



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Nov 8, 2017 – 10:49 PM EST

PDB ID : 5M54
EMDB ID: : EMD-4156
Title : Mechanism of microtubule minus-end recognition and protection by CAMSAP proteins
Authors : Akhmanova, A.; Moores, C.A.; Baldus, M.; Steinmetz, M.O.; Topf, M.; Roberts, A.J.; Grant, B.J.; Scarabelli, G.; Joseph, A.-J.; van Hooff, J.J.E.; Houben, K.; Hua, S.; Luo, Y.; Stangier, M.M.; Jiang, K.; Atherton, J.
Deposited on : unknown
Resolution : 8.00 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

<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030345

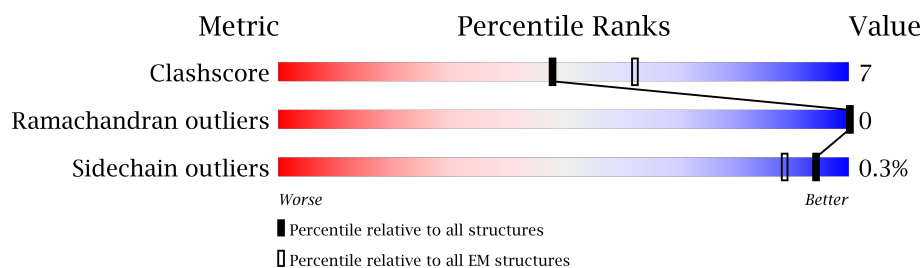
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 8.00 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)	EM structures (#Entries)
Clashscore	125131	1336
Ramachandran outliers	121729	1120
Sidechain outliers	121581	1026

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	C	117	80% 20%
2	A	438	78% 20% .
2	D	438	79% 18% .
3	B	426	82% 18%
3	E	426	83% 17%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 14605 atoms, of which 0 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 Calmodulin-regulated spectrin-associated protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C	117	Total	C	N	O	S	0	0
			947	604	163	173	7		

- Molecule 2 is a protein called Tubulin alpha chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	D	428	Total	C	N	O	S	0	0
			3350	2121	570	638	21		
2	A	428	Total	C	N	O	S	0	0
			3350	2121	570	638	21		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	136	SER	LEU	conflict	UNP F2Z4C1
D	265	GLY	ILE	conflict	UNP F2Z4C1
D	358	GLU	GLN	conflict	UNP F2Z4C1
A	136	SER	LEU	conflict	UNP F2Z4C1
A	265	GLY	ILE	conflict	UNP F2Z4C1
A	358	GLU	GLN	conflict	UNP F2Z4C1

- Molecule 3 is a protein called Tubulin beta-2B chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	E	426	Total	C	N	O	S	0	0
			3352	2105	575	647	25		
3	B	426	Total	C	N	O	S	0	0
			3352	2105	575	647	25		

There are 8 discrepancies between the modelled and reference sequences:

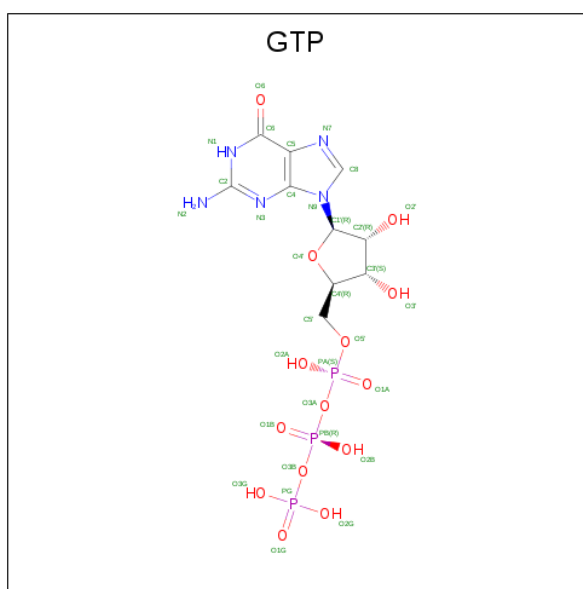
Chain	Residue	Modelled	Actual	Comment	Reference
E	57	ALA	THR	conflict	UNP Q6B856

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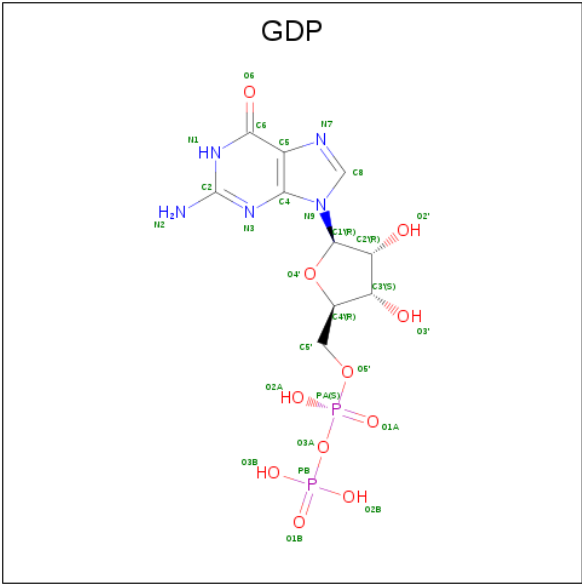
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Chain	Residue	Modelled	Actual	Comment	Reference
E	172	VAL	MET	conflict	UNP Q6B856
E	298	ALA	SER	conflict	UNP Q6B856
E	318	VAL	ILE	conflict	UNP Q6B856
B	57	ALA	THR	conflict	UNP Q6B856
B	172	VAL	MET	conflict	UNP Q6B856
B	298	ALA	SER	conflict	UNP Q6B856
B	318	VAL	ILE	conflict	UNP Q6B856

- Molecule 4 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

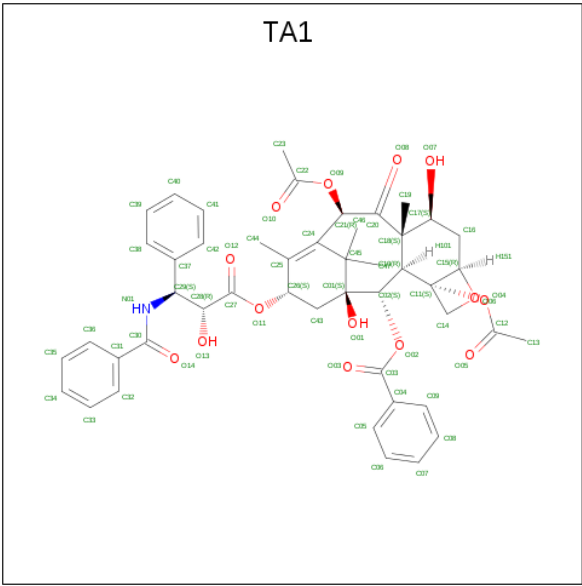


C₁₀H₁₅N₅O₁₁P₂).



Mol	Chain	Residues	Atoms					AltConf
6	E	1	Total	C	N	O	P	0
			28	10	5	11	2	
6	B	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 7 is TAXOL (three-letter code: TA1) (formula: C₄₇H₅₁NO₁₄).



Mol	Chain	Residues	Atoms				AltConf
7	E	1	Total	C	N	O	0
			62	47	1	14	

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Mol	Chain	Residues	Atoms				AltConf
7	B	1	Total	C	N	O	0
			62	47	1	14	


- Molecule 8 is water.

Mol	Chain	Residues	Atoms		AltConf
8	D	4	Total	O	0
			4	4	
8	A	4	Total	O	0
			4	4	

3 Residue-property plots


These plots are drawn for all protein, RNA and DNA 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.

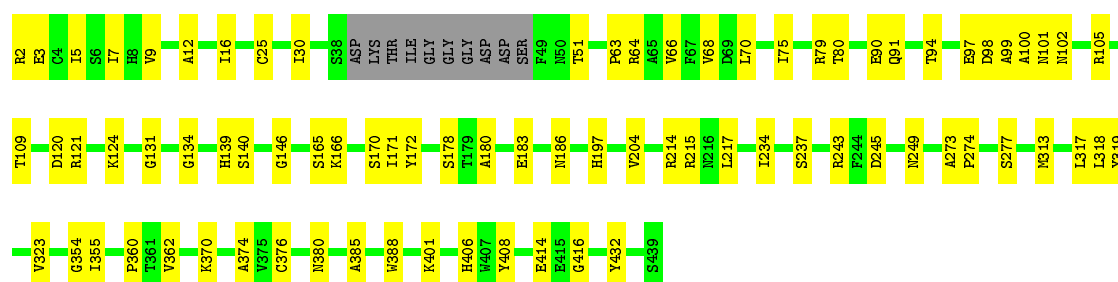
- Molecule 1: Calmodulin-regulated spectrin-associated protein 1

Chain C: 




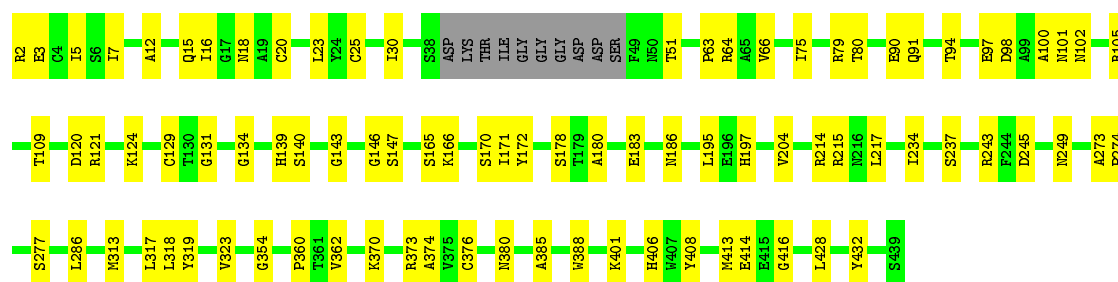
- Molecule 2: Tubulin alpha chain

Chain D: 




- Molecule 2: Tubulin alpha chain

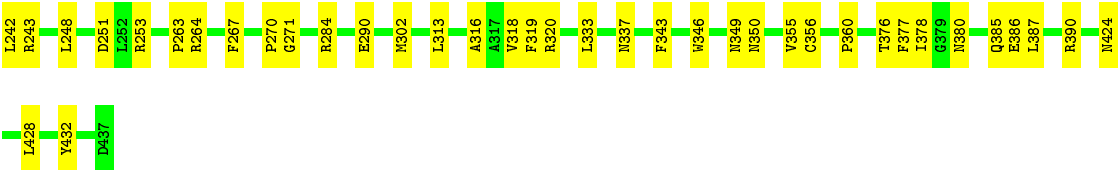
Chain A: 



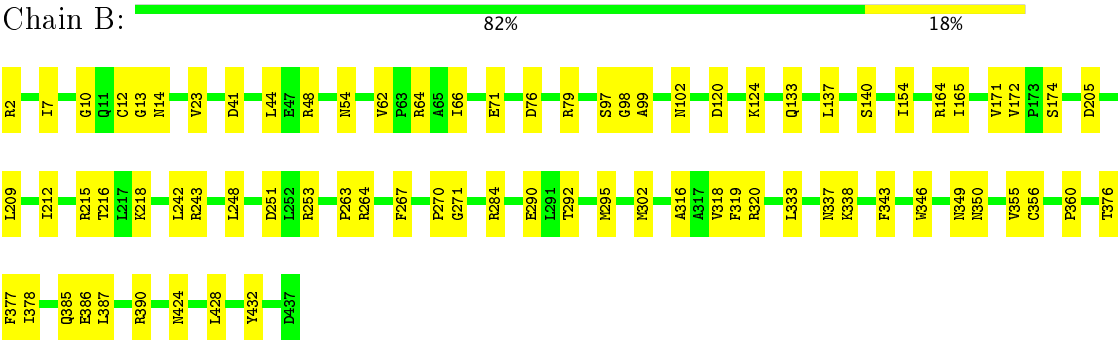
- Molecule 3: Tubulin beta-2B chain

Chain E: 





● Molecule 3: Tubulin beta-2B chain



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of particles used	5954	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	DIRECT ELECTRON DE-20 (5k x 3k)	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GDP, GTP, MG, TA1

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	C	0.26	0/970	0.52	0/1309
2	A	0.27	0/3427	0.46	0/4651
2	D	0.27	0/3427	0.46	0/4651
3	B	0.27	0/3427	0.46	0/4642
3	E	0.27	0/3427	0.46	0/4642
All	All	0.27	0/14678	0.46	0/19895

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
2	A	0	1
2	D	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	273	ALA	Peptide
2	D	273	ALA	Peptide

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	C	947	0	948	13	0
2	A	3350	0	3254	53	0
2	D	3350	0	3254	49	0
3	B	3352	0	3229	51	0
3	E	3352	0	3229	49	0
4	A	32	0	12	0	0
4	D	32	0	12	0	0
5	A	1	0	0	0	0
5	D	1	0	0	0	0
6	B	28	0	12	0	0
6	E	28	0	12	1	0
7	B	62	0	51	6	0
7	E	62	0	51	5	0
8	A	4	0	0	0	0
8	D	4	0	0	0	0
All	All	14605	0	14064	206	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 7.

The worst 5 of 206 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)
7:E:502:TA1:C20	7:E:502:TA1:C21	1.81	1.57
7:B:502:TA1:C21	7:B:502:TA1:C20	1.81	1.57
2:A:51:THR:HG21	2:A:243:ARG:HG2	1.77	0.66
2:D:90:GLU:HG3	2:D:121:ARG:HD2	1.80	0.64
2:D:51:THR:HG21	2:D:243:ARG:HG2	1.78	0.64

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	C	115/117 (98%)	106 (92%)	9 (8%)	0	100	100
2	A	424/438 (97%)	408 (96%)	16 (4%)	0	100	100
2	D	424/438 (97%)	407 (96%)	17 (4%)	0	100	100
3	B	424/426 (100%)	413 (97%)	11 (3%)	0	100	100
3	E	424/426 (100%)	415 (98%)	9 (2%)	0	100	100
All	All	1811/1845 (98%)	1749 (97%)	62 (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 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	C	106/106 (100%)	104 (98%)	2 (2%)	62	82
2	A	360/367 (98%)	359 (100%)	1 (0%)	94	96
2	D	360/367 (98%)	359 (100%)	1 (0%)	94	96
3	B	367/367 (100%)	367 (100%)	0	100	100
3	E	367/367 (100%)	367 (100%)	0	100	100
All	All	1560/1574 (99%)	1556 (100%)	4 (0%)	94	96

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	1484	LYS
1	C	1560	LYS
2	D	101	ASN
2	A	101	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
3	E	334	ASN
2	A	102	ASN
3	B	331	GLN
3	E	337	ASN
2	A	101	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 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 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	GTP	A	501	5	27,34,34	0.93	1 (3%)	27,54,54	2.19	4 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	GDP	B	501	-	25,30,30	0.90	1 (4%)	26,47,47	2.22	4 (15%)
7	TA1	B	502	-	68,68,68	0.81	3 (4%)	105,105,105	1.10	9 (8%)
4	GTP	D	501	5	27,34,34	0.92	1 (3%)	27,54,54	2.18	4 (14%)
6	GDP	E	501	-	25,30,30	0.90	1 (4%)	26,47,47	2.23	4 (15%)
7	TA1	E	502	-	68,68,68	0.80	3 (4%)	105,105,105	1.08	9 (8%)

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	GTP	A	501	5	-	0/18/38/38	0/3/3/3
6	GDP	B	501	-	-	0/12/32/32	0/3/3/3
7	TA1	B	502	-	-	0/41/127/127	0/5/7/7
4	GTP	D	501	5	-	0/18/38/38	0/3/3/3
6	GDP	E	501	-	-	0/12/32/32	0/3/3/3
7	TA1	E	502	-	-	0/41/127/127	0/5/7/7

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	502	TA1	C01-C02	2.20	1.66	1.57
7	E	502	TA1	C01-C02	2.22	1.66	1.57
4	D	501	GTP	C6-N1	2.89	1.38	1.33
6	E	501	GDP	C6-N1	2.97	1.38	1.33
4	A	501	GTP	C6-N1	2.98	1.38	1.33

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	501	GTP	C5-C6-N1	-7.89	112.25	123.48
6	E	501	GDP	C5-C6-N1	-7.85	112.31	123.48
6	B	501	GDP	C5-C6-N1	-7.84	112.32	123.48
4	D	501	GTP	C5-C6-N1	-7.81	112.36	123.48
7	B	502	TA1	C47-C45-C46	-5.06	90.60	106.30

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	502	TA1	6	0
6	E	501	GDP	1	0
7	E	502	TA1	5	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.