



wwPDB/EMDatabank EM Map/Model Validation Summary Report

Jan 19, 2019 – 11:06 AM EST


PDB ID : 6EEC
EMDB ID: : EMD-9041
Title : Mycobacterium tuberculosis RNAP promoter unwinding intermediate complex
with RbpA/CarD and AP3 promoter captured by Coralopyronin
Authors : Darst, S.A.; Campbell, E.A.; Boyaci Selcuk, H.; Chen, J.
Deposited on : 2018-08-13
Resolution : 3.55 Å(reported)

This is a wwPDB/EMDatabank EM Map/Model Validation Summary Report
for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the  symbol.

MolProbity : 4.02b-467
Mogul : 1.7.3 (157068), CSD as539be (2018)
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20031633

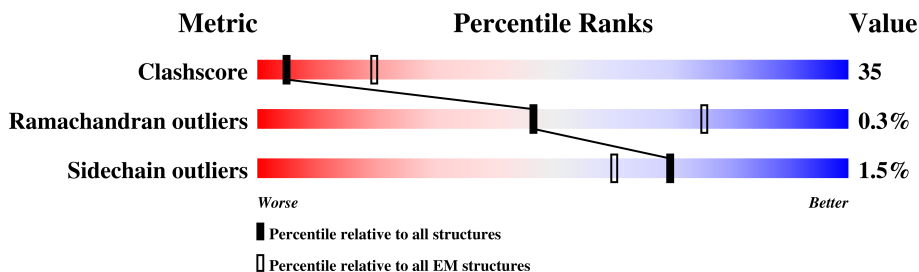
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.55 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.



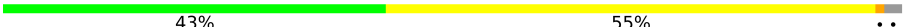
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	1531

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	347	34% 30% 35%
1	B	347	31% 37% 32%
2	C	1179	44% 49% • 6%
3	D	1326	45% 49% • 5%
4	E	110	35% 41% 25%
5	F	531	31% 28% • 40%
6	J	111	55% 40% • •
7	O	90	10% 61% • 28%
8	P	90	12% 58% 30%

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Mol	Chain	Length	Quality of chain
9	M	162	 43% 55% ..

2 Entry composition i

There are 12 unique types of molecules in this entry. The entry contains 29936 atoms, of which 40 are hydrogens and 0 are deuteriums.

In the tables below, 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 DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	225	Total	C	N	O	S	0	0
			1716	1080	296	338	2		
1	B	237	Total	C	N	O	S	0	0
			1759	1112	298	346	3		

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	C	1111	Total	C	N	O	S	0	0
			8593	5381	1507	1666	39		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	1179	LEU	-	expression tag	UNP V9Z879
C	1180	ALA	-	expression tag	UNP V9Z879
C	1181	ARG	-	expression tag	UNP V9Z879
C	1182	HIS	-	expression tag	UNP V9Z879
C	1183	GLY	-	expression tag	UNP V9Z879
C	1184	GLY	-	expression tag	UNP V9Z879
C	1185	SER	-	expression tag	UNP V9Z879

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	D	1266	Total	C	N	O	S	0	0
			9873	6184	1794	1853	42		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	-1	GLY	-	expression tag	UNP A5U053
D	0	ALA	-	expression tag	UNP A5U053

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Chain	Residue	Modelled	Actual	Comment	Reference
D	1317	HIS	-	expression tag	UNP A5U053
D	1318	HIS	-	expression tag	UNP A5U053
D	1319	HIS	-	expression tag	UNP A5U053
D	1320	HIS	-	expression tag	UNP A5U053
D	1321	HIS	-	expression tag	UNP A5U053
D	1322	HIS	-	expression tag	UNP A5U053
D	1323	HIS	-	expression tag	UNP A5U053
D	1324	HIS	-	expression tag	UNP A5U053

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	E	83	649	414	108	127	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	1	GLY	-	expression tag	UNP A0A0T9N9K3

- Molecule 5 is a protein called RNA polymerase sigma factor SigA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	F	319	2518	1571	456	482	9	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-2	GLY	-	expression tag	UNP P9WGI0
F	-1	PRO	-	expression tag	UNP P9WGI0
F	0	HIS	-	expression tag	UNP P9WGI0

- Molecule 6 is a protein called RNA polymerase-binding protein RbpA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	J	108	881	543	168	167	3	0	0

- Molecule 7 is a DNA chain called DNA (65-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
7	O	65	1336	633	243	395	65	0	0

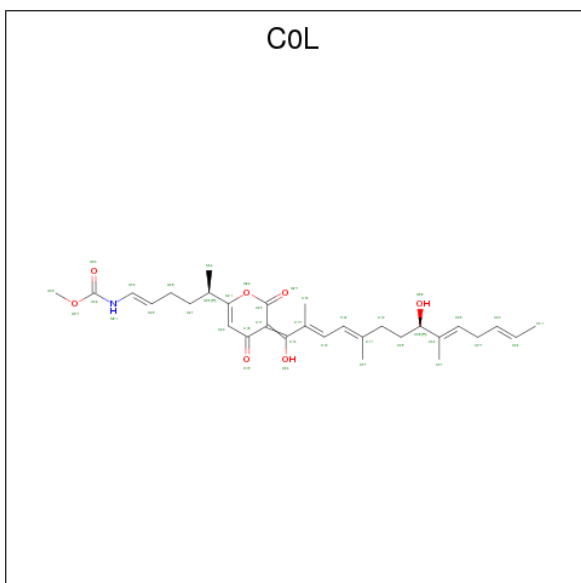
- Molecule 8 is a DNA chain called DNA (63-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
8	P	63	1289	610	242	374	63	0	0

- Molecule 9 is a protein called RNA polymerase-binding transcription factor CarD.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	M	159	1241	777	224	239	1	0	0

- Molecule 10 is methyl [(1E,5R)-5-{(3E)-3-[(2E,4E,8R,9E,12E)-1,8-dihydroxy-2,5,9-trimethyltetradeca-2,4,9,12-tetraen-1-ylidene]-2,4-dioxo-3,4-dihydro-2H-pyran-6-yl}hex-1-en-1-yl]carbamate (three-letter code: C0L) (formula: C₃₀H₄₁NO₇).



Mol	Chain	Residues	Atoms				AltConf	
			Total	C	H	N		O
10	C	1	78	30	40	1	7	0

- Molecule 11 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
11	D	2	Total 2	Zn 2	0

- Molecule 12 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
12	D	1	Total 1	Mg 1	0

V1252	D1182	G1102	T1025	3876	A788	Q540	A466	R357	Q303	L219	H145	K71	G-1
I1253	RL183	D1103	L952	L877	L789	M541	Q467	G588	P309	E220	M146	G72	A0
G1254	F1186	H1104	L953	V878	R790	L545	M469	G390	M310	D221	E147	I73	N5
K1255	E1187	E1106	A954	D879	E791	L546	I468	P390	G311	L222	L148	I74	F6
L1256	A1188	E1108	A955	V880	H792	P547	K470	L399	M312	W223	S149	C75	F7
I1258	E1189	L1111	G956	S881	Y793	L547	S471	L399	V313	T227	T150	E76	D8
G1261	RL190	M1112	I957	V884	M797	E580	A472	S403	L314	K228	L151	E77	E9
T1262	RL191	P1118	V962	I885	P798	V829	K473	D404	V317	L229	E152	C78	L10
G1263	V1192	H1119	R963	V886	I799	E554	V477	L405	P318	L229	A153	G79	R11
I1264	V1194	E1120	R964	I887	I800	E554	A776	L405	P318	A230	V157	V80	I12
M1265	E1199	L1121	L966	V888	V803	I557	R480	K409	V319	Q232	E158	V82	G13
R1266	A1202	L1122	G968	H889	V803	I558	V483	K410	I320	L234	R159	T83	L14
V1267	A1202	R1123	A969	E891	T808	L560	V483	R414	P321	L235	A161	A85	A15
R1268	G1203	R1124	V970	V892	G809	S561	V486	Q415	E322	V236	V162	K86	A17
G1269	G1203	Q1125	S971	H893	G809	S562	V487	M416	L324	D237	E163	V87	R88
I1270	R1204	G1126	S972	E894	L817	N563	R487	M416	D237	E238	D164	R88	Q22
A1271	P1205	P1127	G973	E902	A818	N563	V490	L418	M327	M259	Q165	R89	R21
V1272	V1206	R1128	V974	A902	G819	L586	I491	G419	V328	L240	R166	E90	Q22
Q1273	M1207	E1129	C975	G908	M820	S567	I491	K420	Q329	Y241	R167	R91	Q23
P1274	M1208	V1130	A976	T909	K821	P573	L497	R421	V329	R242	G168	M92	S24
A1282	G1209	Q1131	T977	T909	G822	V643	L498	V422	R334	E243	G168	G93	Y25
THR	I1210	I1132	C978	L910	L823	V644	L498	V422	F335	E243	G168	M92	Y25
THR	I1211	H1133	C979	I911	V824	E645	N499	S425	A336	L244	L170	H94	G26
THR	K1212	L1134	G980	R912	T825	F851	R500	G426	T337	D246	R173	E96	E27
THR	A1213	Q1139	R981	D913	M826	G852	R500	R427	S338	R247	A174	L97	P31
PRO	S1214	Q1139	S982	P914	P827	H652	L504	S428	S339	Y248	L177	A98	E32
SER	L1215	R1143	G986	Y915	I832	S854	H505	V429	L340	Y251	L177	V101	T33
TYR	A1216	R1143	G986	Y916	I832	G855	R506	I430	Y344	F252	A179	I102	I34
GLU	T1217	H1144	V989	E917	R834	G857	L507	V431	Y344	T283	D180	H103	N35
ASP	D1218	Q1145	V989	A920	P835	G858	G608	V432	Y344	L181	L181	I104	G36
GLN	S1219	Q1145	V990	A920	R836	G859	L509	V432	Y344	L181	L181	I104	R37
TYR	M1220	H1152	I991	A921	V836	G859	Q510	Q435	N349	M256	A191	V105	T38
TYR	W1221	H1153	G992	A921	V836	G859	A511	L436	N349	G257	D192	V106	L39
SER	S1222	I1154	E993	R923	S839	A661	F512	K437	R353	E267	D192	F107	K40
PRO	A1223	E1155	G996	T924	F840	V662	F513	L438	L354	S260	A193	R113	P41
ASP	A1224	V1156	G996	L925	R841	M663	P514	H439	K355	I261	R194	L114	E42
PHE	S1225	R1159	Q1001	G926	L844	A664	M515	G440	R356	Q262	K196	L114	F47
GLY	F1226	Q1160	Q1001	D928	T845	E665	L516	C441	L357	P268	V197	L117	C48
ALA	Q1227	M1161	G1004	A929	V846	L668	E518	G442	L360	D268	R198	L118	E49
ALA	E1228	L1162	E1005	V930	L847	L668	D595	L443	L360	I270	R198	L118	E49
THR	E1228	L1162	P1006	D931	E848	V671	G519	P444	L360	D271	D199	D119	K50
GLY	R1231	H1163	R1085	D931	Y849	M672	E598	K445	E364	D271	G200	L120	L51
ALA	V1232	R1164	R1086	G934	Y849	M672	E598	L446	I366	A272	G201	D124	F52
ALA	L1233	V1165	R1087	G934	F850	F673	Q529	M447	I366	E273	E202	D124	F52
VAL	T1234	T1166	V1088	I937	T851	A753	L524	A448	I366	A274	R203	D124	F52
PRO	D1235	I1167	F1089	V938	N852	A753	H525	L449	N368	E275	E204	I129	R56
LEU	A1236	I1168	K1090	T853	T853	K755	H526	L449	N368	S276	M205	Y130	D57
ASP	A1237	D1169	HIS	H854	H854	L676	L527	K453	M373	L277	R206	Y134	M58
ASP	I1238	S1170	THR	R940	R857	L677	V528	K453	M373	R276	Q207	Y134	M58
TYR	R1241	G1171	PHE	R941	R857	Y681	C529	V456	L374	I208	I208	V135	E59
GLY	R1241	G1171	HIS	R942	R857	Y681	C529	V456	L374	I208	I208	V135	E59
TYR	S1242	T1173	GLN	Q942	R857	Y681	C529	V456	L374	I208	I208	V135	E59
SER	A1243	E1174	GLY	R943	A864	F683	E530	M457	E376	T281	R209	I136	G63
ASP	K1244	F1175	VAL	L944	V884	V611	E530	M457	E376	T281	R209	I136	G63
TYR	L1245	L1176	GLY	G945	V885	V612	A534	K458	D379	R282	A212	T137	K64
ARG	E1250	P1177	GLY	D946	T867	S614	F536	L460	D383	K285	E215	V139	K64
HIS	M1251	I1181	ASP	P947	T874	A616	G538	D462	N384	R295	D217	I139	K66
HIS	M1251	I1181	ILE	E948	R875	V775	G538	D462	N384	R295	D217	I139	K66
HIS	M1251	I1181	ILE	E949	R875	V775	G538	D462	N384	R295	D217	I139	K66

4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	246409	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	69.9	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

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: ZN, COL, 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 >2	RMSZ	# Z >2
1	A	0.47	0/1742	0.55	0/2370
1	B	0.43	0/1786	0.53	0/2435
2	C	0.55	0/8751	0.61	5/11869 (0.0%)
3	D	0.56	1/10037 (0.0%)	0.59	6/13570 (0.0%)
4	E	0.44	0/662	0.52	0/901
5	F	0.46	0/2549	0.55	3/3438 (0.1%)
6	J	0.38	0/897	0.55	1/1210 (0.1%)
7	O	0.80	0/1497	0.97	2/2310 (0.1%)
8	P	0.76	0/1445	0.91	0/2224
9	M	0.36	0/1257	0.49	0/1700
All	All	0.55	1/30623 (0.0%)	0.63	17/42027 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	656	TRP	CB-CG	-7.29	1.37	1.50

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	306	LEU	C-N-CA	-7.20	103.71	121.70
3	D	419	GLY	N-CA-C	7.08	130.80	113.10
3	D	655	GLY	N-CA-C	-6.73	96.27	113.10
2	C	275	LEU	CA-CB-CG	-6.63	100.04	115.30
2	C	288	THR	N-CA-C	-6.59	93.21	111.00

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	1716	0	1756	121	0
1	B	1759	0	1783	145	0
2	C	8593	0	8517	695	0
3	D	9873	0	9938	738	0
4	E	649	0	645	54	0
5	F	2518	0	2540	182	0
6	J	881	0	861	62	0
7	O	1336	0	732	116	0
8	P	1289	0	706	88	0
9	M	1241	0	1259	111	0
10	C	38	40	0	1	0
11	D	2	0	0	0	0
12	D	1	0	0	0	0
All	All	29896	40	28737	2075	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 35.

The worst 5 of 2075 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:C:281:LEU:CD2	2:C:295:LEU:HD21	1.62	1.30
2:C:271:ASP:O	2:C:275:LEU:HD12	1.25	1.27
2:C:1067:ARG:CZ	3:D:418:LEU:CD2	2.13	1.25
2:C:278:TYR:CE1	2:C:292:ALA:HB2	1.73	1.23
2:C:1067:ARG:NH1	3:D:418:LEU:CD2	2.04	1.21

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 PDB entries followed by that with respect to all EM

entries.

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	223/347 (64%)	197 (88%)	26 (12%)	0	100	100
1	B	235/347 (68%)	194 (83%)	41 (17%)	0	100	100
2	C	1109/1179 (94%)	937 (84%)	168 (15%)	4 (0%)	36	74
3	D	1260/1326 (95%)	1141 (91%)	115 (9%)	4 (0%)	43	78
4	E	81/110 (74%)	76 (94%)	5 (6%)	0	100	100
5	F	317/531 (60%)	296 (93%)	20 (6%)	1 (0%)	43	78
6	J	106/111 (96%)	87 (82%)	19 (18%)	0	100	100
9	M	157/162 (97%)	144 (92%)	12 (8%)	1 (1%)	27	68
All	All	3488/4113 (85%)	3072 (88%)	406 (12%)	10 (0%)	47	78

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	D	418	LEU
3	D	658	PRO
2	C	274	LEU
3	D	653	HIS
2	C	53	LEU

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 PDB entries followed by that with respect to all EM entries.

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	194/297 (65%)	192 (99%)	2 (1%)	78	90
1	B	194/297 (65%)	193 (100%)	1 (0%)	90	96
2	C	935/997 (94%)	918 (98%)	17 (2%)	62	84
3	D	1042/1103 (94%)	1024 (98%)	18 (2%)	63	85
4	E	69/89 (78%)	68 (99%)	1 (1%)	69	87

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	F	264/429 (62%)	262 (99%)	2 (1%)	83	93
6	J	93/97 (96%)	89 (96%)	4 (4%)	32	67
9	M	129/131 (98%)	129 (100%)	0	100	100
All	All	2920/3440 (85%)	2875 (98%)	45 (2%)	70	87

5 of 45 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	D	5	ASN
3	D	285	LYS
6	J	4	ARG
3	D	140	ASP
3	D	386	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
3	D	239	ASN
3	D	505	HIS
5	F	516	HIS
3	D	307	ASN
3	D	416	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 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
10	C0L	C	1201	-	36,38,38	2.60	13 (36%)	35,49,49	2.98	11 (31%)

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
10	C0L	C	1201	-	-	0/37/57/57	0/1/1/1

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	C	1201	C0L	O36-C16	-4.52	1.18	1.33
10	C	1201	C0L	C17-C18	-3.94	1.35	1.45
10	C	1201	C0L	C20-C18	-3.54	1.34	1.44
10	C	1201	C0L	O34-C35	-3.00	1.38	1.45
10	C	1201	C0L	C17-C23	-2.45	1.38	1.45

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	C	1201	C0L	C23-O22-C21	-6.86	118.03	122.45
10	C	1201	C0L	C35-O34-C32	-5.93	108.38	115.68
10	C	1201	C0L	O33-C32-N31	-4.32	119.36	125.46
10	C	1201	C0L	O34-C32-O33	-2.80	120.35	124.58
10	C	1201	C0L	C28-C27-C25	-2.78	109.25	114.47

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
10	C	1201	C0L	1	0

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.