wwPDB EM Validation Summary Report (i)

Nov 19, 2022 – 09:43 pm GMT

PDB ID	:	6EVY
EMDB ID	:	EMD-3963
Title	:	Cryo-EM structure of GTPgammaS-microtubule co-polymerised with doublecortin
Authors	:	Manka, S.W.
Deposited on	:	2017-11-03
Resolution	:	4.40 Å(reported)

This is a wwPDB EM 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/EMValidationReportHelp
with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

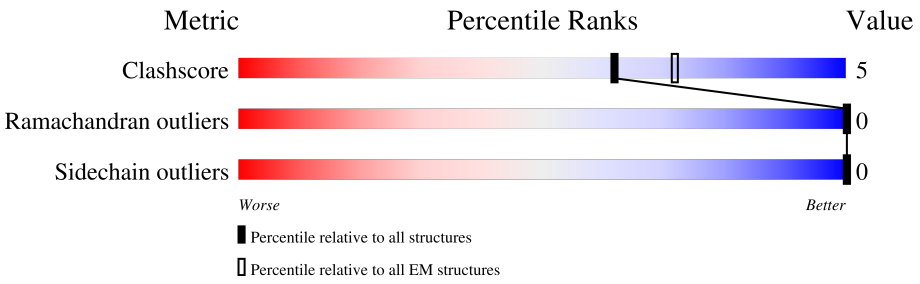
EMDB validation analysis	:	0.0.1.dev43
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

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 4.40 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	451	84% 12% •
1	C	451	83% 13% •
1	E	451	84% 11% •
1	J	451	85% 10% •
1	K	451	85% 11% •
1	L	451	84% 12% •
2	B	445	83% 13% •
2	D	445	84% 13% •

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Mol	Chain	Length	Quality of chain
2	F	445	83% 13%
2	G	445	85% 12%
2	H	445	84% 12%
2	I	445	85% 11%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 40890 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 Tubulin alpha-1B chain.

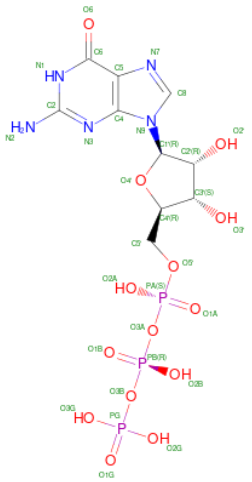
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	E	432	3382	2144	575	642	21	0	0
1	J	432	3382	2144	575	642	21	0	0
1	C	432	3382	2144	575	642	21	0	0
1	L	432	3382	2144	575	642	21	0	0
1	A	432	3382	2144	575	642	21	0	0
1	K	432	3382	2144	575	642	21	0	0

- Molecule 2 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	F	429	3368	2115	578	650	25	0	0
2	G	429	3368	2115	578	650	25	0	0
2	D	429	3368	2115	578	650	25	0	0
2	I	429	3368	2115	578	650	25	0	0
2	B	429	3368	2115	578	650	25	0	0
2	H	429	3368	2115	578	650	25	0	0

- Molecule 3 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).

GTP

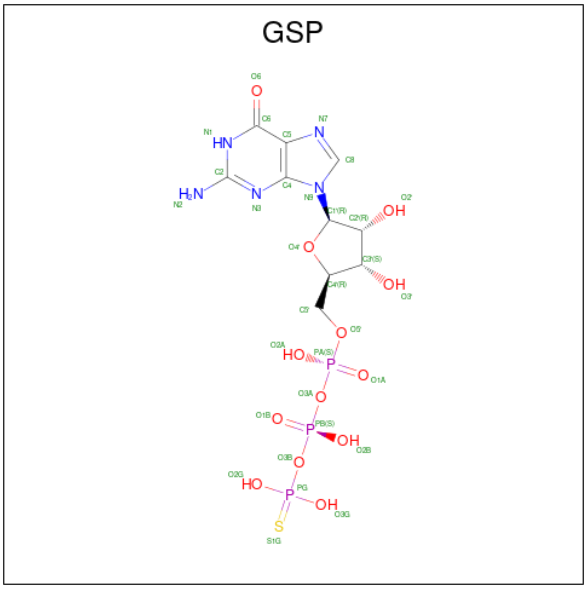


Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
3	E	1	32	10	5	14	3	0
3	J	1	32	10	5	14	3	0
3	C	1	32	10	5	14	3	0
3	L	1	32	10	5	14	3	0
3	A	1	32	10	5	14	3	0
3	K	1	32	10	5	14	3	0

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
4	E	1	1	1	0
4	J	1	1	1	0
4	C	1	1	1	0
4	L	1	1	1	0
4	A	1	1	1	0
4	K	1	1	1	0

- Molecule 5 is 5'-GUANOSINE-DIPHOSPHATE-MONOTHIOPHOSPHATE (three-letter code: GSP) (formula: $C_{10}H_{16}N_5O_{13}P_3S$).



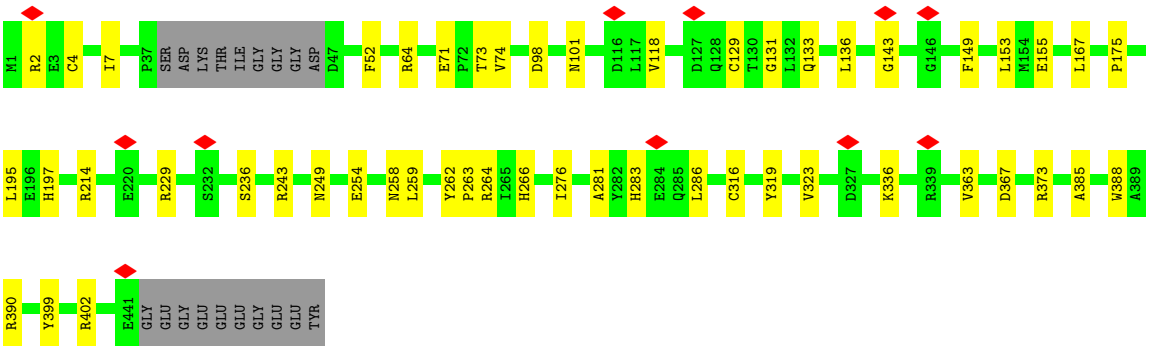
Mol	Chain	Residues	Atoms						AltConf
			Total	C	N	O	P	S	
5	F	1	32	10	5	13	3	1	0
			Total	C	N	O	P	S	
5	G	1	32	10	5	13	3	1	0
			Total	C	N	O	P	S	
5	D	1	32	10	5	13	3	1	0
			Total	C	N	O	P	S	
5	I	1	32	10	5	13	3	1	0
			Total	C	N	O	P	S	
5	B	1	32	10	5	13	3	1	0
			Total	C	N	O	P	S	
5	H	1	32	10	5	13	3	1	0

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 and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

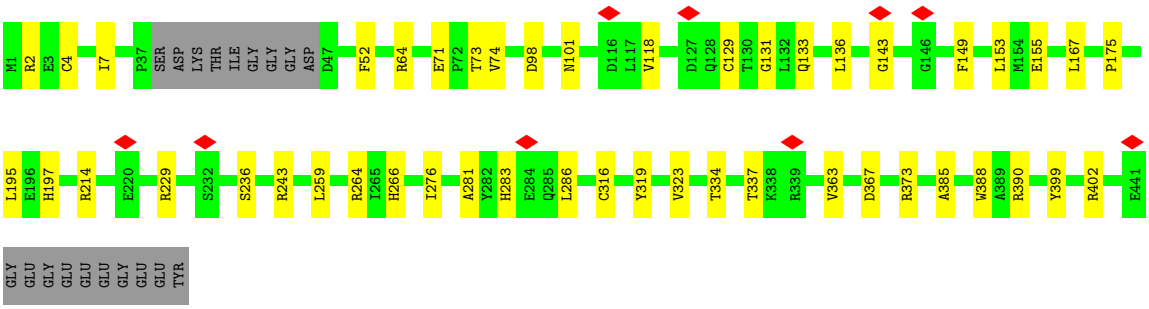
• Molecule 1: Tubulin alpha-1B chain

Chain E:



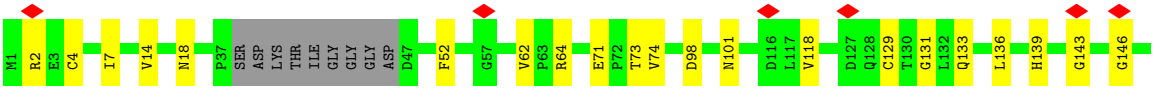
• Molecule 1: Tubulin alpha-1B chain

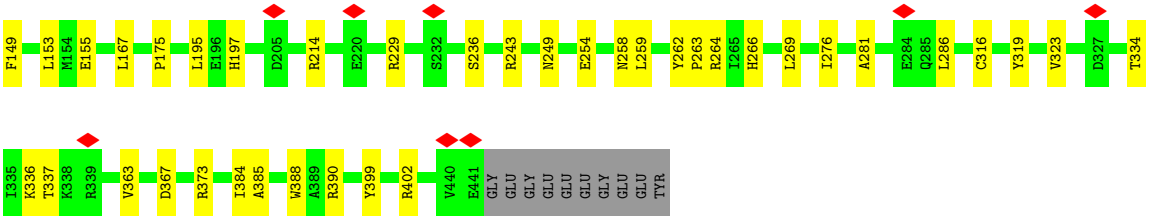
Chain J:



• Molecule 1: Tubulin alpha-1B chain

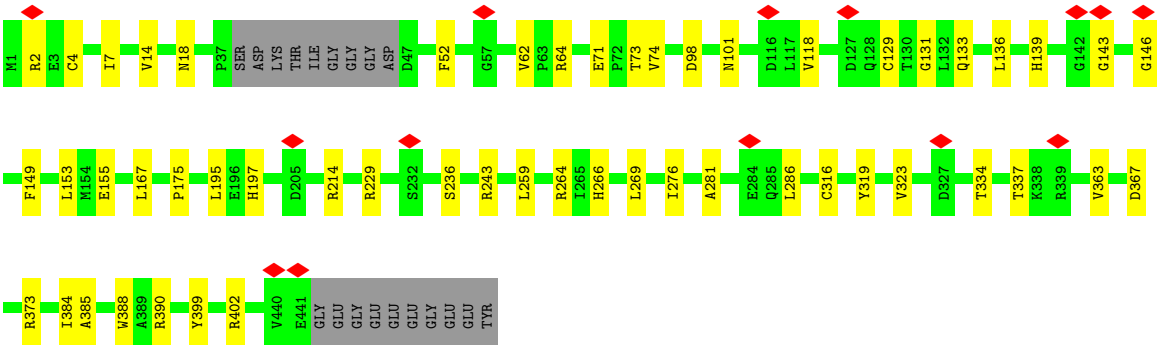
Chain C:





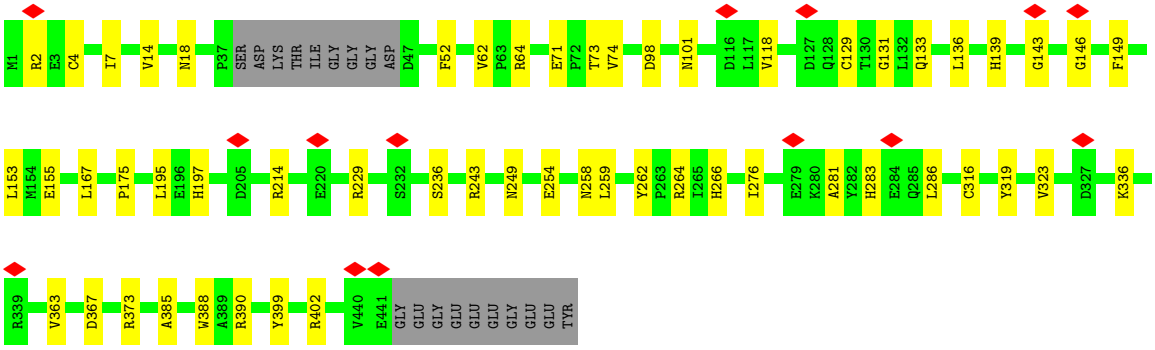
• Molecule 1: Tubulin alpha-1B chain

Chain L:



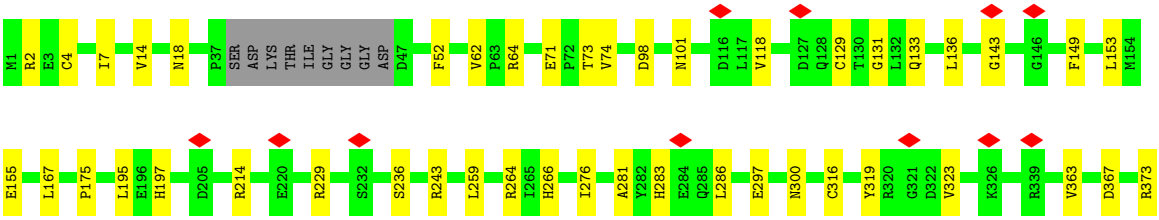
• Molecule 1: Tubulin alpha-1B chain

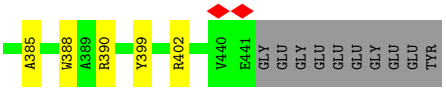
Chain A:



• Molecule 1: Tubulin alpha-1B chain

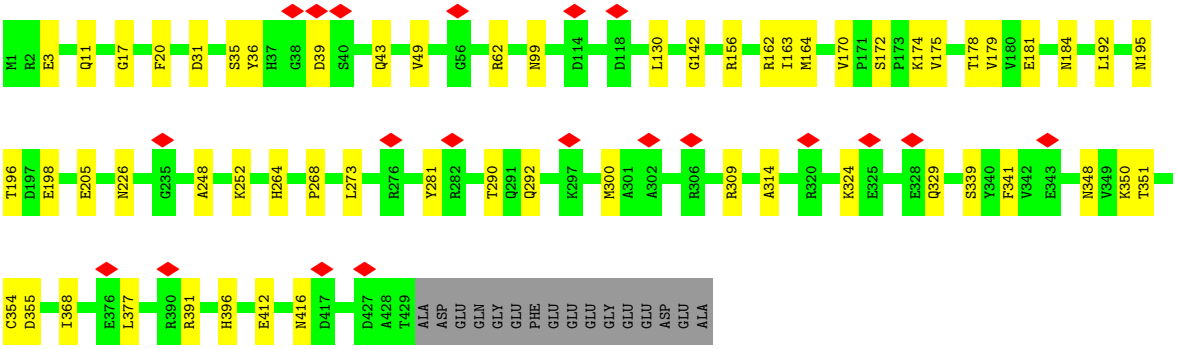
Chain K:





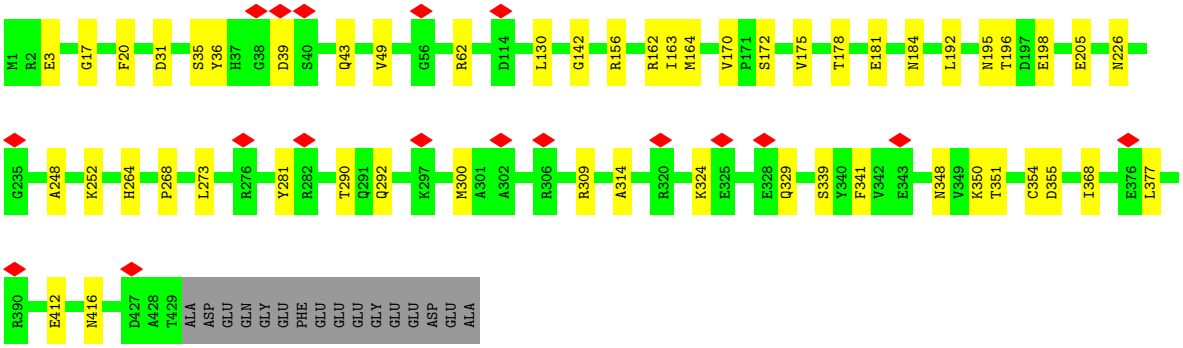
• Molecule 2: Tubulin beta chain

Chain F:



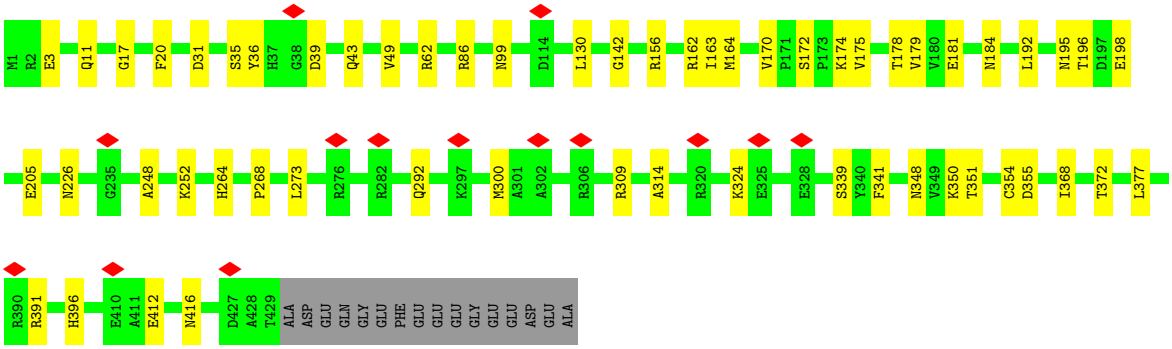
• Molecule 2: Tubulin beta chain

Chain G:



• Molecule 2: Tubulin beta chain

Chain D:



• Molecule 2: Tubulin beta chain

Chain I: 85% 11%

M1 R2 E3 G17 F20 D31 S35 Y36 H37 G38 D39 Q43 V49 R62 R86 D114 L130 G142 R156 R162 I163 M164 V170 P171 S172 V175 T178 E181 N184 L192 N195 T196 D197 E198 E205 N226 G235

A248 K252 H264 P268 L273 R276 R282 Q292 K297 M300 A301 A302 R306 R309 A314 R320 K324 E325 E328 S339 Y340 F341 N348 V349 K350 T351 C354 D355 G360 I368 T372 L377 R390 E410 A411

E412 N416 D427 A428 T429 ALA ASP GLU GLN GLY GLU PHE GLU GLU GLU GLY GLU GLU ASP GLU ALA

- Molecule 2: Tubulin beta chain

Chain B: 83% 13%

M1 R2 E3 Q11 C12 G17 F20 D31 S35 Y36 H37 G38 D39 S40 D41 L42 Q43 V49 R62 R86 N99 D114 L130 S138 G142 R156 R162 I163 M164 V170 P171 S172 P173 K174 V175 T178 V179 V180 E181 N184 L192

N195 T196 D197 E198 E205 N226 G235 A248 K252 H264 P268 L273 R276 Y281 R282 Q292 K297 M300 A301 A302 R306 R309 A314 R320 K324 E325 E328 S339 Y340 F341 N348 V349 K350 T351 C354 D355

I368 T372 L377 R390 R391 E410 A411 E412 N416 D427 A428 T429 ALA ASP GLU GLN GLY GLU PHE GLU GLU GLU GLY GLU GLU ASP GLU ALA

- Molecule 2: Tubulin beta chain

Chain H: 84% 12%

M1 R2 E3 C12 G17 F20 D31 S35 Y36 H37 G38 D39 S40 D41 L42 Q43 V49 R62 R86 D114 L130 S138 G142 R156 R162 I163 M164 V170 P171 S172 V175 T178 E181 N184 L192 N195 T196 D197 E198

E205 N226 G235 A248 K252 H264 P268 L273 R276 Y281 R282 Q292 K297 M300 A301 A302 R306 R309 A314 R320 K324 E325 E328 S339 Y340 F341 N348 V349 K350 T351 C354 D355 G360 I368 T372

L377 R390 E410 A411 E412 N416 D427 A428 T429 ALA ASP GLU GLN GLY GLU PHE GLU GLU GLU GLY GLU GLU ASP GLU ALA

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	72444	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	25	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.502	Depositor
Minimum map value	-0.278	Depositor
Average map value	0.010	Depositor
Map value standard deviation	0.046	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	127.88, 186.26, 233.52	wwPDB
Map dimensions	92, 134, 168	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.39, 1.39, 1.39	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: MG, GSP, GTP

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	0.32	0/3459	0.48	0/4697
1	C	0.32	0/3459	0.48	0/4697
1	E	0.32	0/3459	0.48	0/4697
1	J	0.32	0/3459	0.48	0/4697
1	K	0.32	0/3459	0.48	0/4697
1	L	0.32	0/3459	0.48	0/4697
2	B	0.32	0/3443	0.48	0/4666
2	D	0.32	0/3443	0.48	0/4666
2	F	0.32	0/3443	0.48	0/4666
2	G	0.32	0/3443	0.48	0/4666
2	H	0.32	0/3443	0.48	0/4666
2	I	0.32	0/3443	0.48	0/4666
All	All	0.32	0/41412	0.48	0/56178

There are no bond length outliers.

There are no bond angle outliers.

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	3382	0	3292	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	3382	0	3292	36	0
1	E	3382	0	3292	32	0
1	J	3382	0	3292	27	0
1	K	3382	0	3292	28	0
1	L	3382	0	3292	29	0
2	B	3368	0	3246	39	0
2	D	3368	0	3246	37	0
2	F	3368	0	3246	37	0
2	G	3368	0	3246	31	0
2	H	3368	0	3246	34	0
2	I	3368	0	3246	31	0
3	A	32	0	12	0	0
3	C	32	0	12	1	0
3	E	32	0	12	1	0
3	J	32	0	12	1	0
3	K	32	0	12	0	0
3	L	32	0	12	0	0
4	A	1	0	0	0	0
4	C	1	0	0	0	0
4	E	1	0	0	0	0
4	J	1	0	0	0	0
4	K	1	0	0	0	0
4	L	1	0	0	0	0
5	B	32	0	12	2	0
5	D	32	0	12	2	0
5	F	32	0	12	2	0
5	G	32	0	12	2	0
5	H	32	0	12	2	0
5	I	32	0	12	2	0
All	All	40890	0	39372	363	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 363 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:K:64:ARG:NH2	1:K:129:CYS:SG	2.73	0.62
1:A:64:ARG:NH2	1:A:129:CYS:SG	2.73	0.62
1:C:64:ARG:NH2	1:C:129:CYS:SG	2.73	0.62
1:L:64:ARG:NH2	1:L:129:CYS:SG	2.73	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:64:ARG:NH2	1:E:129:CYS:SG	2.73	0.61

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	428/451 (95%)	409 (96%)	19 (4%)	0	100	100
1	C	428/451 (95%)	408 (95%)	20 (5%)	0	100	100
1	E	428/451 (95%)	408 (95%)	20 (5%)	0	100	100
1	J	428/451 (95%)	408 (95%)	20 (5%)	0	100	100
1	K	428/451 (95%)	408 (95%)	20 (5%)	0	100	100
1	L	428/451 (95%)	408 (95%)	20 (5%)	0	100	100
2	B	427/445 (96%)	406 (95%)	21 (5%)	0	100	100
2	D	427/445 (96%)	406 (95%)	21 (5%)	0	100	100
2	F	427/445 (96%)	406 (95%)	21 (5%)	0	100	100
2	G	427/445 (96%)	407 (95%)	20 (5%)	0	100	100
2	H	427/445 (96%)	406 (95%)	21 (5%)	0	100	100
2	I	427/445 (96%)	407 (95%)	20 (5%)	0	100	100
All	All	5130/5376 (95%)	4887 (95%)	243 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	364/379 (96%)	364 (100%)	0	100	100
1	C	364/379 (96%)	364 (100%)	0	100	100
1	E	364/379 (96%)	364 (100%)	0	100	100
1	J	364/379 (96%)	364 (100%)	0	100	100
1	K	364/379 (96%)	364 (100%)	0	100	100
1	L	364/379 (96%)	364 (100%)	0	100	100
2	B	368/381 (97%)	368 (100%)	0	100	100
2	D	368/381 (97%)	368 (100%)	0	100	100
2	F	368/381 (97%)	368 (100%)	0	100	100
2	G	368/381 (97%)	368 (100%)	0	100	100
2	H	368/381 (97%)	368 (100%)	0	100	100
2	I	368/381 (97%)	368 (100%)	0	100	100
All	All	4392/4560 (96%)	4392 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 83 such sidechains are listed below:

Mol	Chain	Res	Type
1	K	206	ASN
2	I	292	GLN
2	G	226	ASN
2	D	247	ASN
2	B	247	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 18 ligands modelled in this entry, 6 are monoatomic - leaving 12 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	$\#\|Z\| > 2$
3	GTP	E	501	4	26,34,34	1.05	3 (11%)	32,54,54	0.88	1 (3%)
3	GTP	K	501	4	26,34,34	1.01	3 (11%)	32,54,54	0.92	0
3	GTP	L	501	4	26,34,34	0.99	3 (11%)	32,54,54	0.61	0
3	GTP	J	501	4	26,34,34	1.04	3 (11%)	32,54,54	0.76	0
5	GSP	I	501	-	26,34,34	0.95	3 (11%)	27,54,54	0.74	1 (3%)
5	GSP	B	501	-	26,34,34	0.96	3 (11%)	27,54,54	0.74	1 (3%)
3	GTP	A	501	4	26,34,34	1.02	3 (11%)	32,54,54	0.76	0
5	GSP	D	501	-	26,34,34	0.96	3 (11%)	27,54,54	0.76	1 (3%)
3	GTP	C	501	4	26,34,34	1.05	4 (15%)	32,54,54	0.82	1 (3%)
5	GSP	G	501	-	26,34,34	0.96	3 (11%)	27,54,54	0.69	1 (3%)
5	GSP	F	501	-	26,34,34	0.98	3 (11%)	27,54,54	0.72	1 (3%)
5	GSP	H	501	-	26,34,34	0.95	3 (11%)	27,54,54	0.77	1 (3%)

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
3	GTP	E	501	4	-	4/18/38/38	0/3/3/3
3	GTP	K	501	4	-	4/18/38/38	0/3/3/3
3	GTP	L	501	4	-	4/18/38/38	0/3/3/3
3	GTP	J	501	4	-	3/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	GSP	I	501	-	-	1/17/38/38	0/3/3/3
5	GSP	B	501	-	-	1/17/38/38	0/3/3/3
3	GTP	A	501	4	-	4/18/38/38	0/3/3/3
5	GSP	D	501	-	-	1/17/38/38	0/3/3/3
3	GTP	C	501	4	-	3/18/38/38	0/3/3/3
5	GSP	G	501	-	-	1/17/38/38	0/3/3/3
5	GSP	F	501	-	-	1/17/38/38	0/3/3/3
5	GSP	H	501	-	-	1/17/38/38	0/3/3/3

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	501	GTP	C5-C6	-2.62	1.42	1.47
3	J	501	GTP	C5-C6	-2.59	1.42	1.47
3	K	501	GTP	C5-C6	-2.55	1.42	1.47
3	A	501	GTP	C5-C6	-2.53	1.42	1.47
3	L	501	GTP	C5-C6	-2.48	1.42	1.47

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	D	501	GSP	PA-O3A-PB	-2.71	123.53	132.83
5	B	501	GSP	PA-O3A-PB	-2.61	123.88	132.83
5	I	501	GSP	PA-O3A-PB	-2.58	123.97	132.83
5	H	501	GSP	PA-O3A-PB	-2.56	124.05	132.83
5	F	501	GSP	PA-O3A-PB	-2.41	124.54	132.83

There are no chirality outliers.

5 of 28 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	501	GTP	C5'-O5'-PA-O1A
3	E	501	GTP	C5'-O5'-PA-O2A
3	J	501	GTP	C5'-O5'-PA-O3A
3	C	501	GTP	C5'-O5'-PA-O1A
3	C	501	GTP	C5'-O5'-PA-O2A

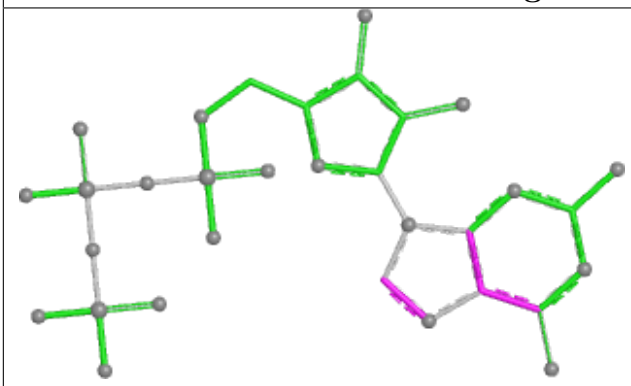
There are no ring outliers.

9 monomers are involved in 15 short contacts:

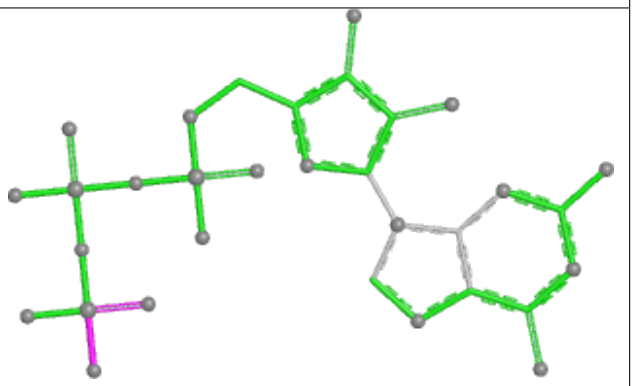
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	501	GTP	1	0
3	J	501	GTP	1	0
5	I	501	GSP	2	0
5	B	501	GSP	2	0
5	D	501	GSP	2	0
3	C	501	GTP	1	0
5	G	501	GSP	2	0
5	F	501	GSP	2	0
5	H	501	GSP	2	0

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 then 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.

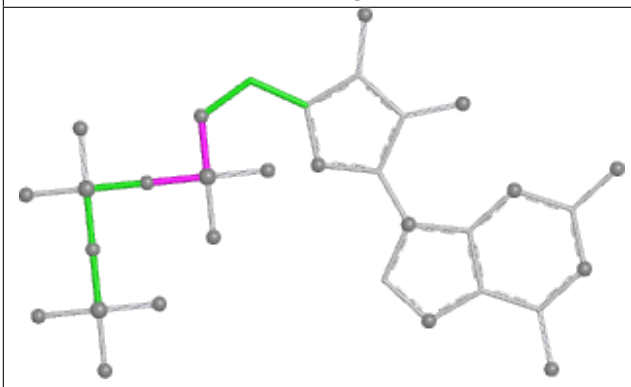
Ligand GTP E 501



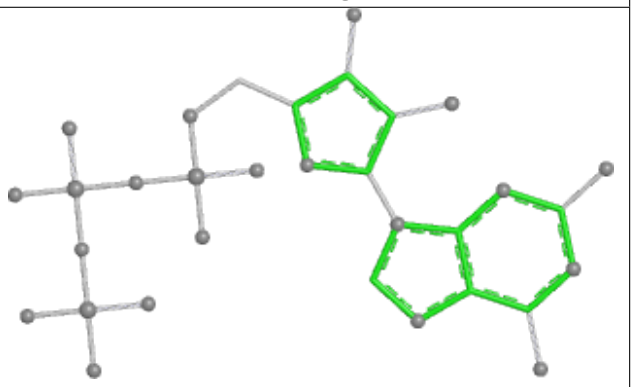
Bond lengths



Bond angles

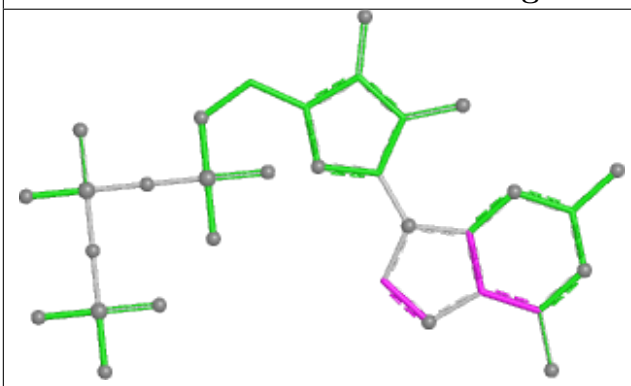


Torsions



Rings

Ligand GTP K 501



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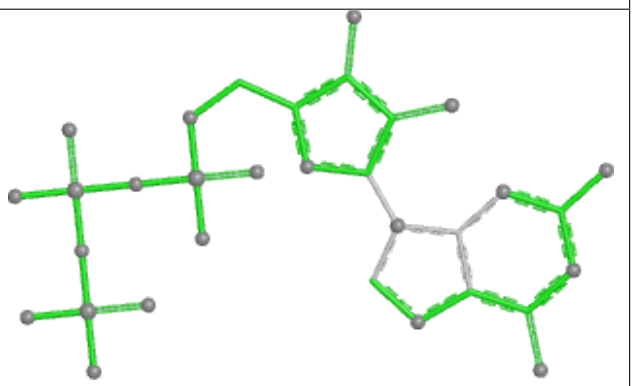

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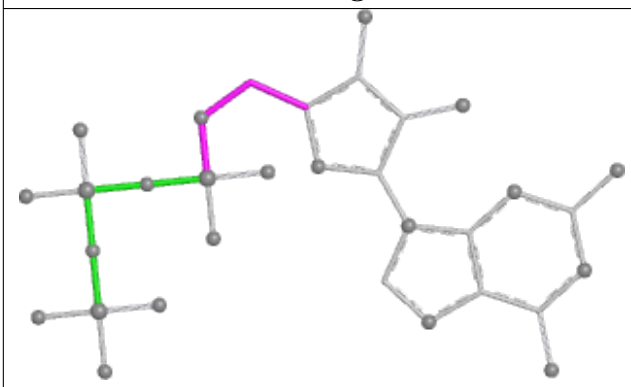

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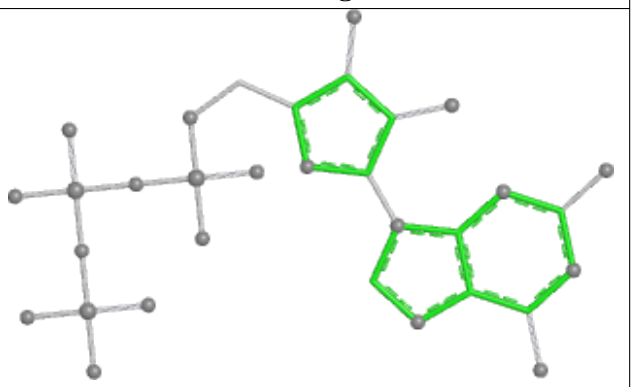

Rings

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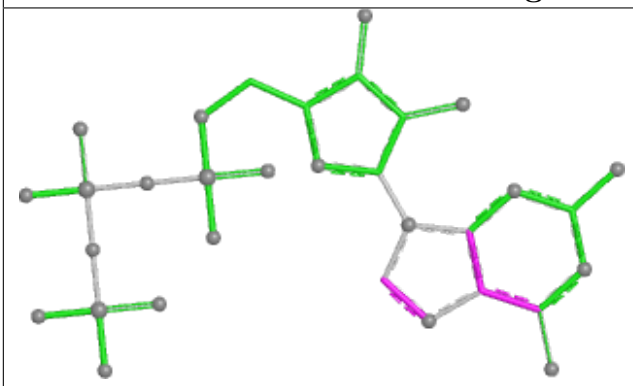

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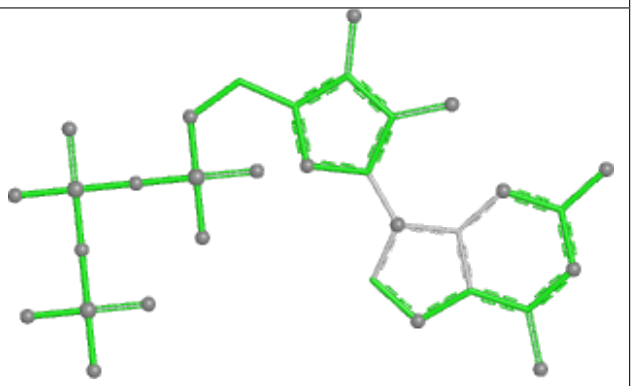

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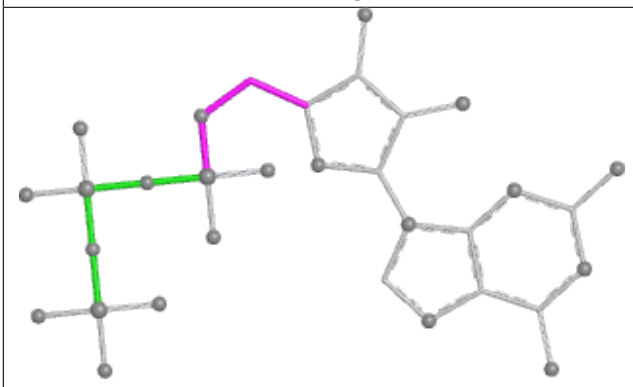

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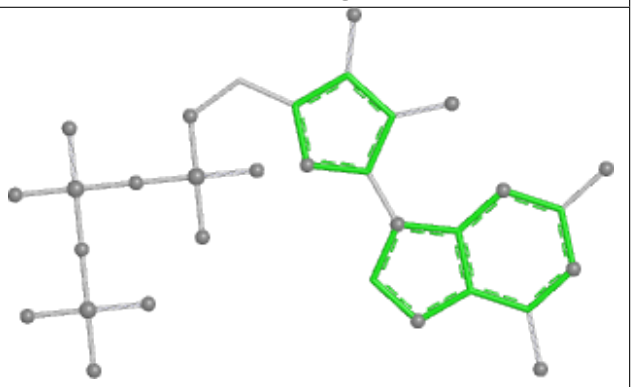
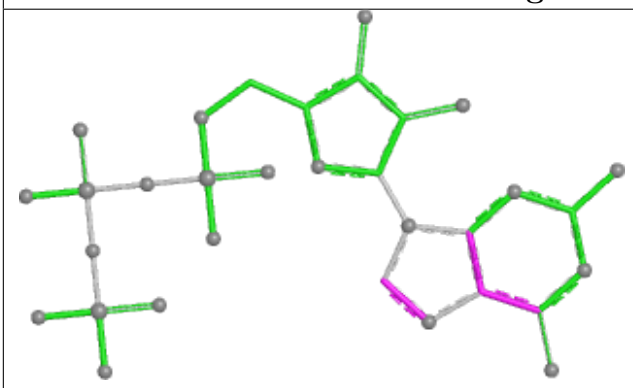


Rings

Ligand GTP J 501



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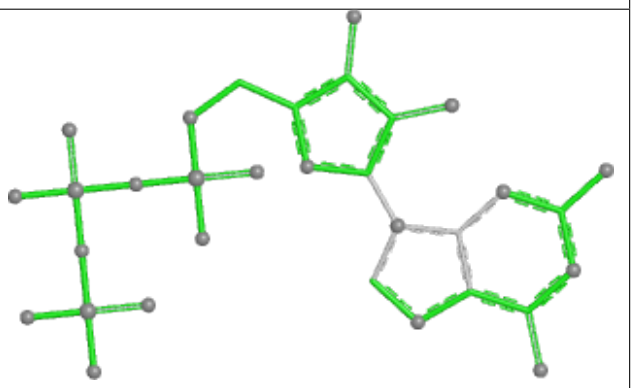

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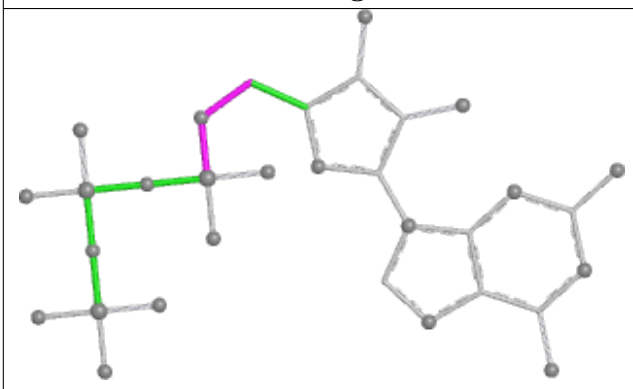

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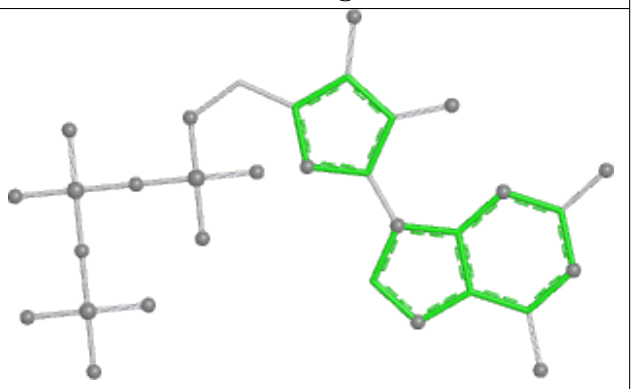
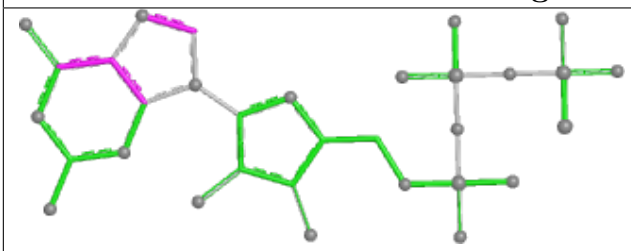
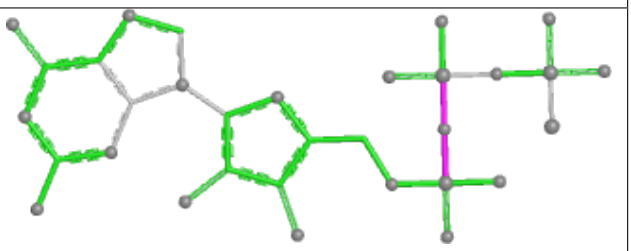
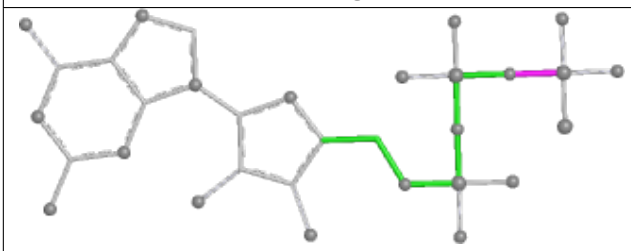
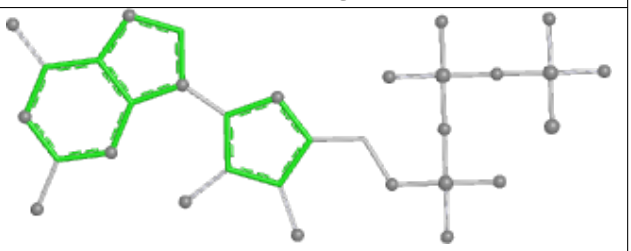


Rings

Ligand GSP I 501	
 Bond lengths	 Bond angles
 Torsions	 Rings

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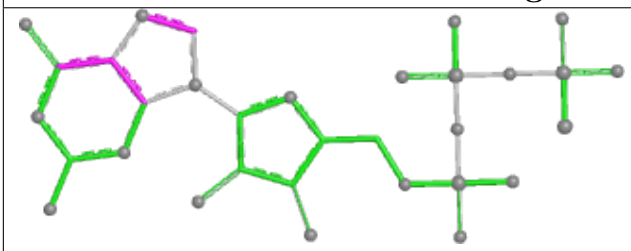
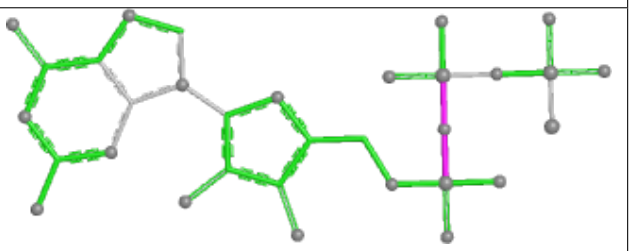
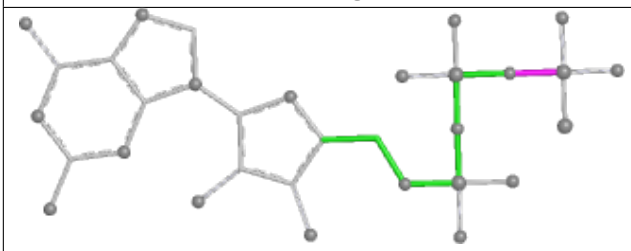
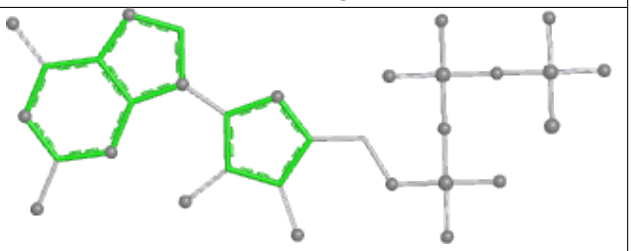
 Bond lengths	 Bond angles
 Torsions	 Rings

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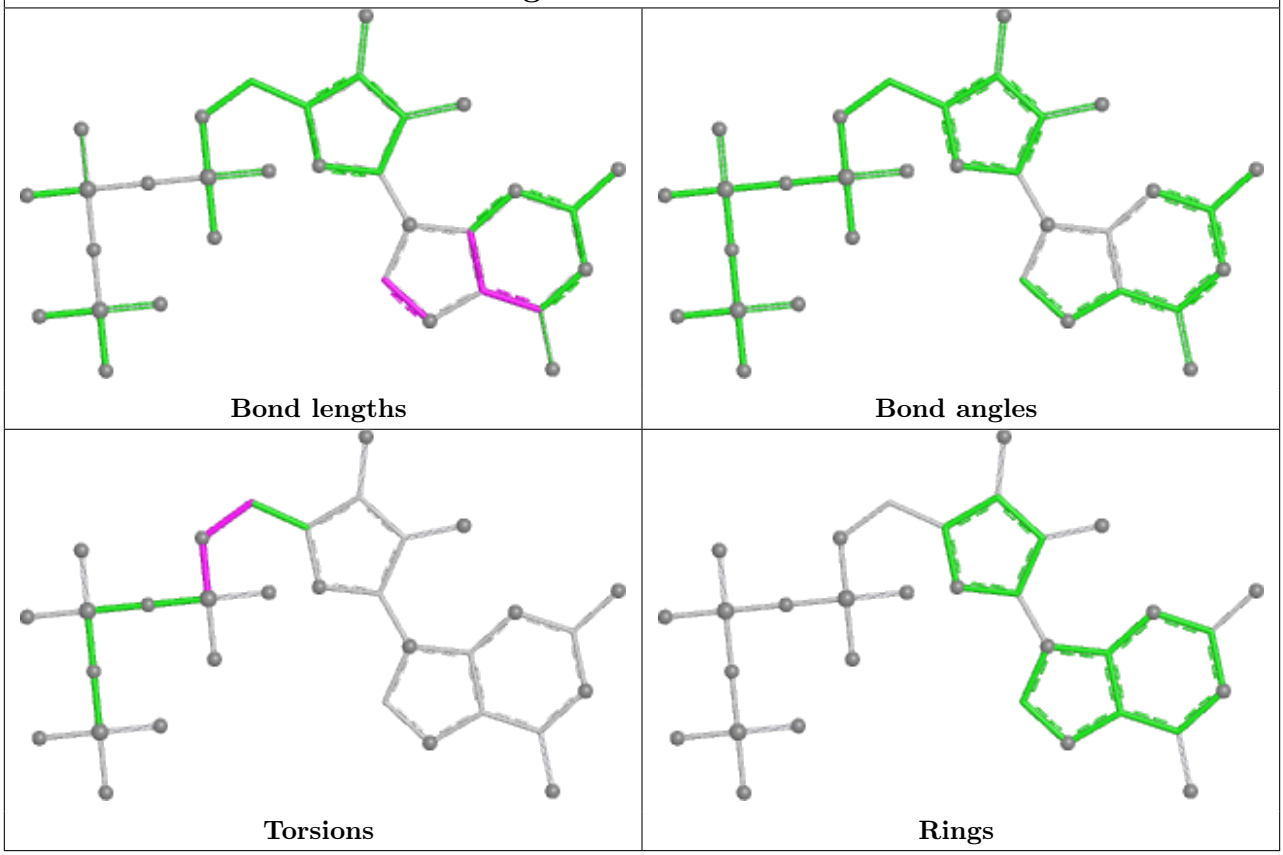

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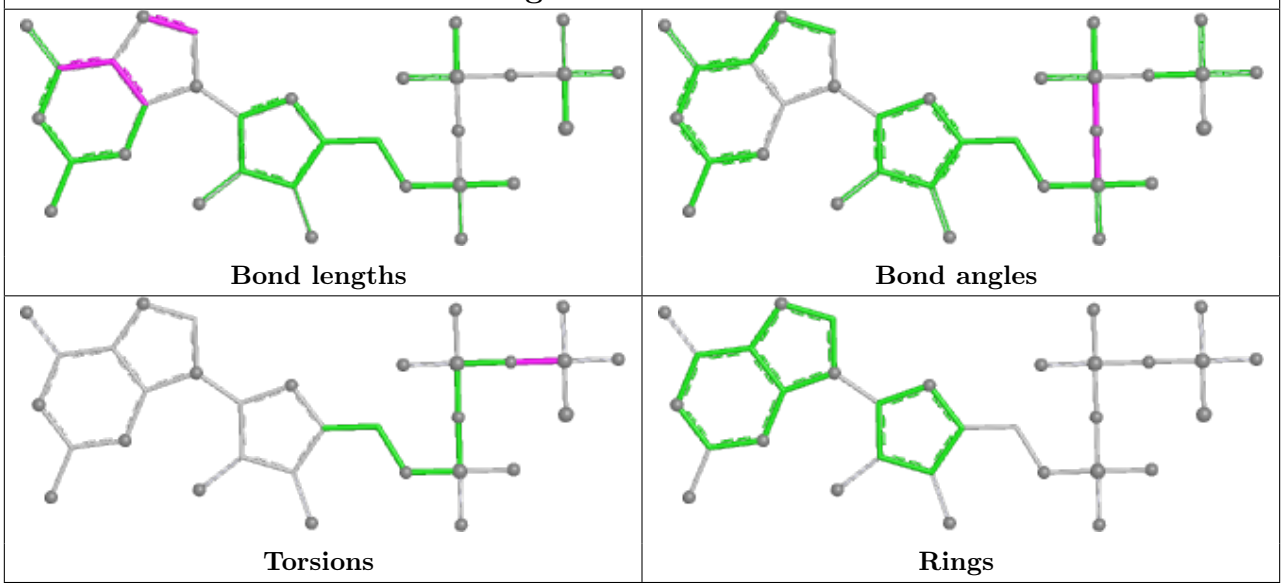

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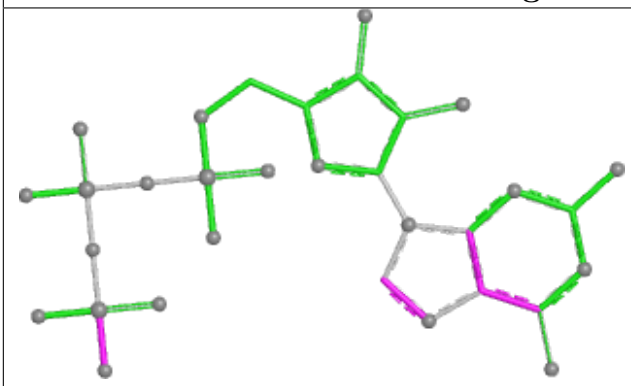
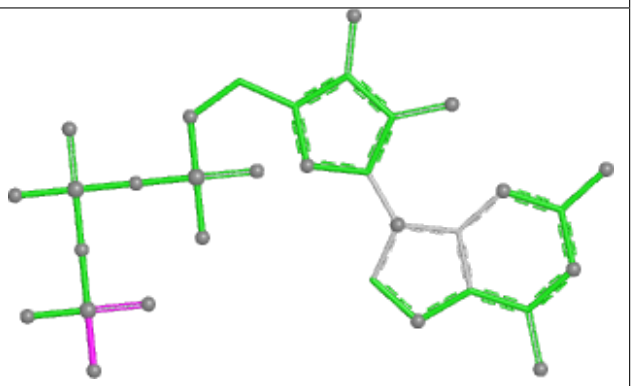
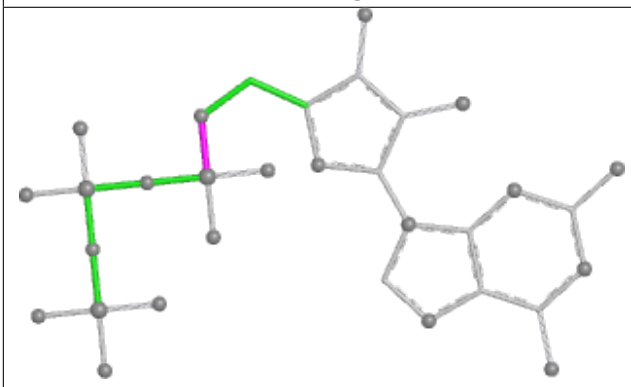
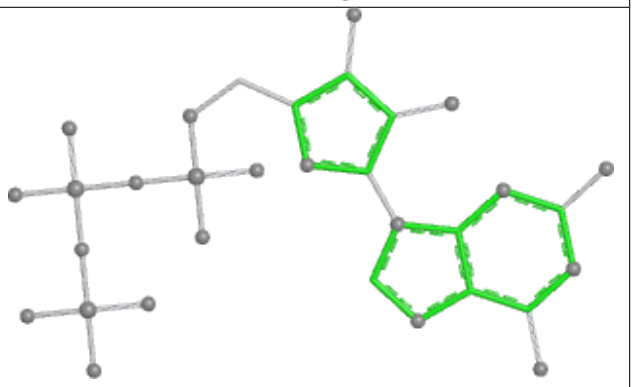
 Bond lengths	 Bond angles
 Torsions	 Rings

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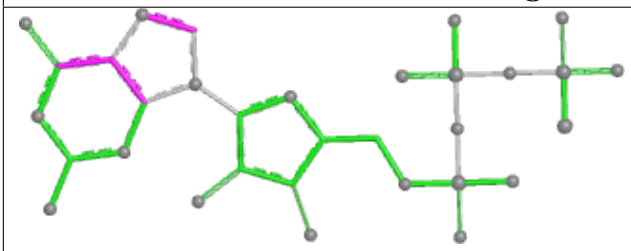
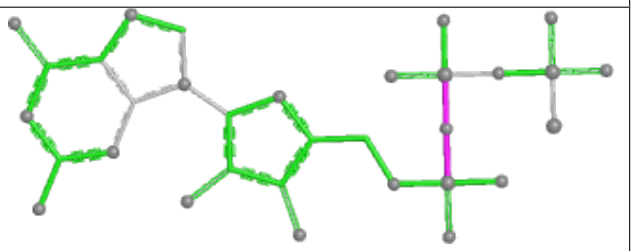
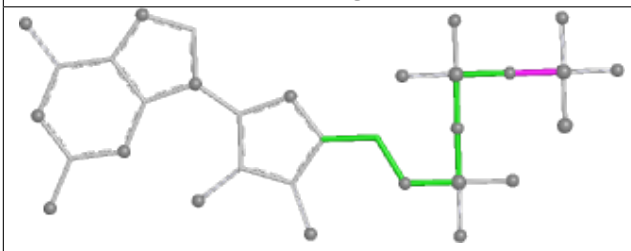
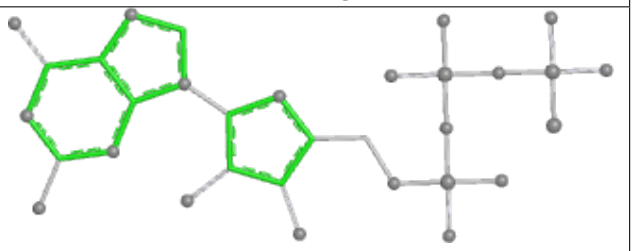
 Bond lengths	 Bond angles
 Torsions	 Rings

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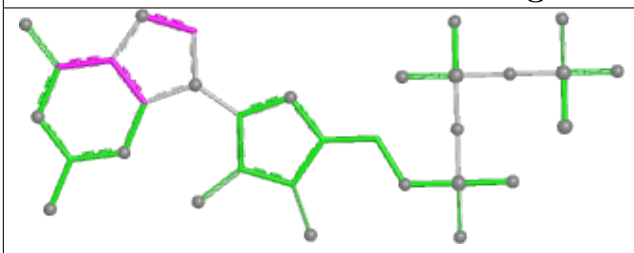
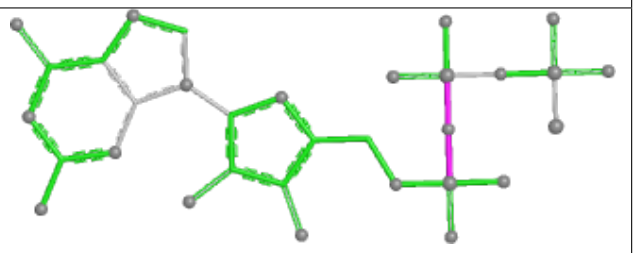
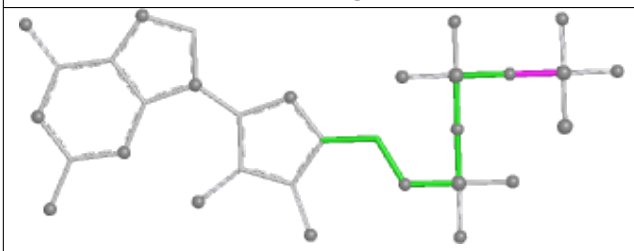
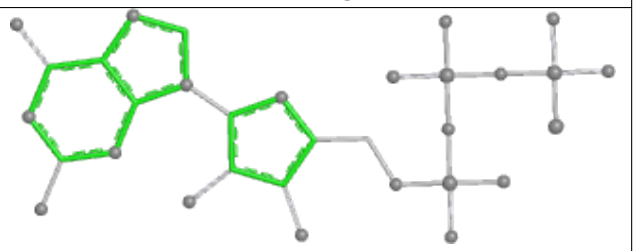
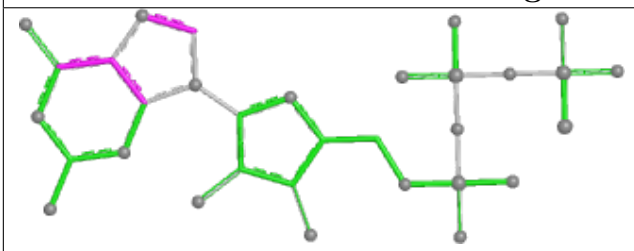
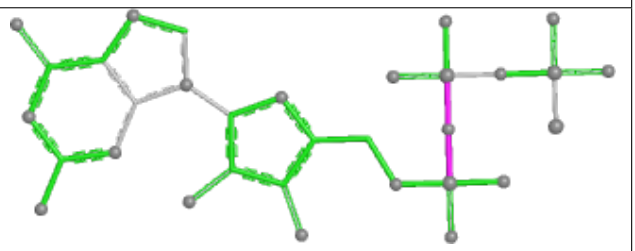
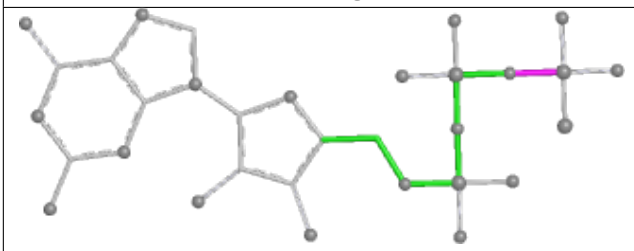
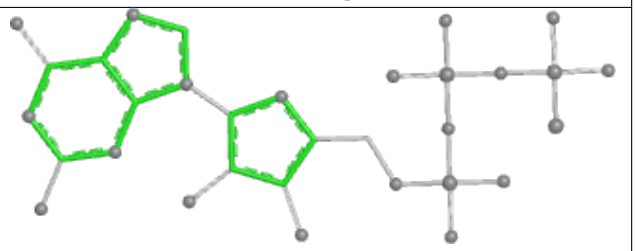
 Bond lengths	 Bond angles
 Torsions	 Rings

Ligand GSP H 501	
 Bond lengths	 Bond angles
 Torsions	 Rings

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.

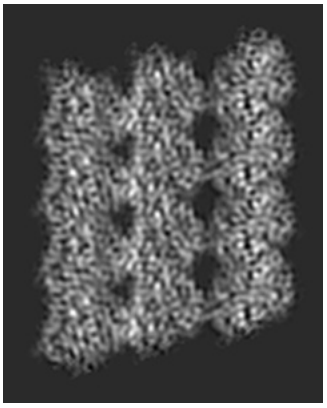
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-3963. These allow visual inspection of the internal detail of the map and identification of artifacts.

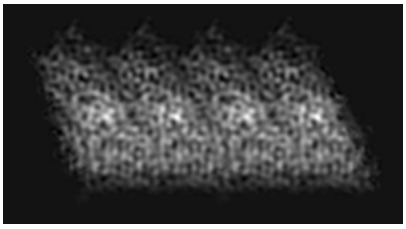
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

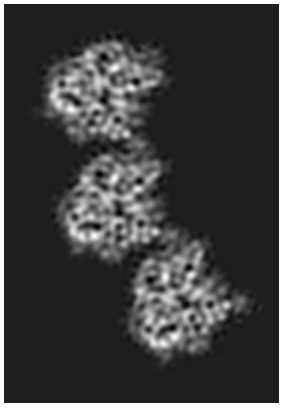
6.1.1 Primary map



X



Y

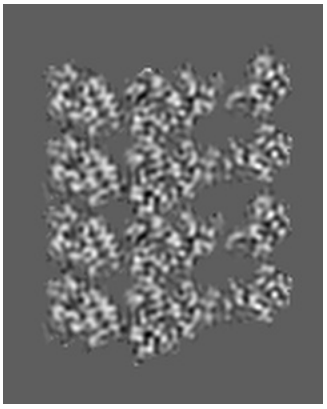


Z

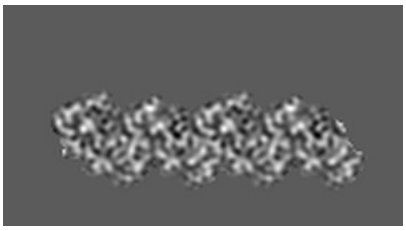
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

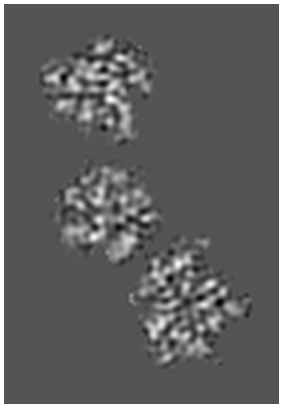
6.2.1 Primary map



X Index: 46



Y Index: 67

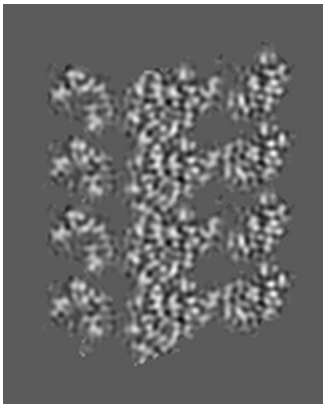


Z Index: 84

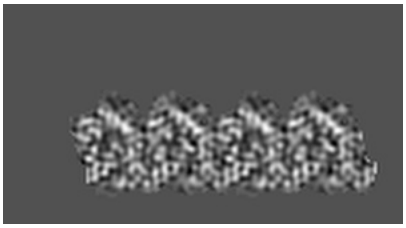
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

6.3.1 Primary map



X Index: 44



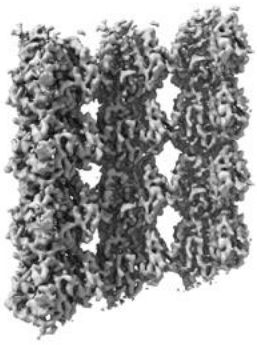
Y Index: 105

Z Index: 96

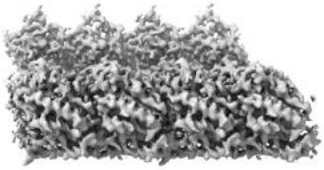
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

6.4.1 Primary map



X



Y

Z

The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

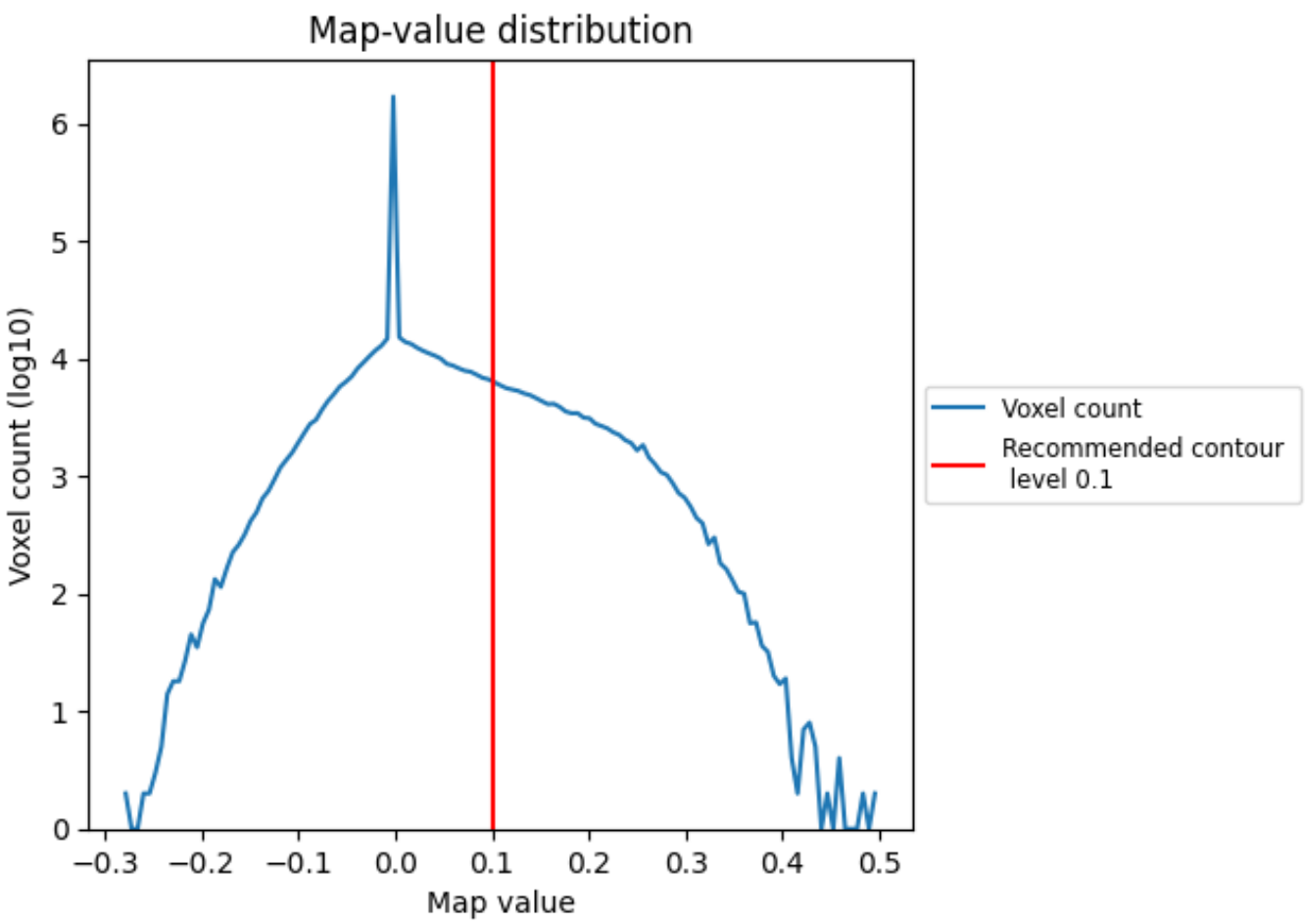
6.5 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis (i)

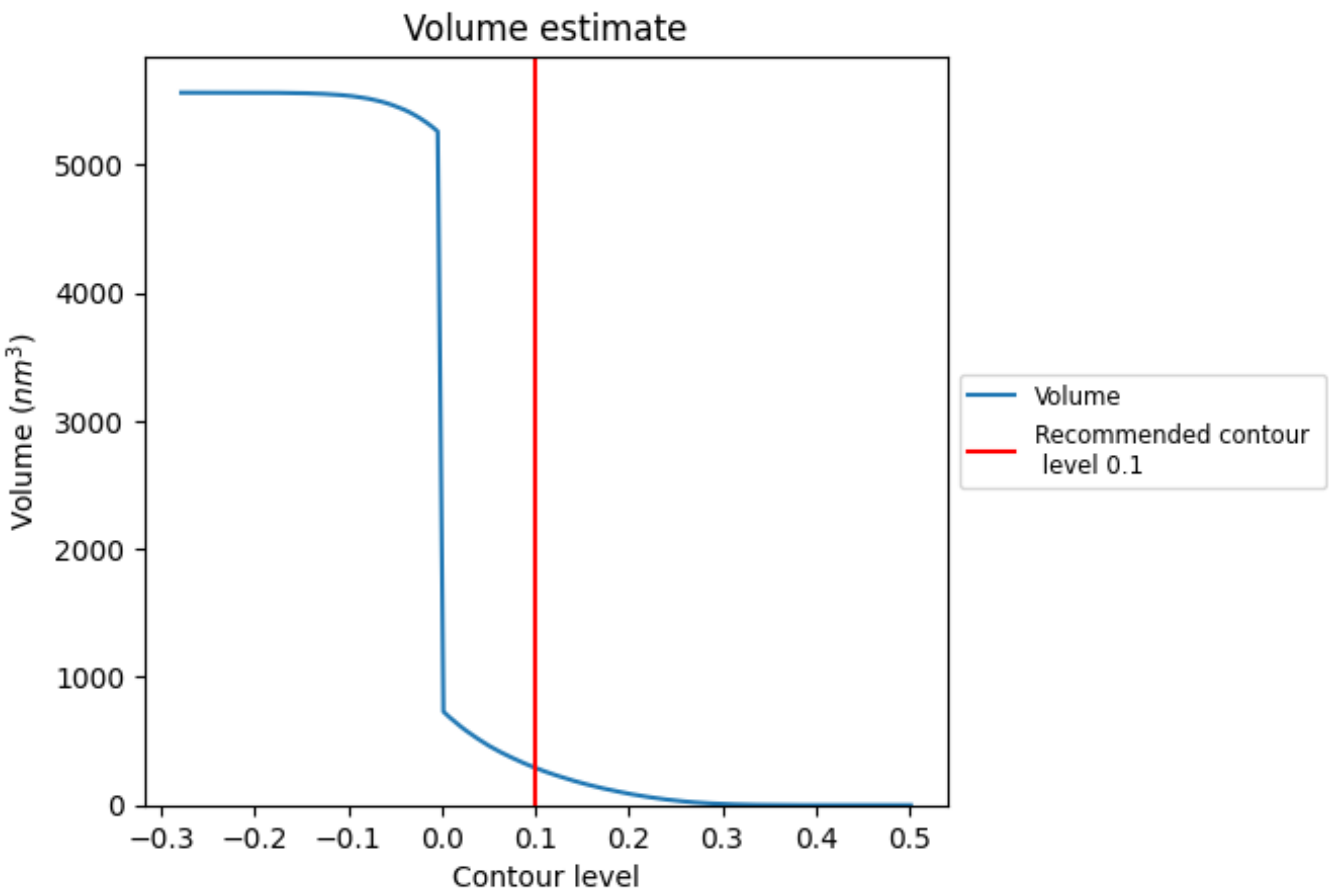
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

7.2 Volume estimate (i)



The volume at the recommended contour level is 292 nm^3; this corresponds to an approximate mass of 263 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

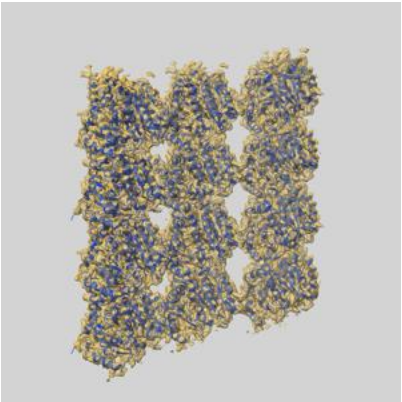
8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.

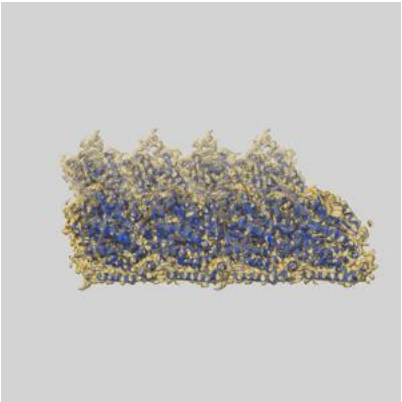
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-3963 and PDB model 6EVY. Per-residue inclusion information can be found in section 3 on page 7.

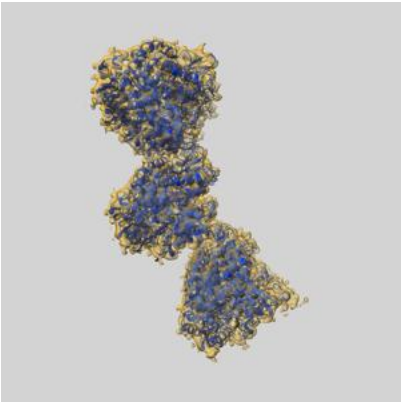
9.1 Map-model overlay (i)



X



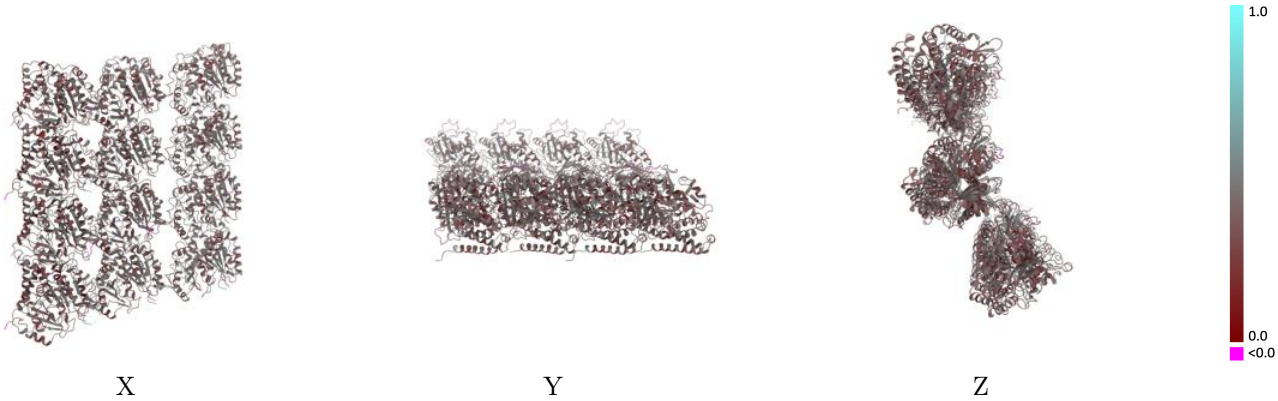
Y



Z

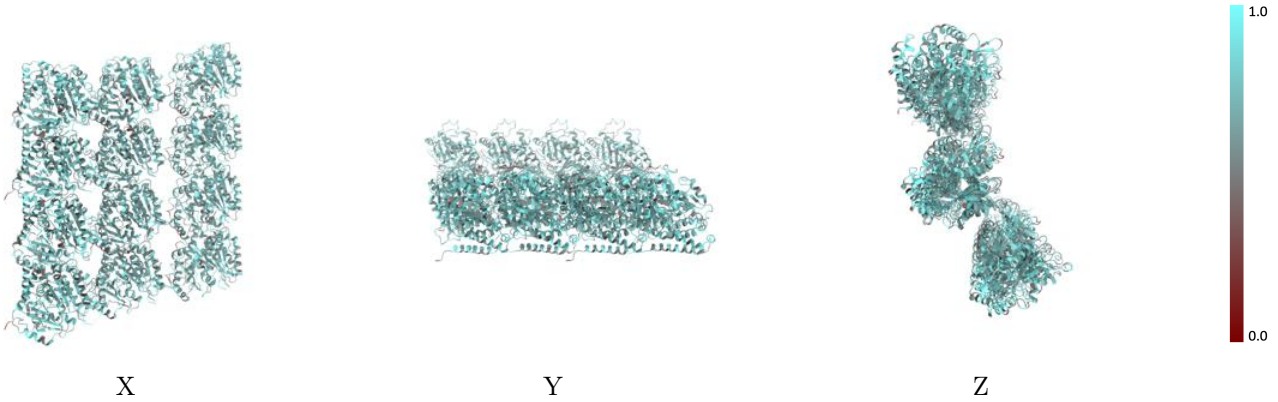
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



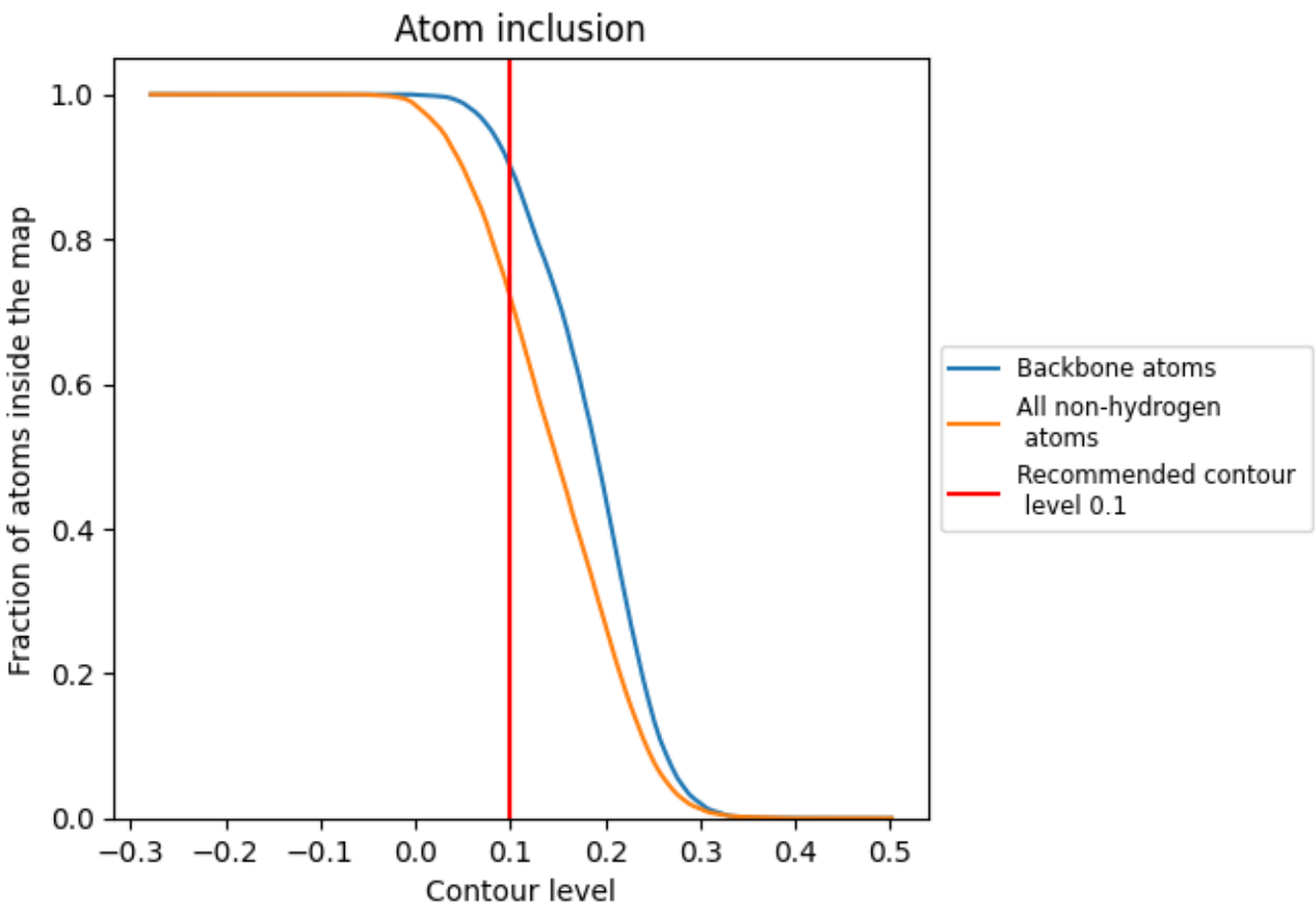
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model (i)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.1).

9.4 Atom inclusion (i)



At the recommended contour level, 90% of all backbone atoms, 72% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7198	0.3860
A	0.7084	0.3850
B	0.7230	0.3830
C	0.7141	0.3870
D	0.7281	0.3860
E	0.7192	0.3910
F	0.7254	0.3870
G	0.7278	0.3870
H	0.7260	0.3830
I	0.7260	0.3860
J	0.7177	0.3900
K	0.7087	0.3850
L	0.7126	0.3860