



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:07 PM UTC

PDB ID : 1VBD / pdb_00001vbd
Title : POLIOVIRUS (TYPE 1, MAHONEY STRAIN) COMPLEXED WITH R78206
Authors : Grant, R.A.; Hiremath, C.N.; Filman, D.J.; Syed, R.; Andries, K.; Hogle, J.M.
Deposited on : 1996-01-02
Resolution : 2.90 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 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

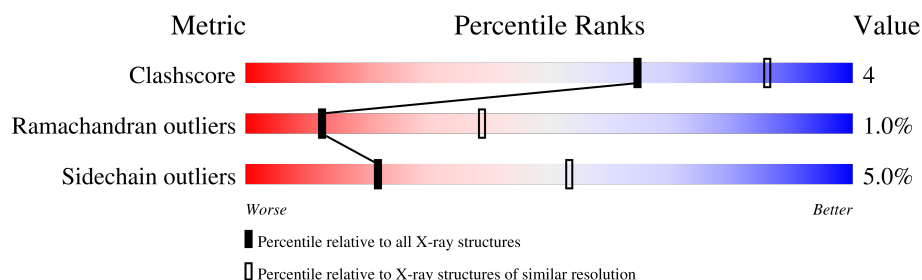
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)

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	0	5	40% 20% 40%
2	1	302	67% 22% . . 6%
3	2	272	67% 28% . .
4	3	238	74% 22% . .
5	4	68	56% 28% 6% . 9%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6675 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 POLIOVIRUS TYPE 1 MAHONEY.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	0	5	Total	C	N	O	0	0	0
			29	15	5	9			

- Molecule 2 is a protein called POLIOVIRUS TYPE 1 MAHONEY.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	1	283	Total	C	N	O	S	0	0	0
			2222	1416	378	423	5			

- Molecule 3 is a protein called POLIOVIRUS TYPE 1 MAHONEY.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	2	266	Total	C	N	O	S	0	0	0
			2071	1309	356	392	14			

- Molecule 4 is a protein called POLIOVIRUS TYPE 1 MAHONEY.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	3	235	Total	C	N	O	S	0	0	0
			1834	1169	299	349	17			

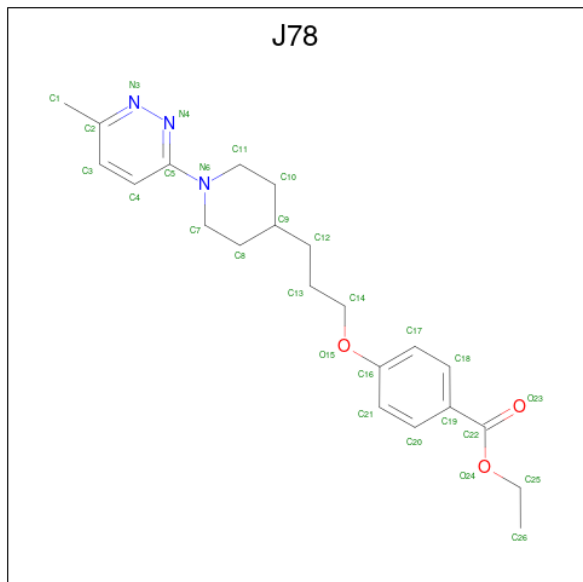
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3	123	SER	PHE	conflict	UNP P03300

- Molecule 5 is a protein called POLIOVIRUS TYPE 1 MAHONEY.

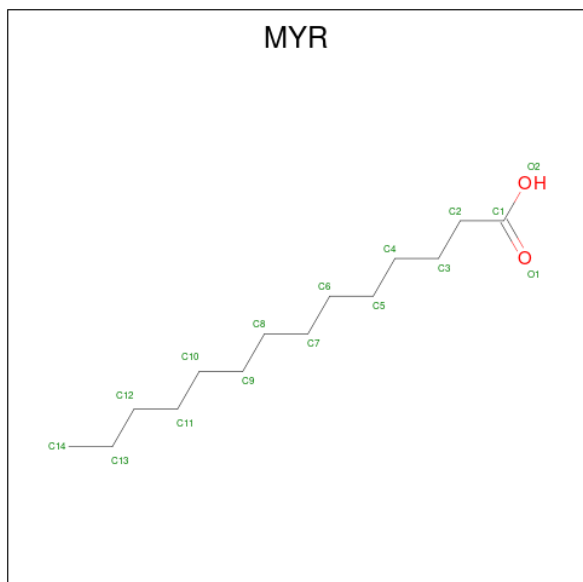
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	4	62	Total	C	N	O	S	0	0	0
			476	293	81	101	1			

- Molecule 6 is (METHYLPYRIDAZINE PIPERIDINE PROPYLOXYPHENYL)ETHYLACETATE (CCD ID: J78) (formula: $C_{22}H_{29}N_3O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	1	1	Total	C	N	O	0	0
			28	22	3	3		

- Molecule 7 is MYRISTIC ACID (CCD ID: MYR) (formula: $C_{14}H_{28}O_2$).



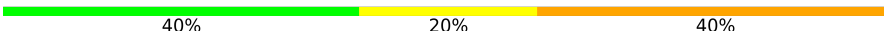
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	4	1	Total	C	O	0	0
			15	14	1		

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.

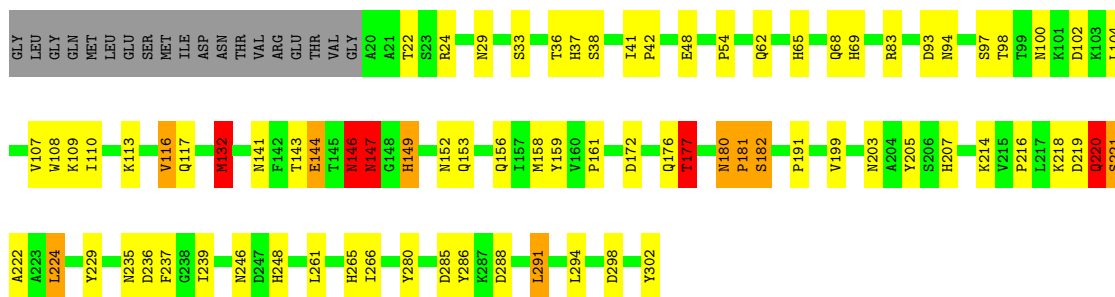
• Molecule 1: POLIOVIRUS TYPE 1 MAHONEY

Chain 0: 



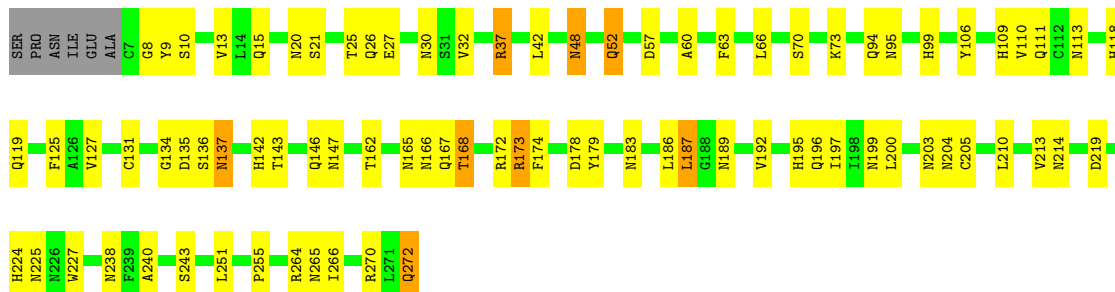
• Molecule 2: POLIOVirus TYPE 1 MAHONEY

Chain 1: 



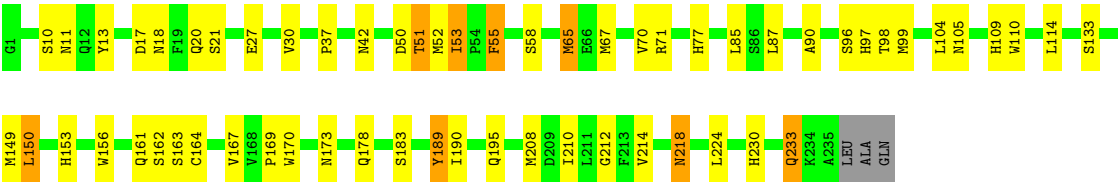
• Molecule 3: POLIOVirus TYPE 1 MAHONEY

Chain 2: 

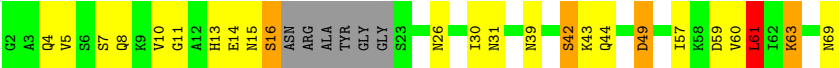


• Molecule 4: POLIOVirus TYPE 1 MAHONEY

Chain 3: 



● Molecule 5: POLIOVIRUS TYPE 1 MAHONEY



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	322.94Å 358.04Å 380.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.90	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.90)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 2.1	Depositor
R, R_{free}	0.287 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6675	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MYR, J78

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	0	0.87	0/28	2.26	3/36 (8.3%)
2	1	0.94	10/2285 (0.4%)	1.81	56/3124 (1.8%)
3	2	0.91	7/2128 (0.3%)	1.89	69/2909 (2.4%)
4	3	0.89	5/1881 (0.3%)	1.72	35/2562 (1.4%)
5	4	0.95	1/483 (0.2%)	2.01	21/651 (3.2%)
All	All	0.92	23/6805 (0.3%)	1.83	184/9282 (2.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
3	2	0	1

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	2	224	HIS	CD2-NE2	-7.48	1.29	1.37
2	1	69	HIS	CD2-NE2	-7.04	1.30	1.37
2	1	37	HIS	CD2-NE2	-6.84	1.30	1.37
4	3	77	HIS	CD2-NE2	-6.82	1.30	1.37
4	3	97	HIS	CD2-NE2	-6.75	1.30	1.37
2	1	149	HIS	CD2-NE2	-6.68	1.30	1.37
5	4	13	HIS	CD2-NE2	-6.58	1.30	1.37
2	1	65	HIS	CD2-NE2	-6.57	1.30	1.37
2	1	207	HIS	CD2-NE2	-6.49	1.30	1.37
4	3	153	HIS	CD2-NE2	-6.28	1.30	1.37
3	2	195	HIS	CD2-NE2	-6.23	1.30	1.37
3	2	99	HIS	CD2-NE2	-6.09	1.31	1.37
2	1	54	PRO	CA-CB	-6.08	1.49	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	2	142	HIS	CD2-NE2	-6.07	1.31	1.37
2	1	265	HIS	CD2-NE2	-6.01	1.31	1.37
4	3	109	HIS	CD2-NE2	-5.89	1.31	1.37
3	2	118	HIS	CD2-NE2	-5.81	1.31	1.37
3	2	109	HIS	CD2-NE2	-5.70	1.31	1.37
4	3	230	HIS	CD2-NE2	-5.61	1.31	1.37
3	2	224	HIS	CG-ND1	-5.31	1.32	1.38
2	1	265	HIS	CG-ND1	-5.10	1.32	1.38
2	1	69	HIS	CG-ND1	-5.09	1.32	1.38
2	1	248	HIS	CD2-NE2	-5.06	1.32	1.37

All (184) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	3	233	GLN	OE1-CD-NE2	-10.54	112.06	122.60
4	3	218	ASN	OD1-CG-ND2	-10.50	112.10	122.60
3	2	204	ASN	CB-CG-ND2	9.77	131.06	116.40
2	1	116	VAL	N-CA-C	9.68	120.14	111.81
4	3	173	ASN	OD1-CG-ND2	-9.49	113.11	122.60
2	1	266	ILE	N-CA-C	9.27	121.81	109.21
3	2	204	ASN	CA-CB-CG	9.19	121.79	112.60
2	1	117	GLN	OE1-CD-NE2	-9.14	113.46	122.60
2	1	153	GLN	OE1-CD-NE2	-8.94	113.66	122.60
3	2	48	ASN	OD1-CG-ND2	-8.91	113.69	122.60
3	2	214	ASN	OD1-CG-ND2	-8.61	113.99	122.60
5	4	31	ASN	OD1-CG-ND2	-8.61	113.99	122.60
3	2	52	GLN	OE1-CD-NE2	-8.57	114.03	122.60
4	3	53	ILE	N-CA-C	8.57	116.00	108.63
3	2	146	GLN	OE1-CD-NE2	-8.54	114.06	122.60
3	2	204	ASN	OD1-CG-ND2	-8.52	114.08	122.60
2	1	220	GLN	OE1-CD-NE2	-8.43	114.17	122.60
3	2	203	ASN	OD1-CG-ND2	-8.38	114.22	122.60
4	3	17	ASP	CA-CB-CG	8.26	120.86	112.60
4	3	105	ASN	OD1-CG-ND2	-8.16	114.44	122.60
5	4	39	ASN	OD1-CG-ND2	-8.09	114.51	122.60
3	2	219	ASP	CA-CB-CG	8.00	120.60	112.60
4	3	218	ASN	CB-CG-ND2	7.73	127.99	116.40
3	2	167	GLN	OE1-CD-NE2	-7.68	114.92	122.60
5	4	8	GLN	OE1-CD-NE2	-7.52	115.08	122.60
2	1	104	LEU	N-CA-C	7.52	119.97	109.15
3	2	224	HIS	N-CA-C	7.49	120.69	108.26
2	1	219	ASP	CA-CB-CG	7.46	120.06	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	1	199	VAL	N-CA-C	7.45	119.29	112.29
5	4	69	ASN	OD1-CG-ND2	-7.44	115.16	122.60
3	2	20	ASN	OD1-CG-ND2	-7.39	115.21	122.60
2	1	68	GLN	OE1-CD-NE2	-7.39	115.21	122.60
2	1	176	GLN	OE1-CD-NE2	-7.38	115.22	122.60
3	2	10	SER	N-CA-C	7.37	120.56	108.99
2	1	146	ASN	CA-CB-CG	7.36	119.96	112.60
3	2	94	GLN	OE1-CD-NE2	-7.36	115.24	122.60
4	3	178	GLN	OE1-CD-NE2	-7.34	115.26	122.60
3	2	119	GLN	OE1-CD-NE2	-7.33	115.27	122.60
4	3	162	SER	N-CA-C	7.32	121.12	111.75
3	2	26	GLN	OE1-CD-NE2	-7.28	115.32	122.60
2	1	117	GLN	N-CA-C	7.27	118.90	110.97
3	2	203	ASN	N-CA-C	7.27	120.41	108.99
3	2	178	ASP	N-CA-C	7.26	119.83	111.11
2	1	147	ASN	OD1-CG-ND2	-7.18	115.42	122.60
3	2	204	ASN	CB-CA-C	-7.16	96.92	110.67
3	2	225	ASN	OD1-CG-ND2	-7.15	115.45	122.60
2	1	172	ASP	CA-CB-CG	7.02	119.62	112.60
5	4	10	VAL	N-CA-C	7.01	118.91	108.54
2	1	152	ASN	OD1-CG-ND2	-6.98	115.62	122.60
3	2	137	ASN	OD1-CG-ND2	-6.96	115.64	122.60
2	1	113	LYS	N-CA-C	6.95	121.75	113.28
3	2	127	VAL	N-CA-C	6.92	115.52	107.77
2	1	93	ASP	CA-CB-CG	6.92	119.52	112.60
2	1	236	ASP	CA-CB-CG	6.89	119.49	112.60
3	2	265	ASN	OD1-CG-ND2	-6.89	115.71	122.60
3	2	178	ASP	CA-CB-CG	6.87	119.47	112.60
3	2	199	ASN	OD1-CG-ND2	-6.87	115.73	122.60
3	2	266	ILE	N-CA-C	6.86	117.87	109.30
4	3	96	SER	N-CA-C	6.82	120.47	111.75
3	2	113	ASN	OD1-CG-ND2	-6.81	115.79	122.60
2	1	102	ASP	N-CA-C	6.77	120.05	110.23
3	2	189	ASN	OD1-CG-ND2	-6.74	115.86	122.60
2	1	100	ASN	OD1-CG-ND2	-6.69	115.91	122.60
3	2	63	PHE	N-CA-C	6.64	119.66	108.23
2	1	94	ASN	OD1-CG-ND2	-6.60	116.00	122.60
2	1	182	SER	N-CA-C	6.56	120.16	109.59
3	2	165	ASN	N-CA-C	6.55	121.02	112.89
2	1	62	GLN	OE1-CD-NE2	-6.48	116.12	122.60
4	3	11	ASN	OD1-CG-ND2	-6.44	116.16	122.60
4	3	55	PHE	N-CA-C	6.44	118.30	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	4	13	HIS	CB-CG-CD2	-6.44	122.83	131.20
5	4	39	ASN	CB-CG-ND2	6.40	126.01	116.40
3	2	119	GLN	CG-CD-NE2	6.39	125.98	116.40
4	3	133	SER	N-CA-C	6.32	119.48	109.50
3	2	15	GLN	OE1-CD-NE2	-6.30	116.30	122.60
5	4	4	GLN	OE1-CD-NE2	-6.28	116.32	122.60
3	2	165	ASN	OD1-CG-ND2	-6.24	116.36	122.60
4	3	195	GLN	OE1-CD-NE2	-6.23	116.37	122.60
3	2	136	SER	N-CA-C	6.19	119.56	109.59
5	4	49	ASP	CA-CB-CG	6.19	118.79	112.60
2	1	156	GLN	OE1-CD-NE2	-6.16	116.44	122.60
3	2	205	CYS	N-CA-C	6.16	117.59	108.60
4	3	20	GLN	OE1-CD-NE2	-6.15	116.45	122.60
4	3	21	SER	O-C-N	-6.14	117.55	121.85
3	2	272	GLN	OE1-CD-NE2	-6.12	116.48	122.60
5	4	44	GLN	OE1-CD-NE2	-6.12	116.48	122.60
4	3	18	ASN	OD1-CG-ND2	-6.10	116.50	122.60
2	1	98	THR	N-CA-C	6.10	118.01	111.36
2	1	161	PRO	O-C-N	-6.02	118.32	121.15
2	1	29	ASN	OD1-CG-ND2	-6.00	116.59	122.60
2	1	149	HIS	CB-CG-CD2	-5.96	123.45	131.20
4	3	153	HIS	N-CA-C	5.93	118.09	109.07
4	3	173	ASN	CB-CG-ND2	5.90	125.26	116.40
2	1	235	ASN	OD1-CG-ND2	-5.90	116.70	122.60
3	2	9	TYR	N-CA-C	5.87	118.33	110.35
2	1	180	ASN	OD1-CG-ND2	-5.86	116.74	122.60
5	4	63	LYS	N-CA-C	5.86	118.45	111.71
2	1	153	GLN	CG-CD-NE2	5.83	125.14	116.40
2	1	117	GLN	CG-CD-NE2	5.82	125.13	116.40
4	3	189	TYR	N-CA-C	5.82	118.59	108.76
2	1	222	ALA	N-CA-C	5.81	118.08	111.11
4	3	161	GLN	OE1-CD-NE2	-5.78	116.82	122.60
1	0	7	SER	N-CA-C	5.77	118.20	107.99
4	3	42	ASN	OD1-CG-ND2	-5.75	116.85	122.60
4	3	30	VAL	N-CA-C	5.73	117.10	109.37
3	2	8	GLY	N-CA-C	5.72	121.58	114.37
4	3	153	HIS	CB-CG-CD2	-5.67	123.83	131.20
2	1	141	ASN	OD1-CG-ND2	-5.67	116.93	122.60
3	2	135	ASP	CA-CB-CG	5.64	118.24	112.60
5	4	42	SER	N-CA-C	5.64	118.16	111.33
1	0	10	THR	CA-CB-CG2	5.61	120.04	110.50
3	2	147	ASN	OD1-CG-ND2	-5.61	116.99	122.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	3	27	GLU	N-CA-C	5.61	119.43	112.47
3	2	48	ASN	CB-CG-ND2	5.58	124.76	116.40
2	1	236	ASP	N-CA-C	5.57	120.51	111.37
3	2	183	ASN	OD1-CG-ND2	-5.57	117.03	122.60
3	2	52	GLN	CG-CD-NE2	5.57	124.76	116.40
2	1	108	TRP	CG-CD2-CE3	5.56	139.46	133.90
5	4	49	ASP	N-CA-CB	-5.55	102.79	110.29
5	4	61	LEU	N-CA-C	5.53	118.26	109.24
2	1	147	ASN	CA-CB-CG	-5.52	107.08	112.60
2	1	69	HIS	CB-CG-CD2	-5.50	124.06	131.20
3	2	125	PHE	N-CA-C	5.50	117.92	109.07
5	4	4	GLN	CG-CD-NE2	5.50	124.64	116.40
3	2	200	LEU	N-CA-C	5.49	118.77	111.75
2	1	181	PRO	N-CA-CB	5.45	105.97	102.92
4	3	183	SER	N-CA-C	5.43	117.90	111.33
5	4	49	ASP	CB-CA-C	5.43	116.52	108.87
4	3	150	LEU	N-CA-C	5.41	119.14	112.54
2	1	54	PRO	N-CA-CB	5.39	106.35	102.79
3	2	196	GLN	OE1-CD-NE2	-5.39	117.21	122.60
5	4	26	ASN	N-CA-C	5.37	118.03	110.14
2	1	38	SER	N-CA-C	5.36	116.42	108.86
2	1	221	SER	N-CA-C	5.35	117.99	110.23
3	2	142	HIS	N-CA-C	5.35	119.78	112.88
3	2	27	GLU	N-CA-C	5.33	117.68	110.06
5	4	13	HIS	CB-CG-ND1	5.33	130.69	122.70
3	2	142	HIS	CB-CG-CD2	-5.31	124.29	131.20
2	1	291	LEU	N-CA-C	5.31	119.39	113.02
4	3	233	GLN	CG-CD-NE2	5.31	124.36	116.40
3	2	109	HIS	CB-CG-CD2	-5.31	124.30	131.20
2	1	246	ASN	OD1-CG-ND2	-5.26	117.33	122.60
3	2	118	HIS	CB-CG-CD2	-5.22	124.41	131.20
2	1	108	TRP	CE2-CD2-CG	-5.22	100.94	107.20
4	3	77	HIS	CB-CG-CD2	-5.22	124.42	131.20
5	4	7	SER	N-CA-C	5.22	118.44	110.20
3	2	186	LEU	N-CA-C	5.21	118.05	109.76
3	2	173	ARG	N-CA-C	5.21	117.33	109.41
3	2	70	SER	N-CA-C	5.21	116.89	108.41
2	1	218	LYS	CB-CA-C	-5.20	102.11	110.74
2	1	248	HIS	CB-CG-CD2	-5.19	124.45	131.20
3	2	195	HIS	CB-CG-CD2	-5.19	124.45	131.20
2	1	110	ILE	N-CA-C	5.18	115.78	109.30
1	0	10	THR	CA-CB-OG1	-5.18	101.83	109.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	2	57	ASP	N-CA-C	5.15	116.14	108.31
4	3	65	MET	CG-SD-CE	-5.14	89.58	100.90
3	2	42	LEU	N-CA-C	5.14	117.62	109.96
3	2	227	TRP	CE2-CD2-CG	-5.13	101.04	107.20
2	1	298	ASP	N-CA-C	5.13	118.30	110.20
4	3	52	MET	N-CA-C	5.13	117.91	109.76
2	1	41	ILE	N-CA-C	5.12	119.93	108.88
4	3	98	THR	O-C-N	-5.11	116.97	122.79
5	4	31	ASN	CB-CG-ND2	5.11	124.06	116.40
4	3	50	ASP	CA-CB-CG	5.10	117.70	112.60
2	1	100	ASN	N-CA-C	5.10	118.28	111.75
4	3	110	TRP	CE2-CD2-CG	-5.10	101.08	107.20
3	2	195	HIS	N-CA-C	5.10	116.82	109.07
2	1	203	ASN	OD1-CG-ND2	-5.09	117.51	122.60
2	1	65	HIS	CB-CG-CD2	-5.09	124.58	131.20
5	4	26	ASN	OD1-CG-ND2	-5.09	117.51	122.60
4	3	10	SER	N-CA-C	5.09	117.72	110.24
2	1	153	GLN	N-CA-C	5.08	118.23	110.20
3	2	37	ARG	N-CA-C	5.08	116.98	107.99
3	2	21	SER	N-CA-C	5.07	117.66	109.40
3	2	32	VAL	N-CA-C	5.05	115.59	108.36
2	1	177	THR	N-CA-C	5.05	121.56	110.80
2	1	132	MET	N-CA-C	5.05	117.12	108.90
3	2	111	GLN	OE1-CD-NE2	-5.05	117.55	122.60
3	2	172	ARG	N-CA-C	5.03	118.14	111.30
3	2	162	THR	CA-C-N	5.00	124.91	119.76
3	2	162	THR	C-N-CA	5.00	124.91	119.76
3	2	210	LEU	N-CA-C	5.00	117.51	109.15
3	2	243	SER	N-CA-C	5.00	117.46	111.71
3	2	95	ASN	CA-CB-CG	-5.00	107.60	112.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	2	106	TYR	Sidechain

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	0	29	0	24	1	0
2	1	2222	0	2173	25	0
3	2	2071	0	1989	19	0
4	3	1834	0	1816	19	0
5	4	476	0	457	6	0
6	1	28	0	29	4	0
7	4	15	0	27	1	0
All	All	6675	0	6515	52	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 4.

All (52) 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)
2:1:144:GLU:HB3	2:1:146:ASN:HB2	1.42	1.01
2:1:181:PRO:HB2	6:1:500:J78:H3	1.71	0.72
2:1:158:MET:SD	2:1:177:THR:HG23	2.31	0.69
4:3:51:THR:HG21	4:3:99:MET:H	1.57	0.69
4:3:149:MET:HE2	4:3:150:LEU:HG	1.76	0.67
2:1:177:THR:HG22	2:1:180:ASN:HB2	1.79	0.65
2:1:177:THR:HG21	2:1:182:SER:OG	2.03	0.58
3:2:179:TYR:HA	4:3:65:MET:HE2	1.86	0.57
3:2:187:LEU:HD13	4:3:65:MET:HE1	1.86	0.56
3:2:66:LEU:HD12	3:2:251:LEU:HD23	1.88	0.56
2:1:288:ASP:H	3:2:137:ASN:HD21	1.54	0.55
2:1:22:THR:HG22	2:1:24:ARG:H	1.72	0.54
2:1:107:VAL:HG13	2:1:239:ILE:HD13	1.88	0.54
3:2:110:VAL:HG22	3:2:251:LEU:HD12	1.88	0.54
3:2:143:THR:HG23	3:2:173:ARG:HA	1.88	0.54
3:2:213:VAL:HG22	4:3:37:PRO:HG2	1.90	0.54
5:4:57:ILE:HD11	5:4:61:LEU:HB3	1.89	0.54
2:1:191:PRO:HG2	4:3:13:TYR:HB2	1.90	0.54
1:0:9:SER:HA	5:4:5:VAL:HB	1.91	0.53
3:2:187:LEU:HD22	4:3:65:MET:HE1	1.92	0.52
3:2:192:VAL:HG11	4:3:99:MET:HE2	1.93	0.50
4:3:55:PHE:HE2	4:3:212:GLY:HA3	1.76	0.50
4:3:87:LEU:HD11	4:3:114:LEU:HD12	1.95	0.49
2:1:294:LEU:HD22	4:3:67:MET:SD	2.53	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:205:TYR:CZ	6:1:500:J78:H17	2.49	0.47
2:1:286:TYR:HB2	2:1:291:LEU:HD21	1.96	0.47
4:3:167:VAL:O	4:3:169:PRO:HD3	2.15	0.47
2:1:116:VAL:HG22	4:3:233:GLN:HE21	1.81	0.46
4:3:90:ALA:HB2	4:3:104:LEU:HB3	1.98	0.46
3:2:60:ALA:O	3:2:255:PRO:HG2	2.16	0.45
5:4:30:ILE:HD13	7:4:1:MYR:H72	1.98	0.45
4:3:70:VAL:HB	4:3:210:ILE:HG13	1.98	0.45
3:2:30:ASN:HD21	5:4:59:ASP:HB2	1.82	0.45
2:1:48:GLU:HA	3:2:197:ILE:HB	2.00	0.44
2:1:280:TYR:HB3	2:1:285:ASP:O	2.17	0.44
2:1:132:MET:HE2	2:1:261:LEU:HD11	1.99	0.44
2:1:42:PRO:HA	5:4:63:LYS:O	2.18	0.44
2:1:109:LYS:HA	2:1:239:ILE:HG22	1.98	0.44
2:1:288:ASP:N	3:2:137:ASN:HD21	2.16	0.44
2:1:302:TYR:CE1	4:3:189:TYR:HB3	2.54	0.43
3:2:37:ARG:HG3	4:3:37:PRO:HB3	2.00	0.43
2:1:216:PRO:HB2	3:2:270:ARG:HB3	2.01	0.43
4:3:53:ILE:HD11	4:3:214:VAL:HB	2.01	0.43
2:1:159:TYR:CZ	6:1:500:J78:H102	2.55	0.42
3:2:134:GLY:HA2	3:2:174:PHE:HA	2.02	0.42
3:2:13:VAL:HA	3:2:25:THR:O	2.20	0.41
3:2:166:ASN:OD1	3:2:168:THR:HG22	2.20	0.41
2:1:237:PHE:HB3	6:1:500:J78:H132	2.02	0.41
5:4:14:GLU:C	5:4:16:SER:H	2.29	0.41
2:1:220:GLN:HG3	2:1:224:LEU:HD22	2.03	0.40
2:1:229:TYR:OH	3:2:131:CYS:HA	2.22	0.40
4:3:156:TRP:CD1	4:3:164:CYS:HB2	2.55	0.40

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	0	3/5 (60%)	1 (33%)	1 (33%)	1 (33%)	0	0
2	1	281/302 (93%)	264 (94%)	15 (5%)	2 (1%)	18	48
3	2	264/272 (97%)	245 (93%)	17 (6%)	2 (1%)	16	44
4	3	233/238 (98%)	221 (95%)	11 (5%)	1 (0%)	30	59
5	4	58/68 (85%)	51 (88%)	5 (9%)	2 (3%)	3	12
All	All	839/885 (95%)	782 (93%)	49 (6%)	8 (1%)	12	39

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	0	9	SER
2	1	146	ASN
2	1	147	ASN
3	2	240	ALA
5	4	15	ASN
3	2	48	ASN
4	3	170	TRP
5	4	11	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	0	4/4 (100%)	3 (75%)	1 (25%)	0	2
2	1	245/261 (94%)	231 (94%)	14 (6%)	18	49
3	2	227/232 (98%)	220 (97%)	7 (3%)	35	69
4	3	210/212 (99%)	201 (96%)	9 (4%)	26	60
5	4	54/57 (95%)	48 (89%)	6 (11%)	6	20
All	All	740/766 (97%)	703 (95%)	37 (5%)	22	53

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	0	10	THR
2	1	33	SER
2	1	36	THR
2	1	83	ARG
2	1	97	SER
2	1	132	MET
2	1	143	THR
2	1	144	GLU
2	1	147	ASN
2	1	149	HIS
2	1	177	THR
2	1	214	LYS
2	1	220	GLN
2	1	221	SER
2	1	224	LEU
3	2	52	GLN
3	2	73	LYS
3	2	168	THR
3	2	187	LEU
3	2	238	ASN
3	2	264	ARG
3	2	272	GLN
4	3	51	THR
4	3	58	SER
4	3	71	ARG
4	3	85	LEU
4	3	163	SER
4	3	190	ILE
4	3	208	MET
4	3	218	ASN
4	3	224	LEU
5	4	16	SER
5	4	42	SER
5	4	43	LYS
5	4	49	ASP
5	4	60	VAL
5	4	61	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
2	1	203	ASN
3	2	95	ASN

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Mol	Chain	Res	Type
4	3	6	ASN
4	3	12	GLN
4	3	218	ASN
4	3	230	HIS
4	3	233	GLN
5	4	4	GLN
5	4	13	HIS
5	4	26	ASN

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 oligosaccharides 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	$\# Z > 2$
7	MYR	4	1	5	13,14,15	0.37	0	12,13,15	0.58	0
6	J78	1	500	-	30,30,30	1.51	3 (10%)	37,39,39	1.94	9 (24%)

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
7	MYR	4	1	5	-	4/12/12/13	-
6	J78	1	500	-	-	7/18/28/28	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	1	500	J78	O24-C22	5.17	1.46	1.33
6	1	500	J78	C19-C22	-5.17	1.38	1.50
6	1	500	J78	O24-C25	-2.46	1.39	1.46

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	1	500	J78	O24-C25-C26	5.17	126.94	108.40
6	1	500	J78	C11-N6-C7	4.68	122.09	111.57
6	1	500	J78	C5-N4-N3	4.14	123.14	118.97
6	1	500	J78	C4-C5-N4	-3.96	118.04	123.84
6	1	500	J78	O24-C22-C19	3.50	118.01	112.15
6	1	500	J78	C1-C2-N3	2.62	117.67	116.13
6	1	500	J78	C11-C10-C9	2.46	117.97	111.92
6	1	500	J78	C10-C9-C8	2.41	115.19	109.29
6	1	500	J78	C14-O15-C16	-2.32	111.91	117.93

There are no chirality outliers.

All (11) torsion outliers are listed below:

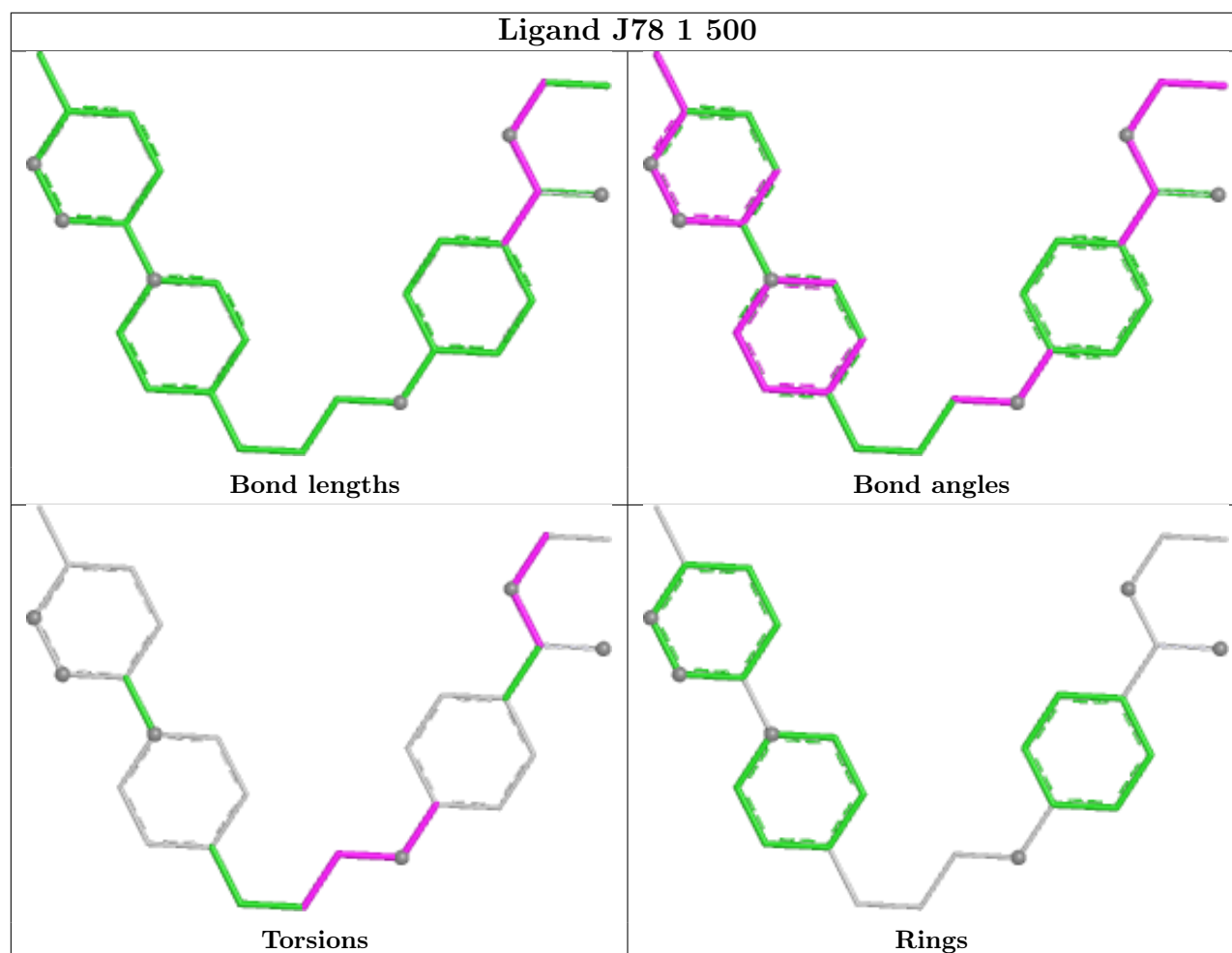
Mol	Chain	Res	Type	Atoms
7	4	1	MYR	O1-C1-C2-C3
6	1	500	J78	C19-C22-O24-C25
6	1	500	J78	O23-C22-O24-C25
6	1	500	J78	C26-C25-O24-C22
6	1	500	J78	C21-C16-O15-C14
6	1	500	J78	C17-C16-O15-C14
7	4	1	MYR	C6-C7-C8-C9
6	1	500	J78	C13-C14-O15-C16
7	4	1	MYR	C11-C12-C13-C14
6	1	500	J78	C12-C13-C14-O15
7	4	1	MYR	C10-C11-C12-C13

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	4	1	MYR	1	0
6	1	500	J78	4	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.



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

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.