	All	838/880 (95%)	823 (98%)	15 (2%)	53	43

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	370[A]	ARG
1	B	1123	ARG
1	A	370[B]	ARG
1	B	1364	LEU
1	B	1086	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1423	ASN
1	B	1408	HIS
1	B	1020	GLN
1	B	1258	ASN
1	A	423	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 19 ligands modelled in this entry, 4 are monoatomic - leaving 15 for Mogul analysis.

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$
4	ANP	B	1504[A]	2	33,33,33	2.15	11 (33%)	45,52,52	2.54	14 (31%)
4	ANP	A	504[B]	2	28,29,33	1.97	5 (17%)	40,45,52	2.39	13 (32%)
5	3GC	B	1501[A]	-	14,15,15	1.28	2 (14%)	16,19,19	0.81	1 (6%)
3	SO4	B	509	-	4,4,4	0.43	0	6,6,6	0.04	0
3	SO4	B	510	-	4,4,4	0.39	0	6,6,6	0.10	0
3	SO4	B	512	-	4,4,4	0.34	0	6,6,6	0.11	0
3	SO4	A	511	-	4,4,4	0.37	0	6,6,6	0.07	0
5	3GC	A	501[A]	-	14,15,15	1.27	2 (14%)	16,19,19	0.76	1 (6%)
3	SO4	B	508	-	4,4,4	0.39	0	6,6,6	0.14	0
4	ANP	A	504[A]	2	33,33,33	1.99	9 (27%)	45,52,52	2.31	14 (31%)
4	ANP	B	1504[B]	2	28,29,33	2.15	6 (21%)	40,45,52	2.29	11 (27%)
3	SO4	A	506	-	4,4,4	0.38	0	6,6,6	0.11	0
5	3GC	B	1501[B]	-	14,15,15	1.05	1 (7%)	16,19,19	1.25	2 (12%)
5	3GC	A	501[B]	-	14,15,15	1.17	1 (7%)	16,19,19	1.00	2 (12%)
3	SO4	A	507	-	4,4,4	0.38	0	6,6,6	0.11	0

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
4	ANP	B	1504[A]	2	-	4/18/38/38	0/3/3/3
4	ANP	A	504[B]	2	-	2/13/32/38	0/3/3/3
5	3GC	B	1501[A]	-	-	0/19/19/19	-
5	3GC	A	501[A]	-	-	0/19/19/19	-
4	ANP	A	504[A]	2	-	4/18/38/38	0/3/3/3
4	ANP	B	1504[B]	2	-	1/13/32/38	0/3/3/3
5	3GC	B	1501[B]	-	-	0/19/19/19	-
5	3GC	A	501[B]	-	-	0/19/19/19	-

The worst 5 of 37 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1504[B]	ANP	PB-O3A	7.99	1.69	1.59
4	B	1504[A]	ANP	PB-O3A	7.46	1.68	1.59
4	A	504[B]	ANP	PB-O3A	6.55	1.67	1.59
4	A	504[A]	ANP	PB-O3A	6.52	1.67	1.59
4	B	1504[A]	ANP	PG-O1G	3.70	1.51	1.46

The worst 5 of 58 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1504[A]	ANP	C5-C4-N3	-6.87	117.26	126.72
4	A	504[B]	ANP	C5-C4-N3	-6.72	117.47	126.72
4	B	1504[B]	ANP	C5-C4-N3	-6.70	117.49	126.72
4	A	504[A]	ANP	C5-C4-N3	-6.58	117.66	126.72
4	B	1504[A]	ANP	N3-C4-N9	6.15	137.62	127.17

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

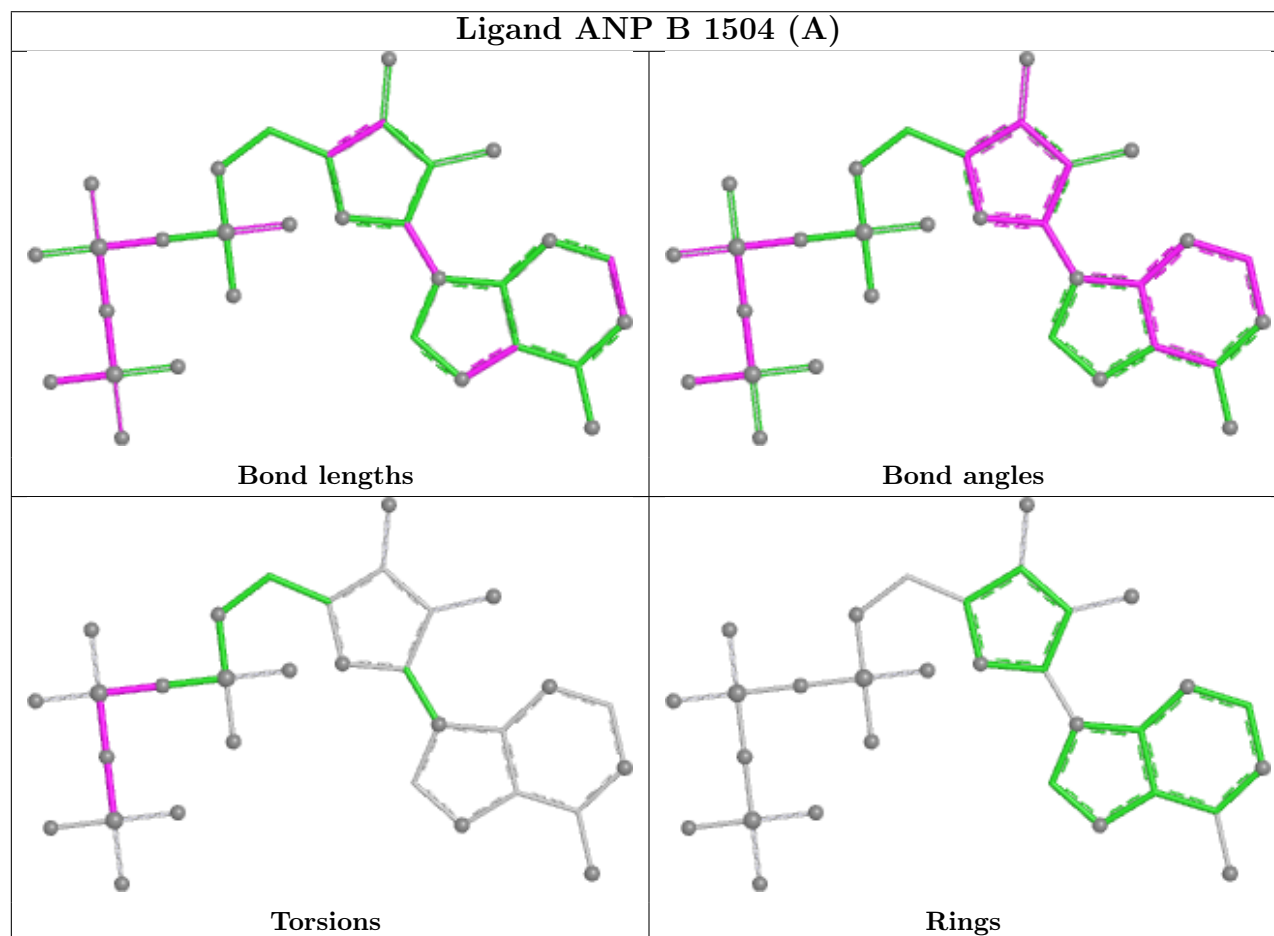
Mol	Chain	Res	Type	Atoms
4	A	504[A]	ANP	PB-N3B-PG-O1G
4	A	504[A]	ANP	PG-N3B-PB-O1B
4	A	504[A]	ANP	PA-O3A-PB-O1B
4	A	504[A]	ANP	PA-O3A-PB-O2B
4	B	1504[A]	ANP	PB-N3B-PG-O1G

There are no ring outliers.

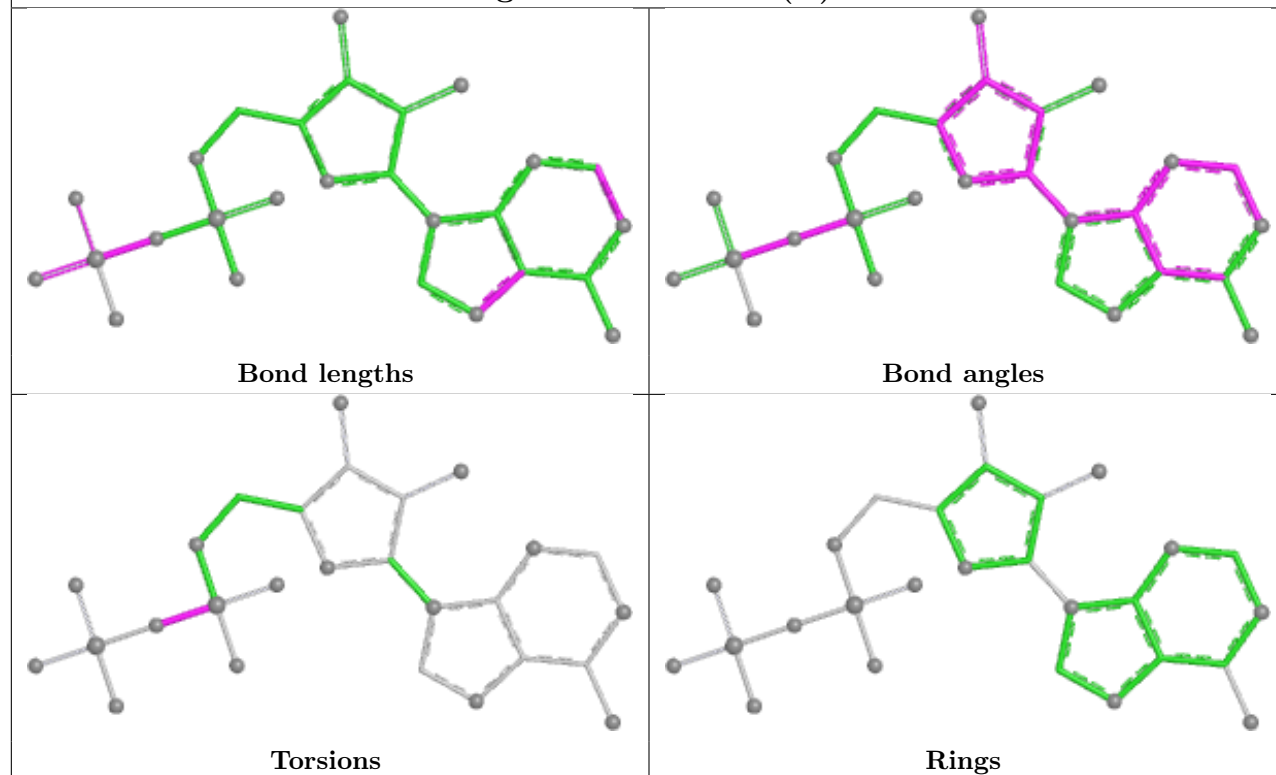
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	1504[A]	ANP	1	0

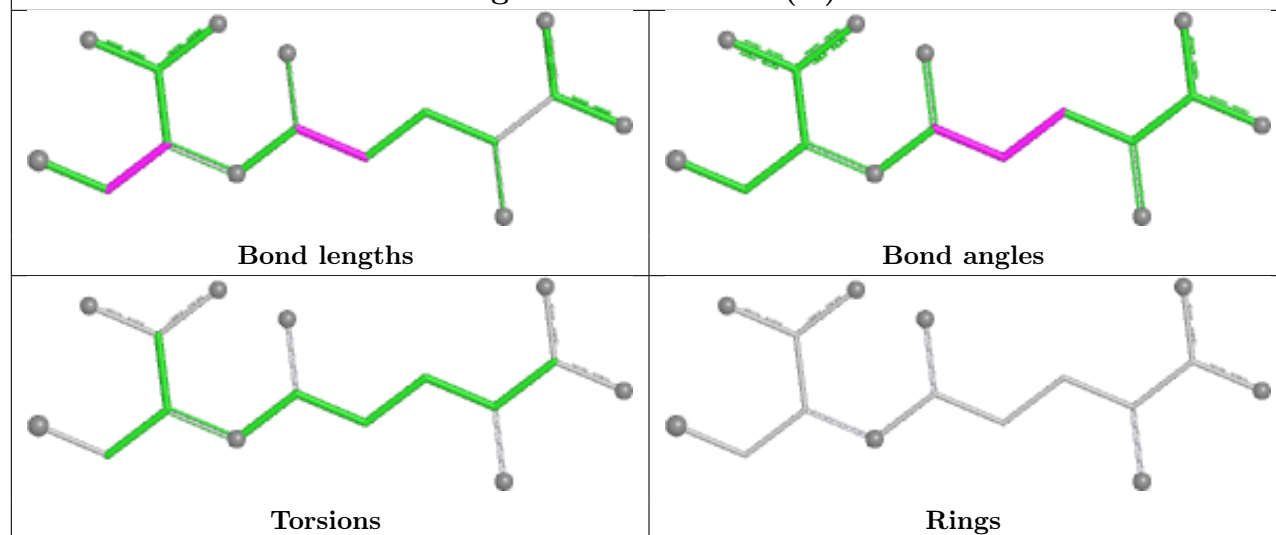
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



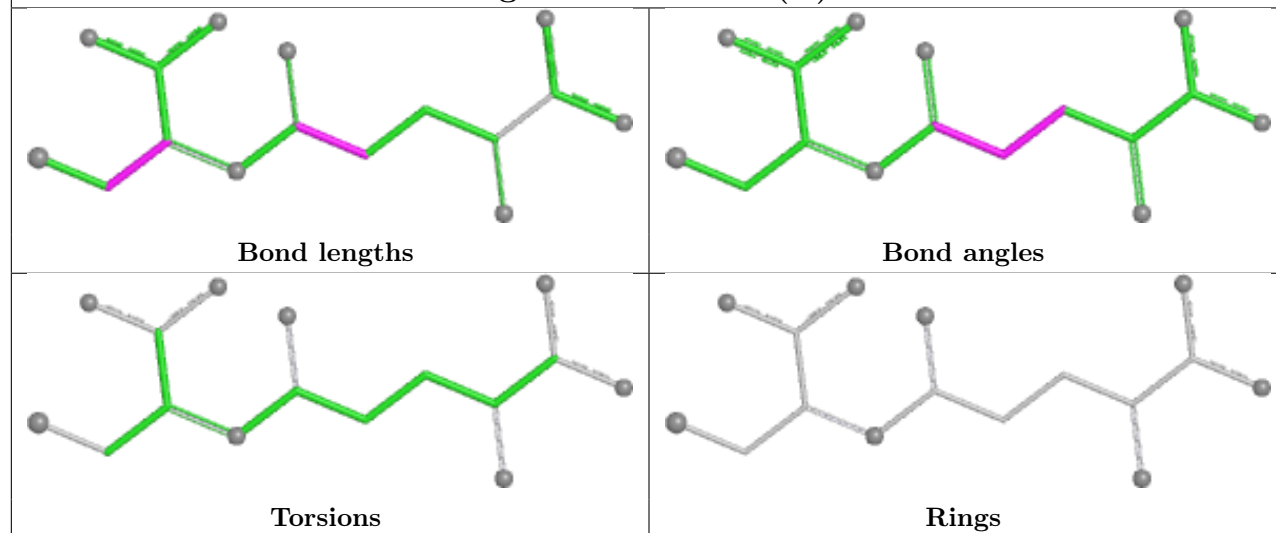
Ligand ANP A 504 (B)



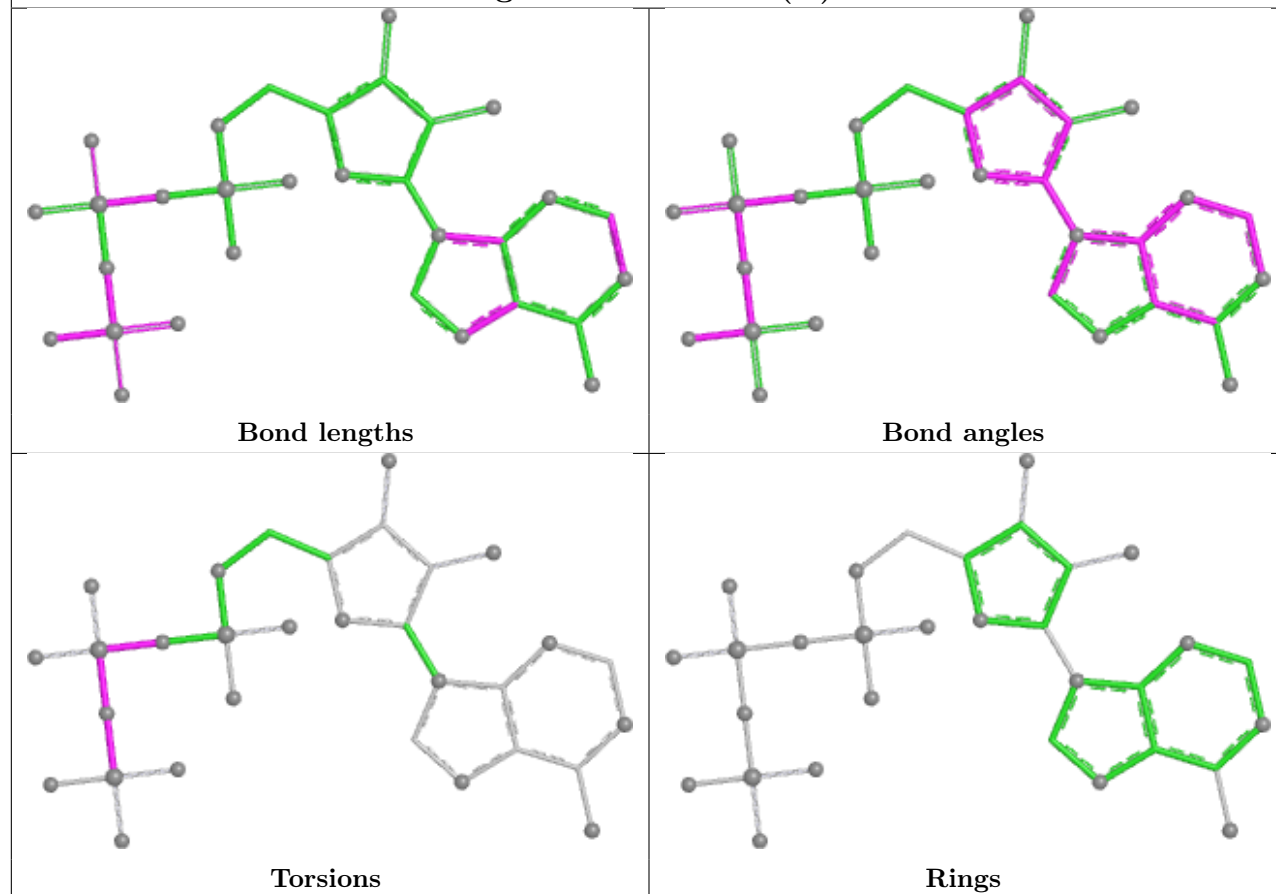
Ligand 3GC B 1501 (A)



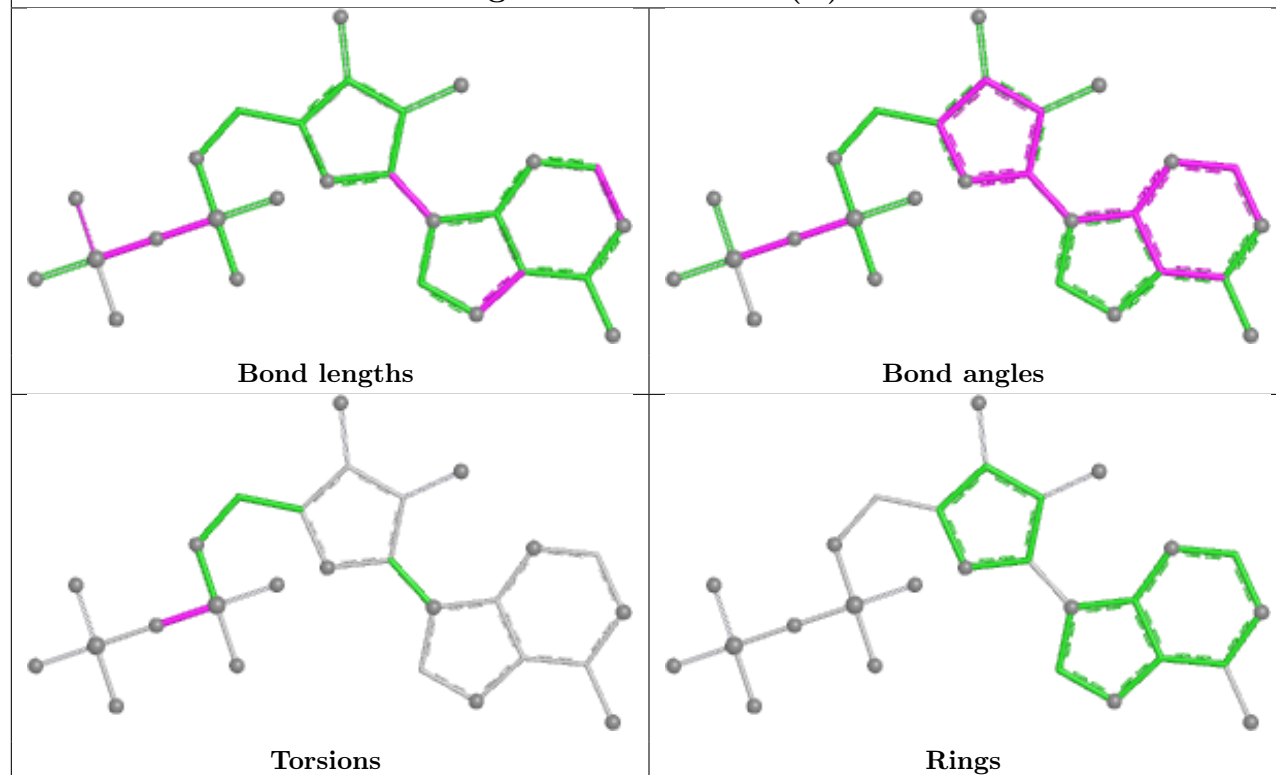
Ligand 3GC A 501 (A)



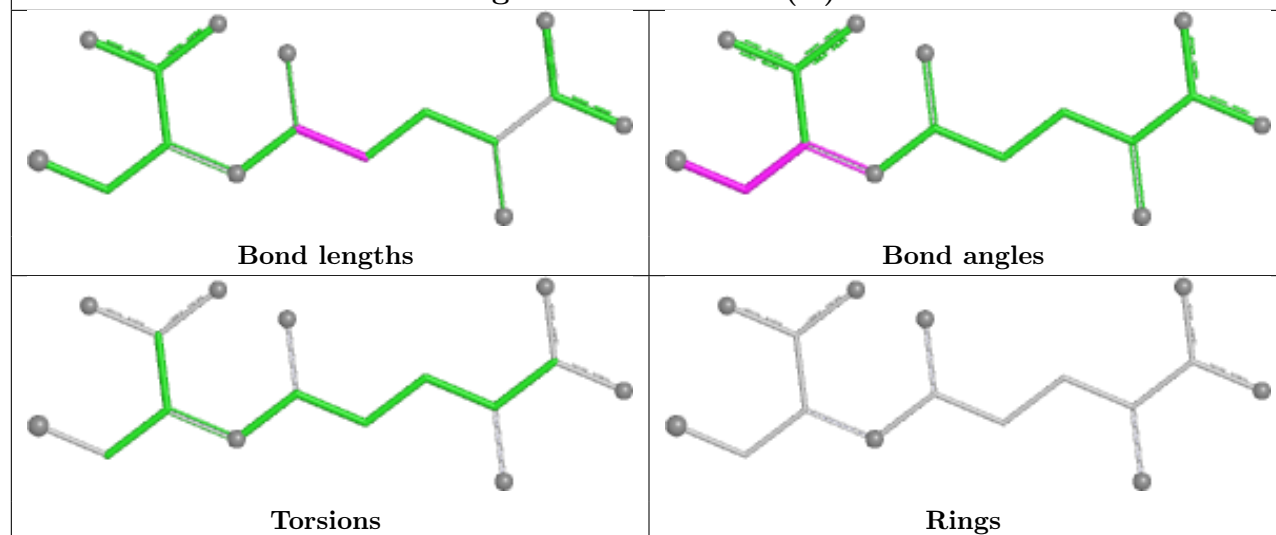
Ligand ANP A 504 (A)

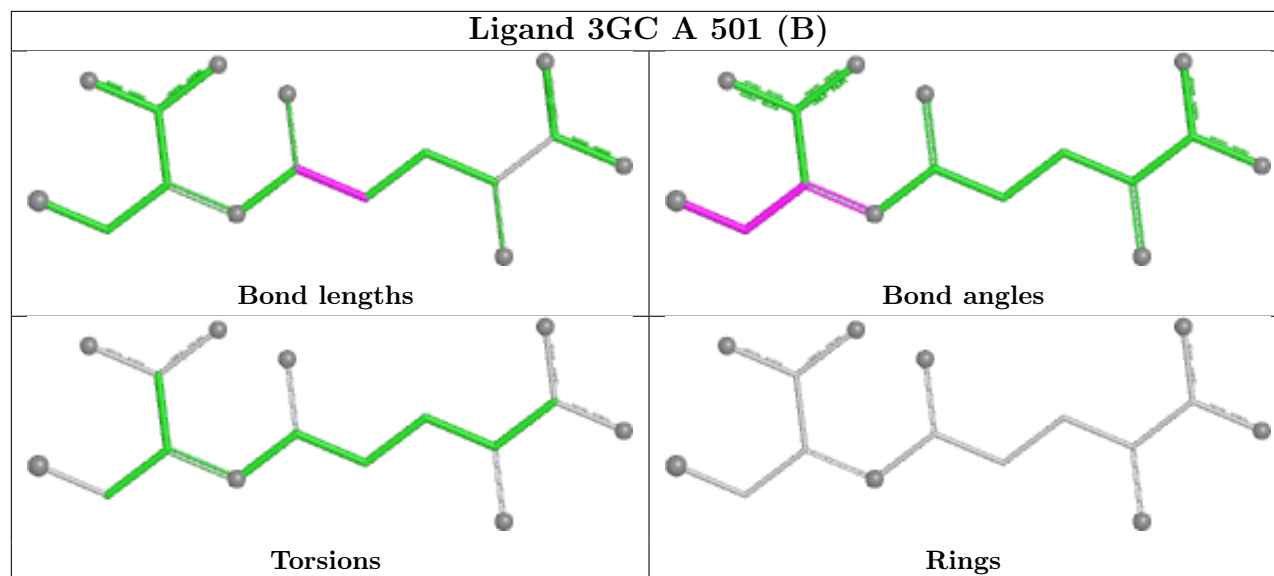


Ligand ANP B 1504 (B)



Ligand 3GC B 1501 (B)





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](#)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.