Full wwPDB EM Validation Report (i)

May 19, 2024 – 10:16 AM EDT

PDB ID	:	7MGZ
EMDB ID	:	EMD-23831
Title	:	Human CTPS1 bound to UTP, AMPPNP, and glutamine
Authors	:	Lynch, E.M.; Dimattia, M.A.; Kollman, J.M.
Deposited on	:	2021-04-14
Resolution	:	2.80 Å(reported)

This is a Full wwPDB EM 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/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:

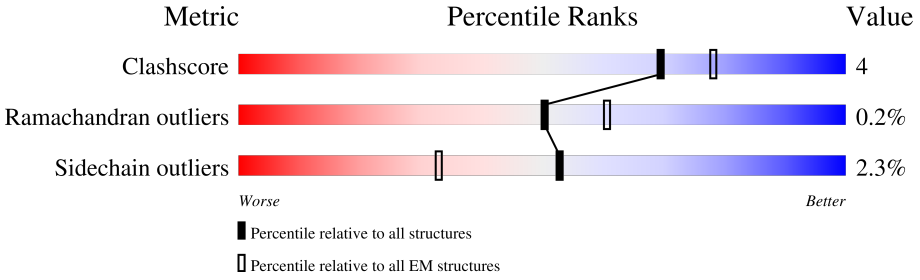
EMDB validation analysis	:	0.0.1.dev92
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 2.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	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	F	591	• 83% 7% • 8%
1	O	591	5% 83% 7% • 8%
1	P	591	• 83% 7% • 8%
1	Q	591	5% 83% 7% • 8%

2 Entry composition (i)

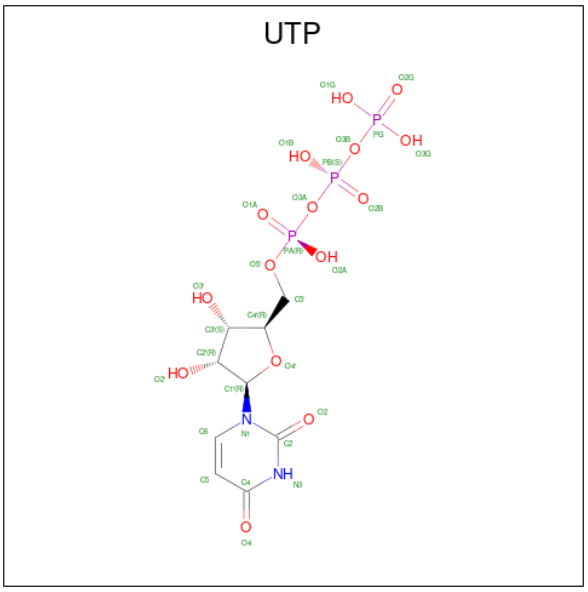
There are 5 unique types of molecules in this entry. The entry contains 34948 atoms, of which 17412 are hydrogens and 0 are deuteriums.

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 CTP synthase 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
			Total	C	H	N	O	S		
1	F	542	8631	2752	4319	738	799	23	0	0
1	O	542	8631	2752	4319	738	799	23	0	0
1	P	542	8631	2752	4319	738	799	23	0	0
1	Q	542	8631	2752	4319	738	799	23	0	0

- Molecule 2 is URIDINE 5'-TRIPHOSPHATE (three-letter code: UTP) (formula: $C_9H_{15}N_2O_{15}P_3$).



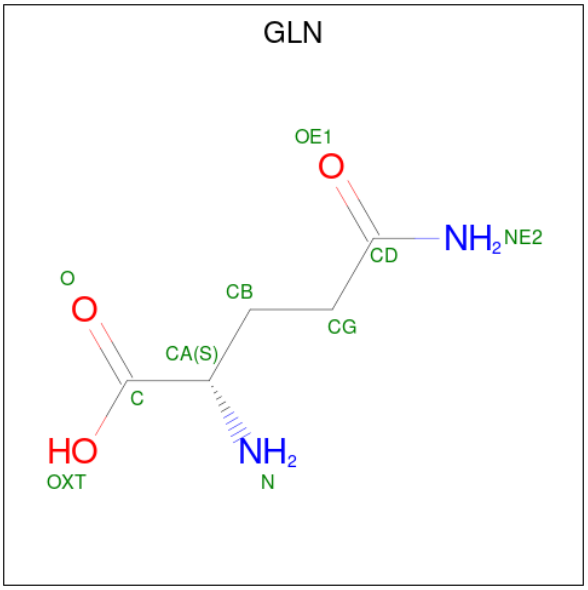
Mol	Chain	Residues	Atoms						AltConf
			Total	C	H	N	O	P	
2	F	1	40	9	11	2	15	3	0
2	O	1	40	9	11	2	15	3	0
2	P	1	40	9	11	2	15	3	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms						AltConf
			Total	C	H	N	O	P	
2	Q	1	40	9	11	2	15	3	0

- Molecule 3 is GLUTAMINE (three-letter code: GLN) (formula: $C_5H_{10}N_2O_3$).

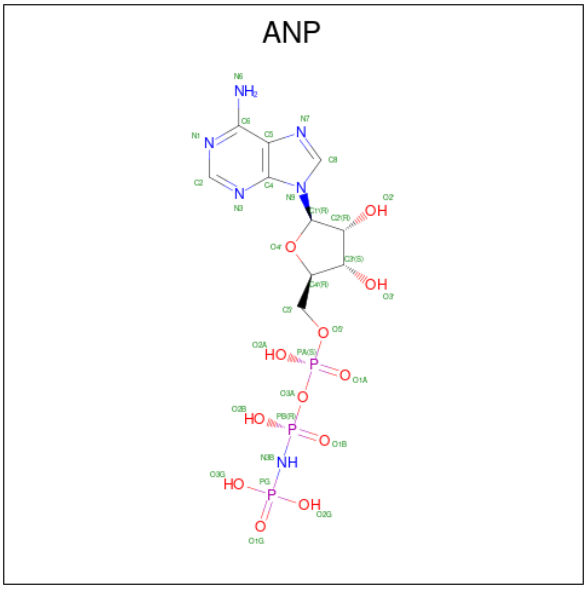


Mol	Chain	Residues	Atoms					AltConf
			Total	C	H	N	O	
3	F	1	20	5	10	2	3	0
3	O	1	20	5	10	2	3	0
3	P	1	20	5	10	2	3	0
3	Q	1	20	5	10	2	3	0

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

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
4	F	2	2	2	0
4	O	2	2	2	0
4	P	2	2	2	0
4	Q	2	2	2	0

- Molecule 5 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$).



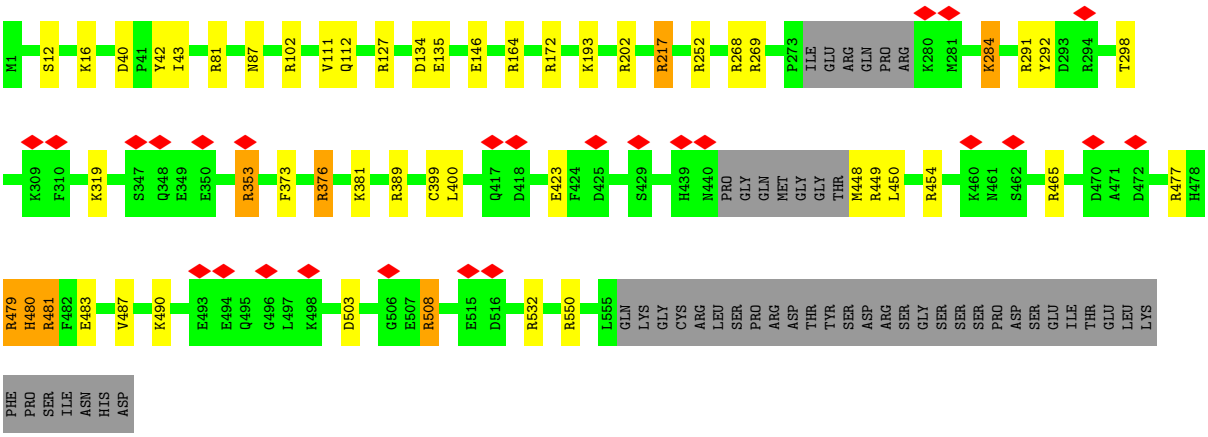
Mol	Chain	Residues	Atoms						AltConf
			Total	C	H	N	O	P	
5	F	1	44	10	13	6	12	3	0
			Total	C	H	N	O	P	
5	O	1	44	10	13	6	12	3	0
			Total	C	H	N	O	P	
5	P	1	44	10	13	6	12	3	0
			Total	C	H	N	O	P	
5	Q	1	44	10	13	6	12	3	0

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.

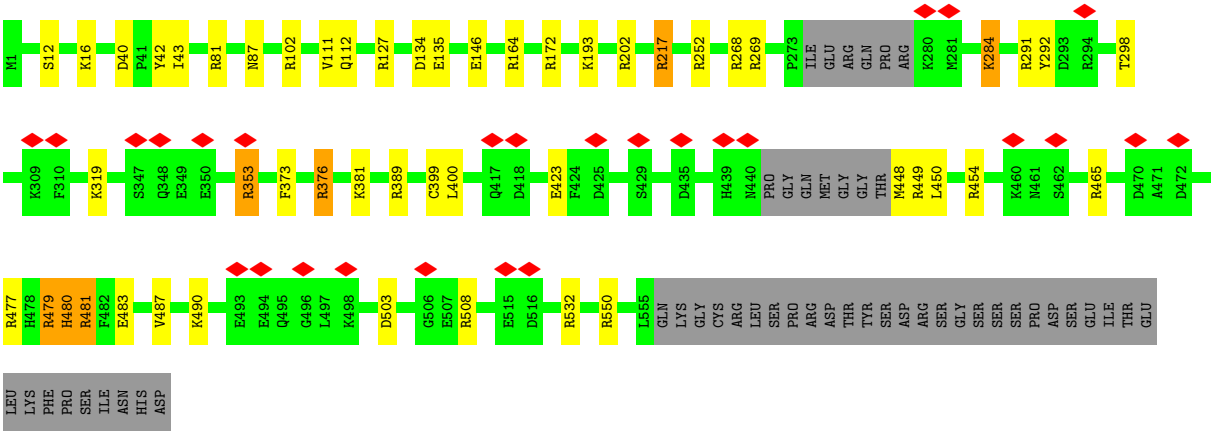
• Molecule 1: CTP synthase 1

Chain F:



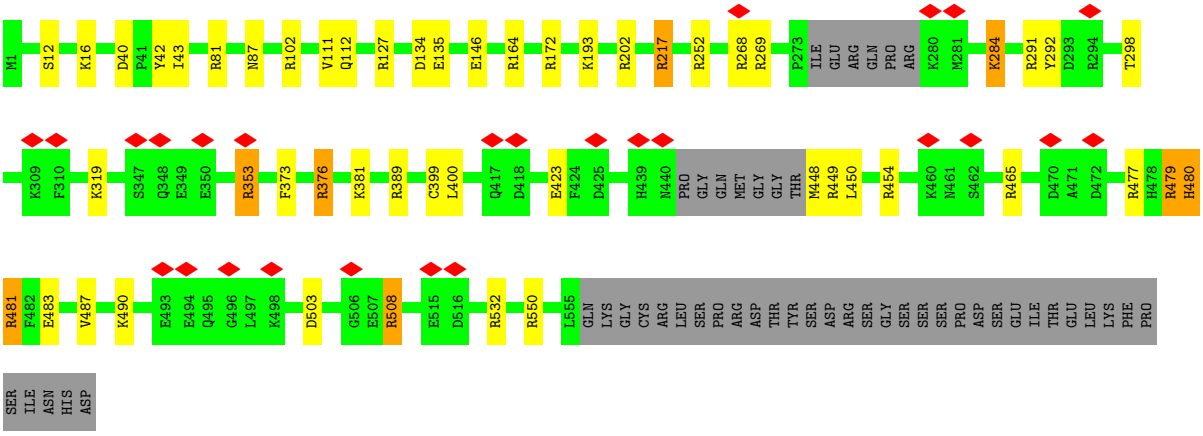
• Molecule 1: CTP synthase 1

Chain O:



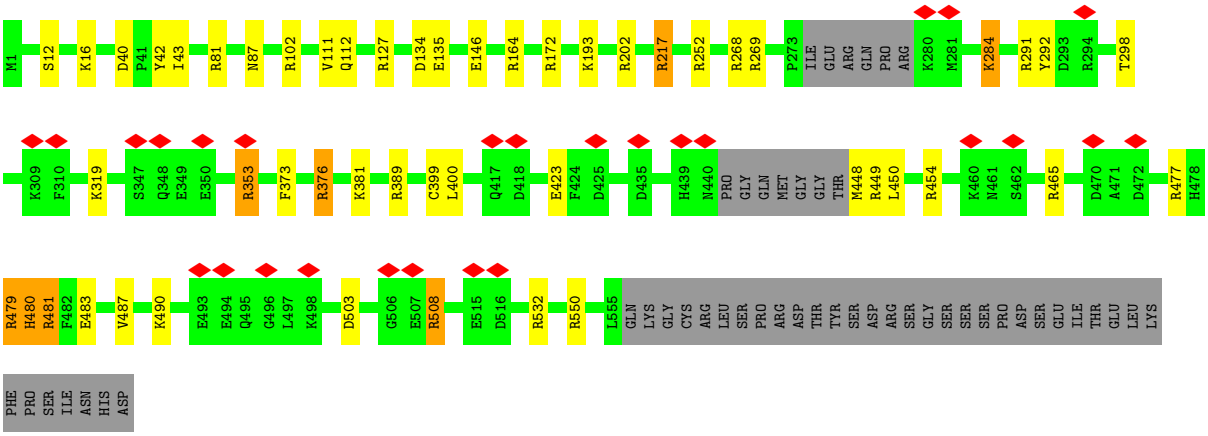
• Molecule 1: CTP synthase 1

Chain P:



- Molecule 1: CTP synthase 1

Chain Q:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D2	Depositor
Number of particles used	147336	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	90	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	13.117	Depositor
Minimum map value	-7.567	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.263	Depositor
Recommended contour level	1.21	Depositor
Map size (Å)	315.0, 315.0, 315.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	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, ANP, UTP

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	F	0.68	3/4407 (0.1%)	1.10	25/5963 (0.4%)
1	O	0.68	3/4407 (0.1%)	1.10	24/5963 (0.4%)
1	P	0.68	3/4407 (0.1%)	1.10	25/5963 (0.4%)
1	Q	0.68	3/4407 (0.1%)	1.10	25/5963 (0.4%)
All	All	0.68	12/17628 (0.1%)	1.10	99/23852 (0.4%)

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
1	F	0	4
1	O	0	4
1	P	0	4
1	Q	0	4
All	All	0	16

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Q	483	GLU	CD-OE2	8.05	1.34	1.25
1	F	483	GLU	CD-OE2	8.04	1.34	1.25
1	P	483	GLU	CD-OE2	8.04	1.34	1.25
1	O	483	GLU	CD-OE2	7.99	1.34	1.25
1	Q	146	GLU	CD-OE2	7.96	1.34	1.25
1	O	146	GLU	CD-OE2	7.96	1.34	1.25
1	F	146	GLU	CD-OE2	7.95	1.34	1.25
1	P	146	GLU	CD-OE2	7.95	1.34	1.25
1	O	487	VAL	CB-CG2	-7.64	1.36	1.52
1	F	487	VAL	CB-CG2	-7.64	1.36	1.52

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	P	487	VAL	CB-CG2	-7.64	1.36	1.52
1	Q	487	VAL	CB-CG2	-7.64	1.36	1.52

All (99) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	F	252	ARG	NE-CZ-NH1	10.16	125.38	120.30
1	O	252	ARG	NE-CZ-NH1	10.14	125.37	120.30
1	P	252	ARG	NE-CZ-NH1	10.14	125.37	120.30
1	Q	252	ARG	NE-CZ-NH1	10.14	125.37	120.30
1	Q	487	VAL	CA-CB-CG1	9.54	125.20	110.90
1	F	487	VAL	CA-CB-CG1	9.52	125.17	110.90
1	O	487	VAL	CA-CB-CG1	9.52	125.17	110.90
1	P	487	VAL	CA-CB-CG1	9.52	125.17	110.90
1	O	477	ARG	NE-CZ-NH1	8.35	124.47	120.30
1	Q	477	ARG	NE-CZ-NH1	8.29	124.45	120.30
1	F	477	ARG	NE-CZ-NH1	8.28	124.44	120.30
1	P	477	ARG	NE-CZ-NH1	8.28	124.44	120.30
1	P	353	ARG	NE-CZ-NH1	7.77	124.19	120.30
1	Q	353	ARG	NE-CZ-NH1	7.71	124.15	120.30
1	F	353	ARG	NE-CZ-NH1	7.69	124.15	120.30
1	O	353	ARG	NE-CZ-NH1	7.66	124.13	120.30
1	Q	532	ARG	NE-CZ-NH1	7.66	124.13	120.30
1	O	479	ARG	NE-CZ-NH1	7.64	124.12	120.30
1	F	479	ARG	NE-CZ-NH1	7.62	124.11	120.30
1	F	532	ARG	NE-CZ-NH1	7.59	124.10	120.30
1	O	532	ARG	NE-CZ-NH1	7.59	124.10	120.30
1	P	532	ARG	NE-CZ-NH1	7.59	124.10	120.30
1	P	479	ARG	NE-CZ-NH1	7.54	124.07	120.30
1	Q	479	ARG	NE-CZ-NH1	7.54	124.07	120.30
1	O	81	ARG	NE-CZ-NH1	7.43	124.01	120.30
1	P	81	ARG	NE-CZ-NH1	7.41	124.01	120.30
1	Q	81	ARG	NE-CZ-NH1	7.41	124.01	120.30
1	F	389	ARG	NE-CZ-NH1	7.39	123.99	120.30
1	Q	389	ARG	NE-CZ-NH1	7.38	123.99	120.30
1	O	389	ARG	NE-CZ-NH1	7.34	123.97	120.30
1	F	81	ARG	NE-CZ-NH1	7.33	123.97	120.30
1	P	389	ARG	NE-CZ-NH1	7.32	123.96	120.30
1	F	449	ARG	NE-CZ-NH1	6.96	123.78	120.30
1	P	449	ARG	NE-CZ-NH1	6.93	123.77	120.30
1	Q	449	ARG	NE-CZ-NH1	6.93	123.77	120.30
1	O	449	ARG	NE-CZ-NH1	6.90	123.75	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	F	550	ARG	NE-CZ-NH1	6.48	123.54	120.30
1	O	550	ARG	NE-CZ-NH1	6.48	123.54	120.30
1	P	550	ARG	NE-CZ-NH1	6.48	123.54	120.30
1	Q	550	ARG	NE-CZ-NH1	6.48	123.54	120.30
1	P	268	ARG	NE-CZ-NH1	6.11	123.35	120.30
1	Q	268	ARG	NE-CZ-NH1	6.11	123.35	120.30
1	F	268	ARG	NE-CZ-NH1	6.08	123.34	120.30
1	O	268	ARG	NE-CZ-NH1	6.08	123.34	120.30
1	Q	164	ARG	NE-CZ-NH1	6.02	123.31	120.30
1	F	164	ARG	NE-CZ-NH1	5.98	123.29	120.30
1	O	164	ARG	NE-CZ-NH1	5.98	123.29	120.30
1	P	164	ARG	NE-CZ-NH1	5.98	123.29	120.30
1	P	291	ARG	NE-CZ-NH1	5.67	123.13	120.30
1	P	217	ARG	NE-CZ-NH1	5.64	123.12	120.30
1	Q	172	ARG	NE-CZ-NH1	5.63	123.11	120.30
1	Q	217	ARG	NE-CZ-NH1	5.62	123.11	120.30
1	O	172	ARG	NE-CZ-NH1	5.62	123.11	120.30
1	O	217	ARG	NE-CZ-NH1	5.60	123.10	120.30
1	F	291	ARG	NE-CZ-NH1	5.59	123.09	120.30
1	P	172	ARG	NE-CZ-NH1	5.59	123.09	120.30
1	F	217	ARG	NE-CZ-NH1	5.56	123.08	120.30
1	F	202	ARG	NE-CZ-NH1	5.53	123.06	120.30
1	P	202	ARG	NE-CZ-NH1	5.53	123.06	120.30
1	Q	202	ARG	NE-CZ-NH1	5.53	123.06	120.30
1	O	202	ARG	NE-CZ-NH1	5.53	123.06	120.30
1	O	102	ARG	NE-CZ-NH1	5.52	123.06	120.30
1	O	291	ARG	NE-CZ-NH1	5.52	123.06	120.30
1	Q	291	ARG	NE-CZ-NH1	5.52	123.06	120.30
1	F	172	ARG	NE-CZ-NH1	5.52	123.06	120.30
1	F	269	ARG	NE-CZ-NH1	5.52	123.06	120.30
1	Q	102	ARG	NE-CZ-NH1	5.51	123.05	120.30
1	Q	269	ARG	NE-CZ-NH1	5.50	123.05	120.30
1	F	481	ARG	NE-CZ-NH1	5.50	123.05	120.30
1	O	269	ARG	NE-CZ-NH1	5.49	123.04	120.30
1	P	481	ARG	NE-CZ-NH1	5.46	123.03	120.30
1	Q	481	ARG	NE-CZ-NH1	5.46	123.03	120.30
1	O	481	ARG	NE-CZ-NH1	5.43	123.02	120.30
1	P	269	ARG	NE-CZ-NH1	5.41	123.00	120.30
1	F	102	ARG	NE-CZ-NH1	5.40	123.00	120.30
1	P	376	ARG	NE-CZ-NH1	5.38	122.99	120.30
1	P	102	ARG	NE-CZ-NH1	5.36	122.98	120.30
1	F	449	ARG	NE-CZ-NH2	-5.31	117.64	120.30

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	P	449	ARG	NE-CZ-NH2	-5.31	117.64	120.30
1	Q	449	ARG	NE-CZ-NH2	-5.31	117.64	120.30
1	F	465	ARG	NE-CZ-NH1	5.28	122.94	120.30
1	O	449	ARG	NE-CZ-NH2	-5.25	117.67	120.30
1	F	376	ARG	NE-CZ-NH1	5.24	122.92	120.30
1	Q	376	ARG	NE-CZ-NH1	5.24	122.92	120.30
1	O	465	ARG	NE-CZ-NH1	5.22	122.91	120.30
1	F	127	ARG	NE-CZ-NH1	5.22	122.91	120.30
1	O	127	ARG	NE-CZ-NH1	5.22	122.91	120.30
1	Q	127	ARG	NE-CZ-NH1	5.22	122.91	120.30
1	P	465	ARG	NE-CZ-NH1	5.20	122.90	120.30
1	Q	465	ARG	NE-CZ-NH1	5.20	122.90	120.30
1	O	376	ARG	NE-CZ-NH1	5.19	122.89	120.30
1	P	454	ARG	NE-CZ-NH1	5.16	122.88	120.30
1	Q	454	ARG	NE-CZ-NH1	5.16	122.88	120.30
1	P	127	ARG	NE-CZ-NH1	5.15	122.88	120.30
1	F	454	ARG	NE-CZ-NH1	5.13	122.86	120.30
1	O	454	ARG	NE-CZ-NH1	5.13	122.86	120.30
1	Q	508	ARG	NE-CZ-NH1	5.12	122.86	120.30
1	F	508	ARG	NE-CZ-NH1	5.06	122.83	120.30
1	P	508	ARG	NE-CZ-NH1	5.04	122.82	120.30

There are no chirality outliers.

All (16) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	F	217	ARG	Sidechain
1	F	292	TYR	Sidechain
1	F	353	ARG	Sidechain
1	F	508	ARG	Sidechain
1	O	217	ARG	Sidechain
1	O	292	TYR	Sidechain
1	O	353	ARG	Sidechain
1	O	508	ARG	Sidechain
1	P	217	ARG	Sidechain
1	P	292	TYR	Sidechain
1	P	353	ARG	Sidechain
1	P	508	ARG	Sidechain
1	Q	217	ARG	Sidechain
1	Q	292	TYR	Sidechain
1	Q	353	ARG	Sidechain
1	Q	508	ARG	Sidechain

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	F	4312	4319	4314	32	0
1	O	4312	4319	4314	32	0
1	P	4312	4319	4314	32	0
1	Q	4312	4319	4314	32	0
2	F	29	11	11	6	0
2	O	29	11	11	6	0
2	P	29	11	11	6	0
2	Q	29	11	11	6	0
3	F	10	10	7	4	0
3	O	10	10	7	4	0
3	P	10	10	7	4	0
3	Q	10	10	7	4	0
4	F	2	0	0	0	0
4	O	2	0	0	0	0
4	P	2	0	0	0	0
4	Q	2	0	0	0	0
5	F	31	13	13	1	0
5	O	31	13	13	1	0
5	P	31	13	13	1	0
5	Q	31	13	13	1	0
All	All	17536	17412	17380	128	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 (128) 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:F:448:MET:CE	1:F:481:ARG:HG3	1.33	1.55
1:P:448:MET:CE	1:P:481:ARG:HG3	1.33	1.55
1:Q:448:MET:CE	1:Q:481:ARG:HG3	1.33	1.55
1:O:448:MET:CE	1:O:481:ARG:HG3	1.33	1.54
1:P:448:MET:HE2	1:P:481:ARG:CG	1.44	1.44
1:O:448:MET:HE2	1:O:481:ARG:CG	1.50	1.41
1:Q:448:MET:HE2	1:Q:481:ARG:CG	1.51	1.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:448:MET:HE2	1:F:481:ARG:CG	1.48	1.40
1:P:448:MET:CE	1:P:481:ARG:CG	2.03	1.32
1:F:448:MET:CE	1:F:481:ARG:CG	2.03	1.31
1:Q:448:MET:CE	1:Q:481:ARG:CG	2.03	1.31
1:O:448:MET:CE	1:O:481:ARG:CG	2.03	1.30
1:F:448:MET:HG3	1:F:481:ARG:HG2	1.30	1.09
1:P:448:MET:HG3	1:P:481:ARG:HG2	1.30	1.09
1:O:448:MET:HG3	1:O:481:ARG:HG2	1.30	1.08
1:Q:448:MET:HG3	1:Q:481:ARG:HG2	1.30	1.07
1:Q:448:MET:HE3	1:Q:481:ARG:CD	1.85	1.06
1:O:448:MET:HE3	1:O:481:ARG:CD	1.86	1.05
1:F:448:MET:HE3	1:F:481:ARG:CD	1.87	1.03
1:Q:448:MET:HE3	1:Q:481:ARG:CG	1.86	1.03
1:O:448:MET:HE3	1:O:481:ARG:CG	1.88	1.02
1:P:448:MET:HE3	1:P:481:ARG:CD	1.90	1.01
1:O:40:ASP:OD1	2:O:601:UTP:H5	1.46	0.98
1:Q:40:ASP:OD1	2:Q:602:UTP:H5	1.46	0.97
1:F:40:ASP:OD1	2:F:601:UTP:H5	1.46	0.97
1:P:40:ASP:OD1	2:P:602:UTP:H5	1.46	0.97
1:F:448:MET:HE3	1:F:481:ARG:CG	1.89	0.96
1:P:448:MET:HE3	1:P:481:ARG:CG	1.94	0.92
1:O:448:MET:HE3	1:O:481:ARG:HD3	1.49	0.92
1:Q:448:MET:HE3	1:Q:481:ARG:HD3	1.49	0.92
1:F:448:MET:HE3	1:F:481:ARG:HD3	1.50	0.92
1:P:448:MET:HE3	1:P:481:ARG:HD3	1.52	0.91
1:F:373:PHE:CE1	3:F:602:GLN:OXT	2.26	0.88
1:P:373:PHE:CE1	3:P:603:GLN:O	2.26	0.88
1:O:373:PHE:CE1	3:O:602:GLN:OXT	2.26	0.88
1:Q:373:PHE:CE1	3:Q:603:GLN:O	2.26	0.88
1:O:448:MET:HG2	1:O:480:HIS:O	1.76	0.85
1:Q:448:MET:HG2	1:Q:480:HIS:O	1.76	0.85
1:P:448:MET:HG2	1:P:480:HIS:O	1.76	0.83
1:F:448:MET:HG2	1:F:480:HIS:O	1.76	0.83
1:F:448:MET:SD	1:F:479:ARG:O	2.41	0.78
1:P:448:MET:SD	1:P:479:ARG:O	2.41	0.78
1:O:448:MET:SD	1:O:479:ARG:O	2.41	0.77
1:Q:448:MET:SD	1:Q:479:ARG:O	2.41	0.77
1:F:193:LYS:HD2	2:P:602:UTP:O3G	1.87	0.74
2:F:601:UTP:O2G	1:P:193:LYS:HD2	1.87	0.74
2:O:601:UTP:O2G	1:Q:193:LYS:HD2	1.87	0.74
1:O:193:LYS:HD2	2:Q:602:UTP:O3G	1.87	0.74

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:448:MET:CG	1:O:481:ARG:HG2	2.16	0.73
1:F:40:ASP:OD1	2:F:601:UTP:C5	2.41	0.71
1:P:40:ASP:OD1	2:P:602:UTP:C5	2.41	0.71
1:Q:448:MET:CG	1:Q:481:ARG:HG2	2.16	0.70
1:P:448:MET:CE	1:P:481:ARG:CD	2.60	0.69
1:F:448:MET:CG	1:F:481:ARG:HG2	2.16	0.69
1:P:448:MET:CG	1:P:481:ARG:HG2	2.16	0.69
1:Q:448:MET:CE	1:Q:481:ARG:HG2	2.20	0.68
1:O:448:MET:CE	1:O:481:ARG:HG2	2.20	0.68
1:O:40:ASP:OD1	2:O:601:UTP:C5	2.41	0.67
1:O:111:VAL:HG23	1:P:43:ILE:HB	1.77	0.67
1:Q:40:ASP:OD1	2:Q:602:UTP:C5	2.41	0.67
1:F:43:ILE:HB	1:Q:111:VAL:HG23	1.77	0.66
1:P:448:MET:CE	1:P:481:ARG:HG2	2.20	0.66
1:F:448:MET:CE	1:F:481:ARG:HG2	2.20	0.66
1:O:43:ILE:HB	1:P:111:VAL:HG23	1.78	0.66
1:F:111:VAL:HG23	1:Q:43:ILE:HB	1.78	0.66
1:F:373:PHE:HE1	3:F:602:GLN:OXT	1.81	0.64
1:F:448:MET:HG3	1:F:481:ARG:CG	2.19	0.64
1:P:373:PHE:HE1	3:P:603:GLN:O	1.81	0.64
1:P:448:MET:HG3	1:P:481:ARG:CG	2.19	0.64
1:O:373:PHE:HE1	3:O:602:GLN:OXT	1.81	0.63
1:Q:373:PHE:HE1	3:Q:603:GLN:O	1.81	0.63
1:P:448:MET:HE3	1:P:481:ARG:HH11	1.65	0.61
1:O:448:MET:HG3	1:O:481:ARG:CG	2.19	0.61
1:Q:448:MET:HG3	1:Q:481:ARG:CG	2.19	0.61
1:O:12:SER:O	1:Q:193:LYS:HE3	2.01	0.60
1:O:193:LYS:HE3	1:Q:12:SER:O	2.01	0.60
1:Q:448:MET:HE2	1:Q:481:ARG:HG3	0.62	0.60
1:O:448:MET:CE	1:O:481:ARG:CD	2.60	0.60
1:F:193:LYS:HE3	1:P:12:SER:O	2.01	0.59
1:F:12:SER:O	1:P:193:LYS:HE3	2.01	0.59
1:Q:448:MET:CE	1:Q:481:ARG:CD	2.60	0.59
1:O:448:MET:HE2	1:O:481:ARG:HG3	0.61	0.58
1:F:448:MET:HE3	1:F:481:ARG:HH11	1.69	0.58
1:O:448:MET:HE3	1:O:481:ARG:HH11	1.70	0.56
1:F:448:MET:HE2	1:F:481:ARG:HG3	0.60	0.56
1:Q:448:MET:HE3	1:Q:481:ARG:HH11	1.72	0.55
1:P:448:MET:HE2	1:P:481:ARG:HG3	0.57	0.53
1:F:319:LYS:HE2	1:F:319:LYS:HA	1.92	0.52
1:P:319:LYS:HA	1:P:319:LYS:HE2	1.92	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:601:UTP:O4	5:O:604:ANP:PG	2.68	0.52
2:Q:602:UTP:O4	5:Q:605:ANP:PG	2.68	0.52
2:F:601:UTP:O4	5:F:604:ANP:PG	2.68	0.52
2:P:602:UTP:O4	5:P:605:ANP:PG	2.68	0.52
1:Q:319:LYS:HA	1:Q:319:LYS:HE2	1.92	0.51
1:O:319:LYS:HA	1:O:319:LYS:HE2	1.92	0.51
1:O:284:LYS:HE3	1:O:284:LYS:HA	1.93	0.51
1:Q:284:LYS:HE3	1:Q:284:LYS:HA	1.93	0.51
1:F:284:LYS:HA	1:F:284:LYS:HE3	1.93	0.51
1:F:448:MET:CE	1:F:481:ARG:HH11	2.24	0.51
1:O:448:MET:CE	1:O:481:ARG:HH11	2.24	0.50
1:P:284:LYS:HE3	1:P:284:LYS:HA	1.93	0.50
1:F:112:GLN:OE1	2:Q:602:UTP:H4'	2.11	0.50
1:P:448:MET:CE	1:P:481:ARG:HH11	2.24	0.50
2:O:601:UTP:H4'	1:P:112:GLN:OE1	2.11	0.50
1:Q:448:MET:CE	1:Q:481:ARG:HH11	2.25	0.50
1:O:112:GLN:OE1	2:P:602:UTP:H4'	2.11	0.50
2:F:601:UTP:H4'	1:Q:112:GLN:OE1	2.11	0.50
3:O:602:GLN:OXT	3:O:602:GLN:HG2	2.16	0.45
3:Q:603:GLN:O	3:Q:603:GLN:HG2	2.16	0.45
3:F:602:GLN:OXT	3:F:602:GLN:HG2	2.16	0.45
3:P:603:GLN:O	3:P:603:GLN:HG2	2.16	0.44
1:Q:448:MET:O	1:Q:450:LEU:N	2.50	0.44
1:O:448:MET:O	1:O:450:LEU:N	2.51	0.44
1:F:448:MET:O	1:F:450:LEU:N	2.50	0.43
1:P:448:MET:O	1:P:450:LEU:N	2.51	0.43
1:Q:12:SER:HB2	2:Q:602:UTP:O2A	2.19	0.43
1:O:12:SER:HB2	2:O:601:UTP:O1A	2.19	0.43
1:P:12:SER:HB2	2:P:602:UTP:O2A	2.19	0.42
1:F:12:SER:HB2	2:F:601:UTP:O1A	2.19	0.42
1:O:423:GLU:OE1	3:O:602:GLN:N	2.54	0.41
1:Q:423:GLU:OE1	3:Q:603:GLN:N	2.54	0.41
1:O:381:LYS:HE2	1:O:400:LEU:HD23	2.02	0.40
1:Q:381:LYS:HE2	1:Q:400:LEU:HD23	2.02	0.40
1:F:423:GLU:OE1	3:F:602:GLN:N	2.54	0.40
1:P:423:GLU:OE1	3:P:603:GLN:N	2.54	0.40
1:F:381:LYS:HE2	1:F:400:LEU:HD23	2.02	0.40
1:F:448:MET:CE	1:F:481:ARG:NH1	2.85	0.40
1:P:381:LYS:HE2	1:P:400:LEU:HD23	2.02	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 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	F	536/591 (91%)	517 (96%)	18 (3%)	1 (0%)	47	78
1	O	536/591 (91%)	517 (96%)	18 (3%)	1 (0%)	47	78
1	P	536/591 (91%)	517 (96%)	18 (3%)	1 (0%)	47	78
1	Q	536/591 (91%)	517 (96%)	18 (3%)	1 (0%)	47	78
All	All	2144/2364 (91%)	2068 (96%)	72 (3%)	4 (0%)	50	78

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	399	CYS
1	O	399	CYS
1	P	399	CYS
1	Q	399	CYS

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	F	480/524 (92%)	469 (98%)	11 (2%)	50	82
1	O	480/524 (92%)	469 (98%)	11 (2%)	50	82
1	P	480/524 (92%)	469 (98%)	11 (2%)	50	82
1	Q	480/524 (92%)	469 (98%)	11 (2%)	50	82
All	All	1920/2096 (92%)	1876 (98%)	44 (2%)	53	82

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	16	LYS
1	F	42	TYR
1	F	87	ASN
1	F	134	ASP
1	F	135	GLU
1	F	284	LYS
1	F	298	THR
1	F	376	ARG
1	F	480	HIS
1	F	490	LYS
1	F	503	ASP
1	O	16	LYS
1	O	42	TYR
1	O	87	ASN
1	O	134	ASP
1	O	135	GLU
1	O	284	LYS
1	O	298	THR
1	O	376	ARG
1	O	480	HIS
1	O	490	LYS
1	O	503	ASP
1	P	16	LYS
1	P	42	TYR
1	P	87	ASN
1	P	134	ASP
1	P	135	GLU
1	P	284	LYS
1	P	298	THR
1	P	376	ARG
1	P	480	HIS
1	P	490	LYS
1	P	503	ASP
1	Q	16	LYS
1	Q	42	TYR
1	Q	87	ASN
1	Q	134	ASP
1	Q	135	GLU
1	Q	284	LYS
1	Q	298	THR
1	Q	376	ARG
1	Q	480	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	Q	490	LYS
1	Q	503	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 20 ligands modelled in this entry, 8 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	GLN	O	602	-	8,9,9	1.29	1 (12%)	10,11,11	0.90	1 (10%)
2	UTP	P	602	4	22,30,30	2.41	6 (27%)	27,47,47	1.26	3 (11%)
3	GLN	Q	603	-	8,9,9	1.15	1 (12%)	10,11,11	1.45	2 (20%)
5	ANP	F	604	4	29,33,33	1.82	6 (20%)	31,52,52	2.52	7 (22%)
5	ANP	P	605	4	29,33,33	1.82	6 (20%)	31,52,52	2.52	7 (22%)
3	GLN	F	602	-	8,9,9	1.30	1 (12%)	10,11,11	0.89	1 (10%)
2	UTP	F	601	4	22,30,30	2.38	6 (27%)	27,47,47	1.22	3 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	GLN	P	603	-	8,9,9	1.14	1 (12%)	10,11,11	1.45	2 (20%)
5	ANP	Q	605	4	29,33,33	1.82	6 (20%)	31,52,52	2.52	7 (22%)
2	UTP	O	601	4	22,30,30	2.38	6 (27%)	27,47,47	1.21	3 (11%)
2	UTP	Q	602	4	22,30,30	2.42	6 (27%)	27,47,47	1.26	3 (11%)
5	ANP	O	604	4	29,33,33	1.82	7 (24%)	31,52,52	2.52	7 (22%)

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	GLN	O	602	-	-	3/9/9/9	-
2	UTP	P	602	4	-	5/20/38/38	0/2/2/2
3	GLN	Q	603	-	-	2/9/9/9	-
5	ANP	F	604	4	-	4/14/38/38	0/3/3/3
5	ANP	P	605	4	-	4/14/38/38	0/3/3/3
3	GLN	F	602	-	-	3/9/9/9	-
2	UTP	F	601	4	-	6/20/38/38	0/2/2/2
3	GLN	P	603	-	-	2/9/9/9	-
5	ANP	Q	605	4	-	4/14/38/38	0/3/3/3
2	UTP	O	601	4	-	6/20/38/38	0/2/2/2
2	UTP	Q	602	4	-	5/20/38/38	0/2/2/2
5	ANP	O	604	4	-	4/14/38/38	0/3/3/3

All (53) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	601	UTP	C3'-C2'	-6.70	1.35	1.53
2	Q	602	UTP	C3'-C2'	-6.69	1.35	1.53
2	O	601	UTP	C3'-C2'	-6.66	1.35	1.53
2	P	602	UTP	C3'-C2'	-6.66	1.35	1.53
5	P	605	ANP	PB-N3B	5.73	1.78	1.63
5	O	604	ANP	PB-N3B	5.70	1.78	1.63
5	F	604	ANP	PB-N3B	5.69	1.78	1.63
5	Q	605	ANP	PB-N3B	5.69	1.78	1.63
2	Q	602	UTP	C2'-C1'	4.44	1.60	1.53
2	F	601	UTP	C2'-C1'	4.43	1.60	1.53

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	O	601	UTP	C2'-C1'	4.40	1.60	1.53
2	P	602	UTP	C2'-C1'	4.40	1.60	1.53
2	Q	602	UTP	O4'-C4'	4.09	1.54	1.45
2	F	601	UTP	O4'-C4'	4.06	1.54	1.45
2	O	601	UTP	O4'-C4'	4.06	1.54	1.45
2	P	602	UTP	O4'-C4'	4.06	1.54	1.45
5	O	604	ANP	PG-N3B	3.76	1.73	1.63
5	Q	605	ANP	PG-N3B	3.75	1.73	1.63
5	F	604	ANP	PG-N3B	3.74	1.73	1.63
5	P	605	ANP	PG-N3B	3.73	1.73	1.63
2	F	601	UTP	O4'-C1'	-3.42	1.36	1.41
2	O	601	UTP	O4'-C1'	-3.42	1.36	1.41
2	P	602	UTP	O4'-C1'	-3.42	1.36	1.41
2	Q	602	UTP	O4'-C1'	-3.39	1.36	1.41
3	F	602	GLN	OXT-C	-3.25	1.19	1.30
3	O	602	GLN	OXT-C	-3.24	1.19	1.30
2	F	601	UTP	C5'-C4'	-3.19	1.41	1.51
2	O	601	UTP	C5'-C4'	-3.19	1.41	1.51
2	P	602	UTP	C5'-C4'	-3.19	1.41	1.51
2	Q	602	UTP	C5'-C4'	-3.19	1.41	1.51
5	F	604	ANP	PB-O2B	-3.13	1.48	1.56
5	O	604	ANP	PB-O2B	-3.13	1.48	1.56
5	P	605	ANP	PB-O2B	-3.13	1.48	1.56
5	Q	605	ANP	PB-O2B	-3.13	1.48	1.56
5	F	604	ANP	PG-O2G	-3.03	1.48	1.56
5	P	605	ANP	PG-O2G	-3.03	1.48	1.56
5	Q	605	ANP	PG-O2G	-3.03	1.48	1.56
5	O	604	ANP	PG-O2G	-3.03	1.48	1.56
3	Q	603	GLN	OXT-C	-2.67	1.21	1.30
3	P	603	GLN	OXT-C	-2.64	1.21	1.30
2	P	602	UTP	PG-O2G	2.48	1.58	1.50
2	Q	602	UTP	PG-O2G	2.48	1.58	1.50
2	F	601	UTP	PB-O1B	-2.11	1.45	1.55
2	O	601	UTP	PB-O1B	-2.11	1.45	1.55
5	O	604	ANP	PG-O1G	2.10	1.49	1.46
5	F	604	ANP	PG-O1G	2.09	1.49	1.46
5	P	605	ANP	PG-O1G	2.09	1.49	1.46
5	Q	605	ANP	PG-O1G	2.09	1.49	1.46
5	F	604	ANP	PG-O3G	-2.08	1.51	1.56
5	O	604	ANP	PG-O3G	-2.06	1.51	1.56
5	Q	605	ANP	PG-O3G	-2.06	1.51	1.56
5	P	605	ANP	PG-O3G	-2.03	1.51	1.56

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	O	604	ANP	PB-O1B	2.00	1.49	1.46

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	Q	605	ANP	O1G-PG-N3B	-8.21	99.68	111.77
5	O	604	ANP	O1G-PG-N3B	-8.20	99.69	111.77
5	F	604	ANP	O1G-PG-N3B	-8.20	99.70	111.77
5	P	605	ANP	O1G-PG-N3B	-8.17	99.74	111.77
5	P	605	ANP	O1B-PB-N3B	-6.69	101.92	111.77
5	O	604	ANP	O1B-PB-N3B	-6.67	101.94	111.77
5	F	604	ANP	O1B-PB-N3B	-6.65	101.97	111.77
5	Q	605	ANP	O1B-PB-N3B	-6.65	101.97	111.77
5	Q	605	ANP	PB-O3A-PA	-3.86	119.04	132.62
5	P	605	ANP	PB-O3A-PA	-3.85	119.06	132.62
5	F	604	ANP	PB-O3A-PA	-3.85	119.06	132.62
5	O	604	ANP	PB-O3A-PA	-3.84	119.10	132.62
2	Q	602	UTP	PB-O3B-PG	-3.80	119.79	132.83
2	P	602	UTP	PB-O3B-PG	-3.79	119.83	132.83
2	F	601	UTP	PB-O3B-PG	-3.78	119.86	132.83
2	O	601	UTP	PB-O3B-PG	-3.78	119.86	132.83
5	F	604	ANP	N3-C2-N1	-3.55	123.14	128.68
5	Q	605	ANP	N3-C2-N1	-3.55	123.14	128.68
5	P	605	ANP	N3-C2-N1	-3.53	123.17	128.68
5	O	604	ANP	N3-C2-N1	-3.52	123.17	128.68
5	F	604	ANP	O4'-C1'-C2'	-3.33	102.06	106.93
5	P	605	ANP	O4'-C1'-C2'	-3.31	102.09	106.93
5	Q	605	ANP	O4'-C1'-C2'	-3.31	102.09	106.93
5	O	604	ANP	O4'-C1'-C2'	-3.29	102.12	106.93
3	P	603	GLN	OXT-C-CA	3.13	124.05	113.38
3	Q	603	GLN	OXT-C-CA	3.13	124.04	113.38
5	O	604	ANP	O2G-PG-O3G	2.88	115.31	107.64
5	F	604	ANP	O2G-PG-O3G	2.87	115.28	107.64
5	Q	605	ANP	O2G-PG-O3G	2.87	115.27	107.64
5	P	605	ANP	O2G-PG-O3G	2.86	115.26	107.64
2	F	601	UTP	C3'-C2'-C1'	2.82	105.23	100.98
2	Q	602	UTP	C3'-C2'-C1'	2.78	105.17	100.98
2	O	601	UTP	C3'-C2'-C1'	2.78	105.17	100.98
2	P	602	UTP	C3'-C2'-C1'	2.78	105.17	100.98
5	O	604	ANP	N6-C6-N1	2.48	123.72	118.57
5	F	604	ANP	N6-C6-N1	2.47	123.71	118.57
5	P	605	ANP	N6-C6-N1	2.47	123.71	118.57

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	Q	605	ANP	N6-C6-N1	2.46	123.67	118.57
2	Q	602	UTP	O3G-PG-O3B	2.21	112.05	104.64
2	P	602	UTP	O3G-PG-O3B	2.21	112.03	104.64
2	F	601	UTP	O3G-PG-O1G	2.11	115.72	107.64
2	O	601	UTP	O3G-PG-O1G	2.11	115.71	107.64
3	F	602	GLN	CB-CA-N	2.06	115.57	110.17
3	Q	603	GLN	CB-CA-N	2.05	115.54	110.17
3	P	603	GLN	CB-CA-N	2.05	115.53	110.17
3	O	602	GLN	CB-CA-N	2.04	115.52	110.17

There are no chirality outliers.

All (48) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	601	UTP	PB-O3B-PG-O3G
2	O	601	UTP	PB-O3B-PG-O3G
2	P	602	UTP	PB-O3B-PG-O1G
2	Q	602	UTP	PB-O3B-PG-O1G
3	F	602	GLN	C-CA-CB-CG
3	O	602	GLN	C-CA-CB-CG
3	P	603	GLN	C-CA-CB-CG
3	Q	603	GLN	C-CA-CB-CG
5	F	604	ANP	PB-N3B-PG-O1G
5	F	604	ANP	PG-N3B-PB-O1B
5	F	604	ANP	PA-O3A-PB-O1B
5	O	604	ANP	PB-N3B-PG-O1G
5	O	604	ANP	PG-N3B-PB-O1B
5	O	604	ANP	PA-O3A-PB-O1B
5	P	605	ANP	PB-N3B-PG-O1G
5	P	605	ANP	PG-N3B-PB-O1B
5	P	605	ANP	PA-O3A-PB-O1B
5	Q	605	ANP	PB-N3B-PG-O1G
5	Q	605	ANP	PG-N3B-PB-O1B
5	Q	605	ANP	PA-O3A-PB-O1B
3	F	602	GLN	CA-CB-CG-CD
3	O	602	GLN	CA-CB-CG-CD
3	P	603	GLN	CA-CB-CG-CD
3	Q	603	GLN	CA-CB-CG-CD
2	F	601	UTP	PA-O3A-PB-O2B
2	O	601	UTP	PA-O3A-PB-O2B
2	P	602	UTP	PA-O3A-PB-O1B
2	Q	602	UTP	PA-O3A-PB-O1B

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
2	F	601	UTP	PB-O3A-PA-O2A
2	O	601	UTP	PB-O3A-PA-O2A
2	P	602	UTP	PB-O3B-PG-O2G
2	Q	602	UTP	PB-O3B-PG-O2G
3	F	602	GLN	OXT-C-CA-N
3	O	602	GLN	OXT-C-CA-N
2	F	601	UTP	PB-O3B-PG-O1G
2	O	601	UTP	PB-O3B-PG-O1G
2	P	602	UTP	PB-O3B-PG-O3G
2	Q	602	UTP	PB-O3B-PG-O3G
2	F	601	UTP	PB-O3A-PA-O1A
2	O	601	UTP	PB-O3A-PA-O1A
2	P	602	UTP	PB-O3A-PA-O2A
2	Q	602	UTP	PB-O3A-PA-O2A
2	F	601	UTP	PB-O3B-PG-O2G
2	O	601	UTP	PB-O3B-PG-O2G
5	F	604	ANP	PG-N3B-PB-O3A
5	O	604	ANP	PG-N3B-PB-O3A
5	P	605	ANP	PG-N3B-PB-O3A
5	Q	605	ANP	PG-N3B-PB-O3A

There are no ring outliers.

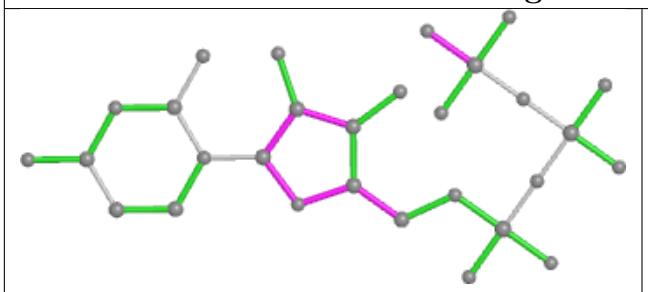
12 monomers are involved in 40 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	O	602	GLN	4	0
2	P	602	UTP	6	0
3	Q	603	GLN	4	0
5	F	604	ANP	1	0
5	P	605	ANP	1	0
3	F	602	GLN	4	0
2	F	601	UTP	6	0
3	P	603	GLN	4	0
5	Q	605	ANP	1	0
2	O	601	UTP	6	0
2	Q	602	UTP	6	0
5	O	604	ANP	1	0

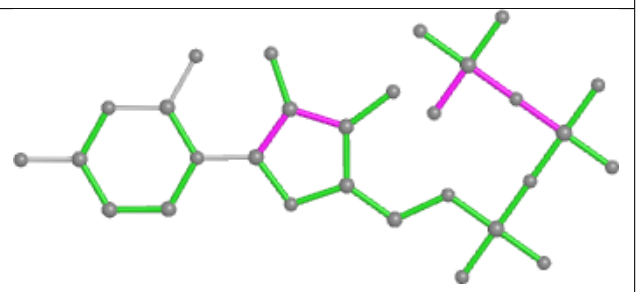
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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.

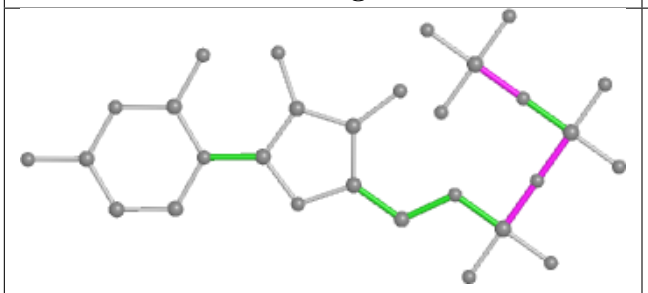
Ligand UTP P 602



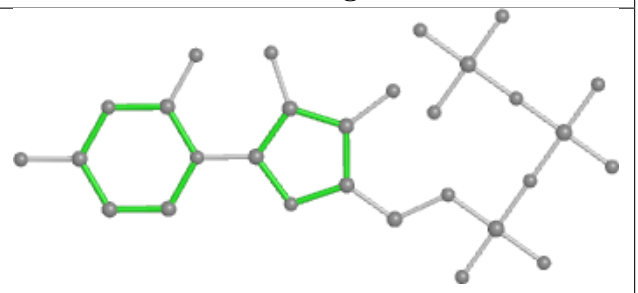
Bond lengths



Bond angles

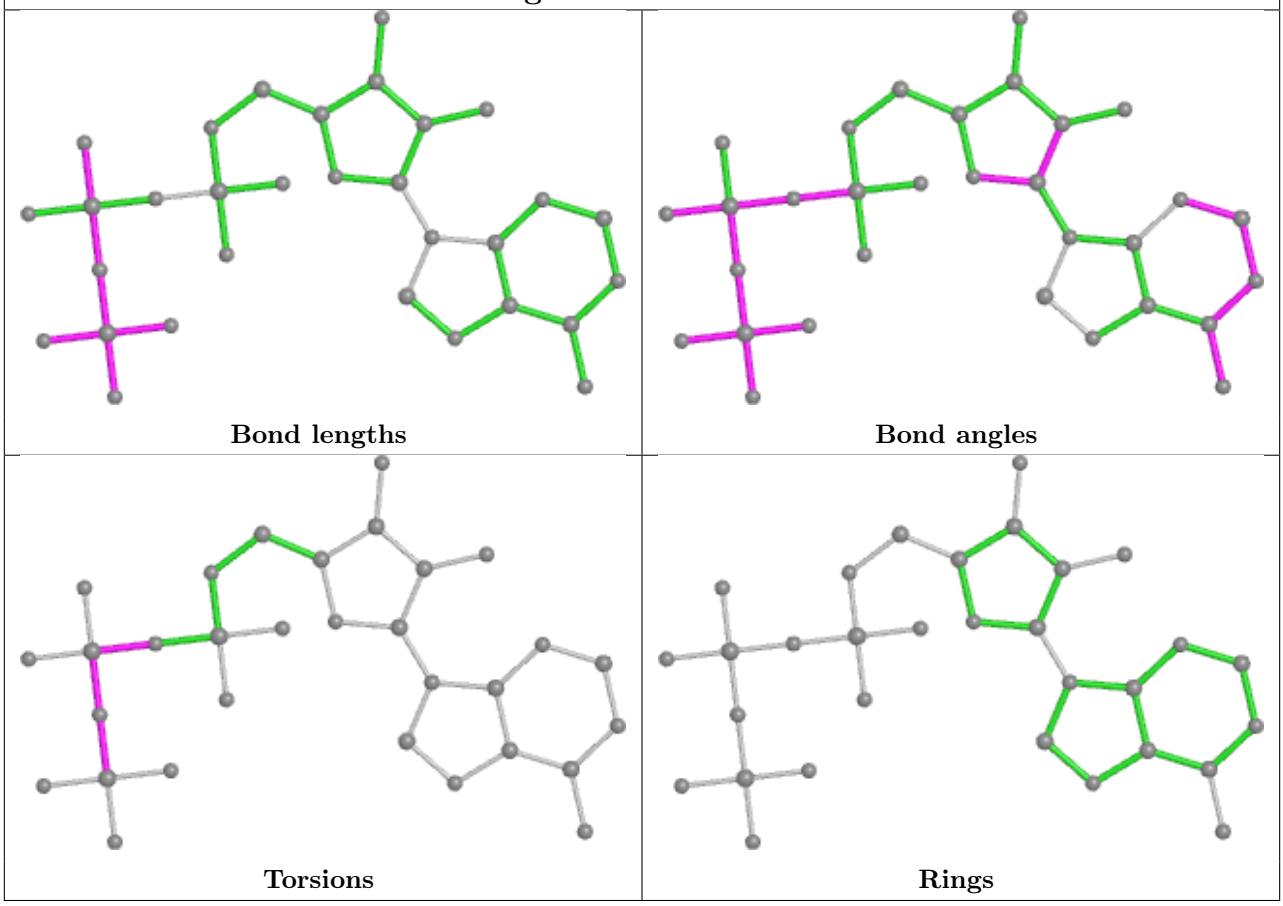


Torsions

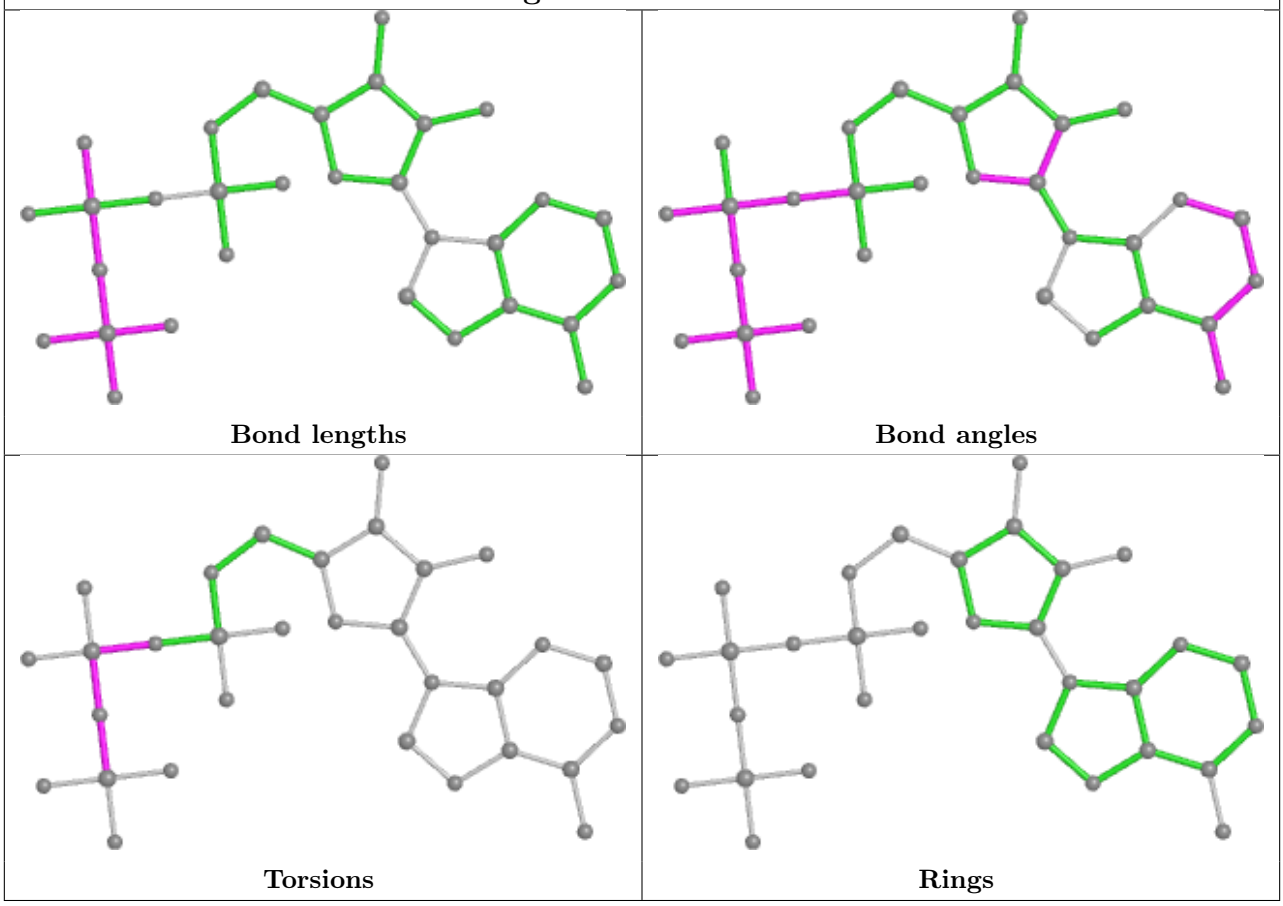


Rings

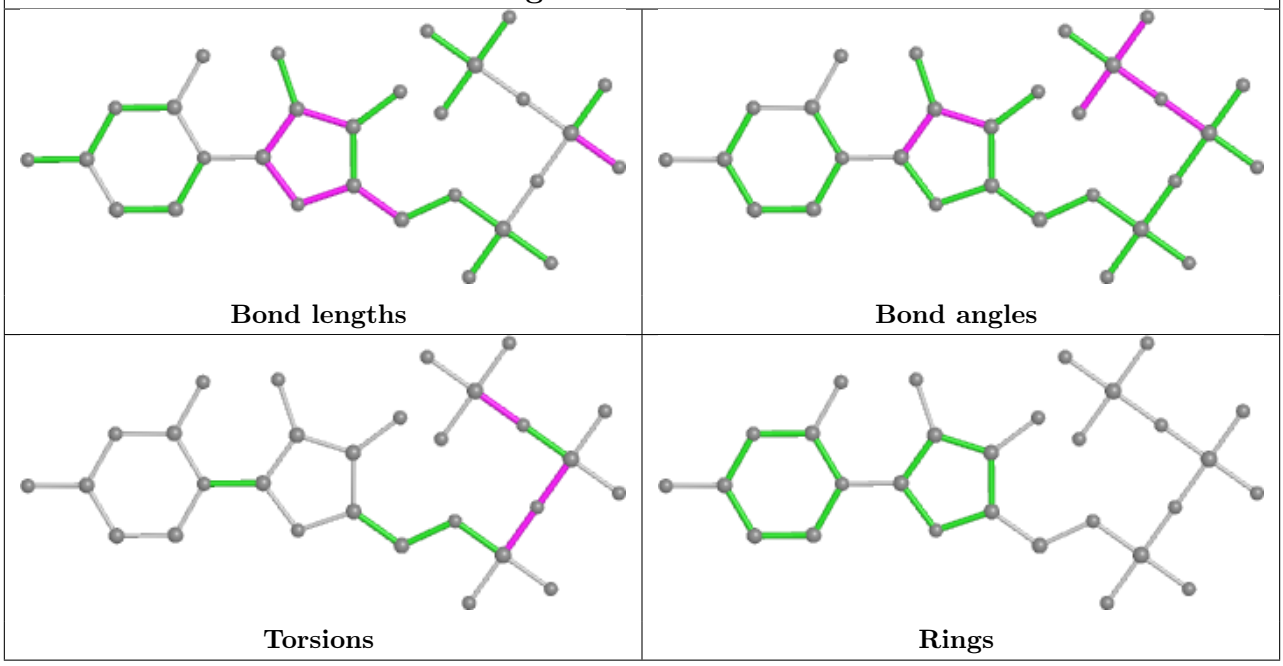
Ligand ANP F 604



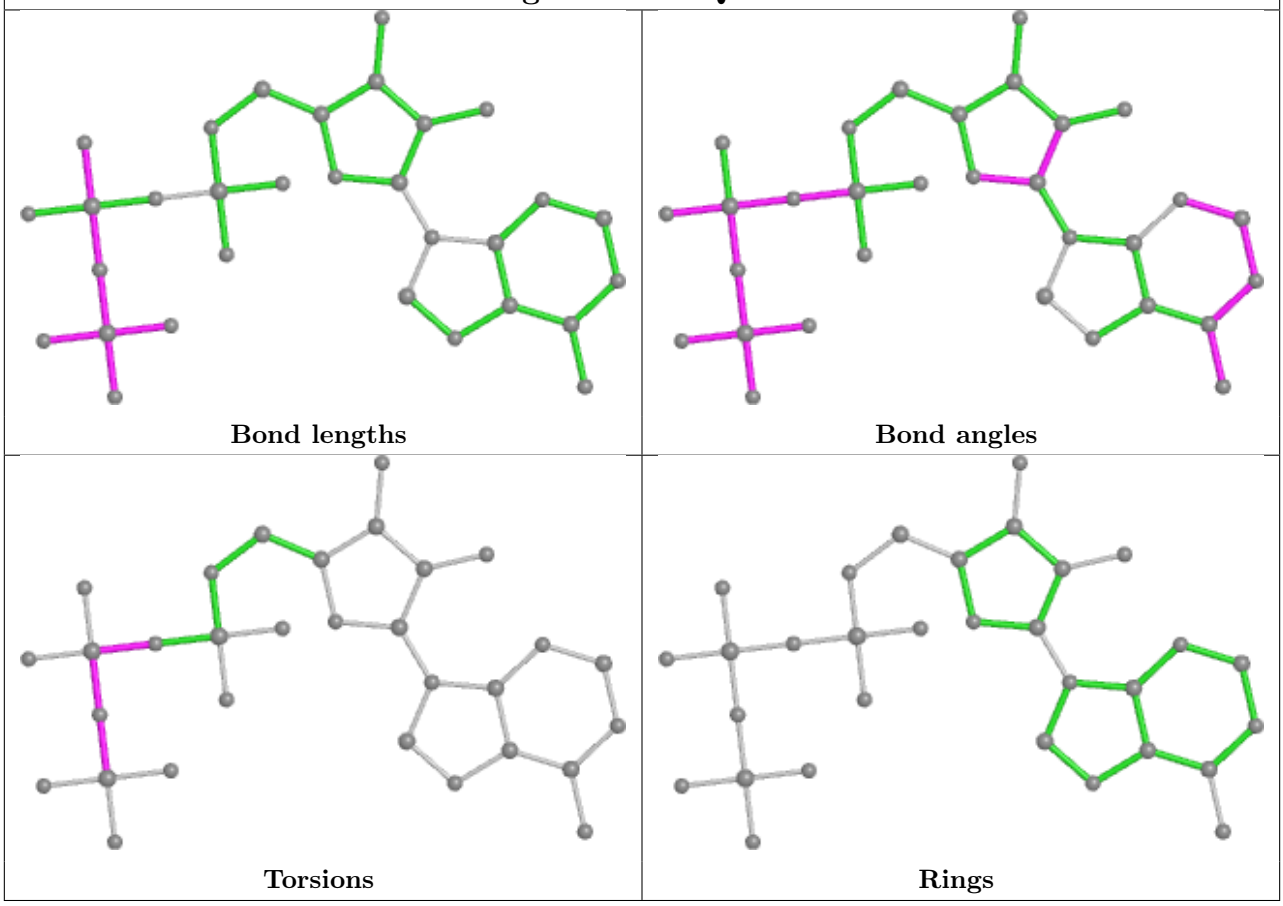
Ligand ANP P 605



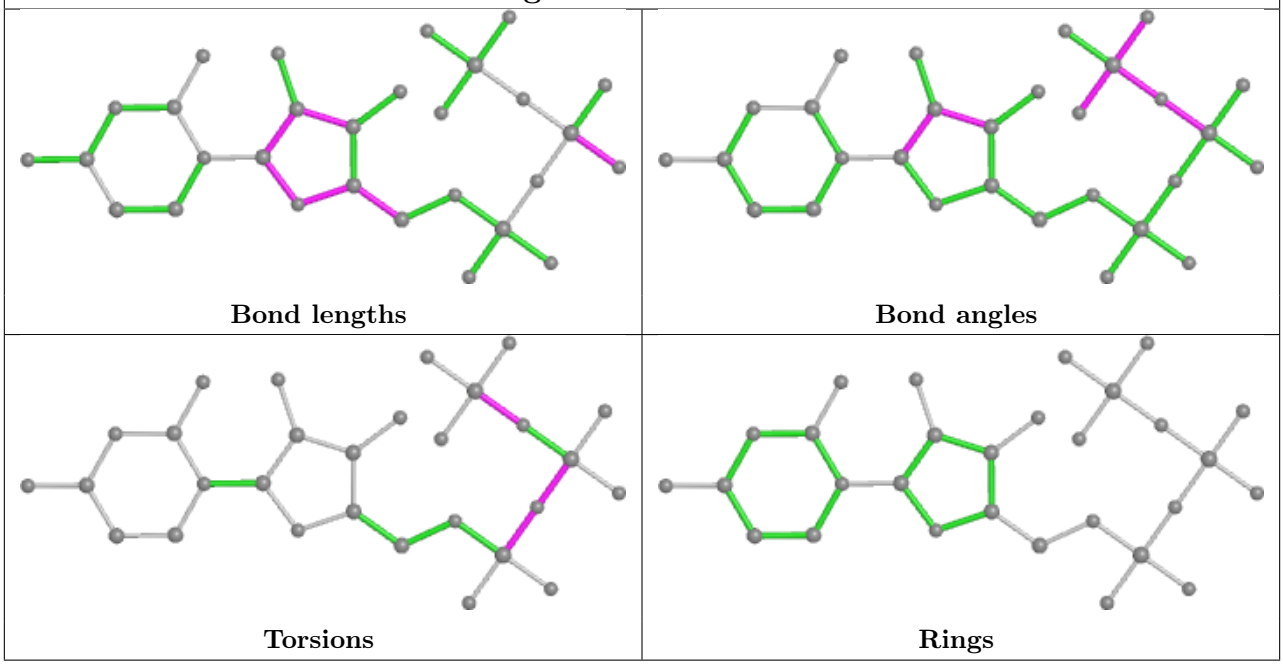
Ligand UTP F 601



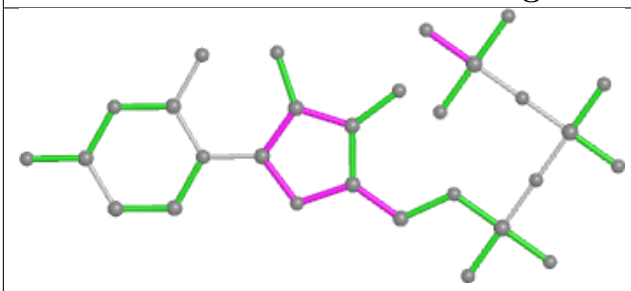
Ligand ANP Q 605



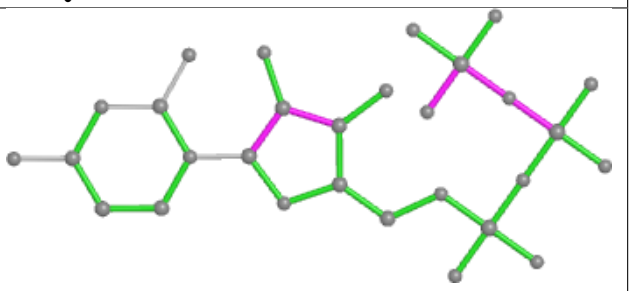
Ligand UTP O 601



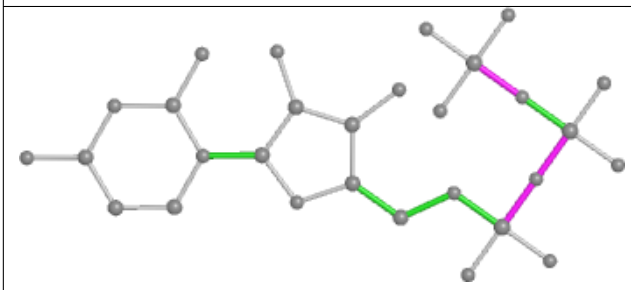
Ligand UTP Q 602



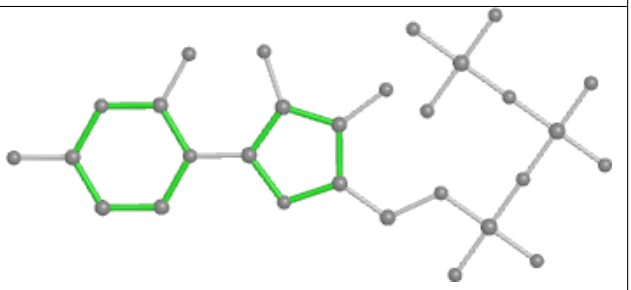
Bond lengths



Bond angles

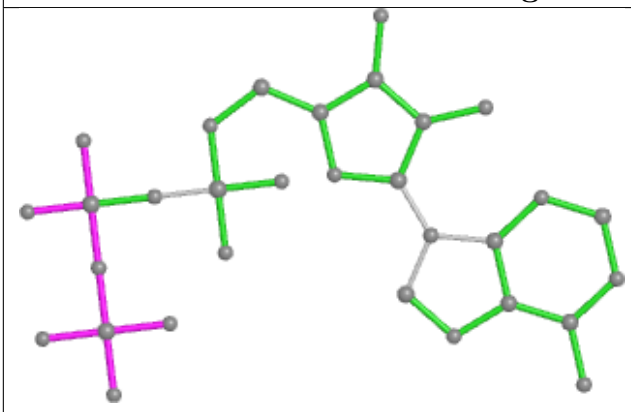


Torsions

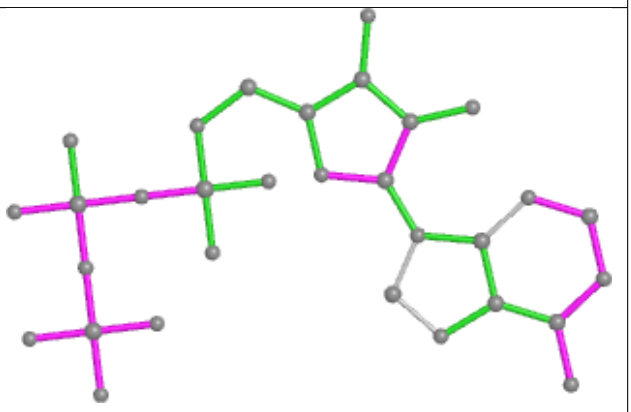


Rings

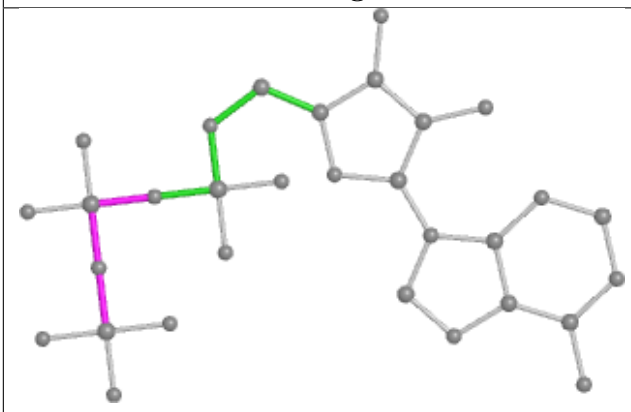
Ligand ANP O 604



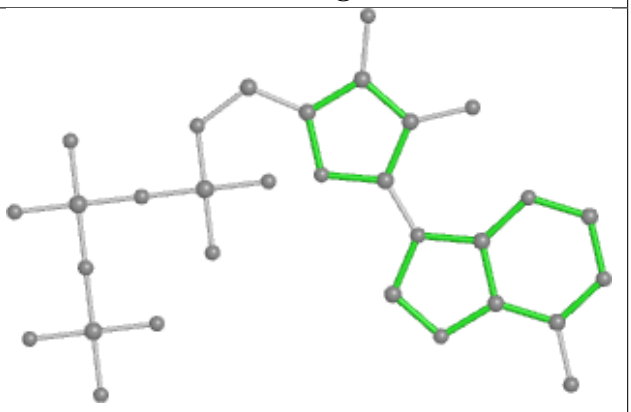
Bond lengths



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.

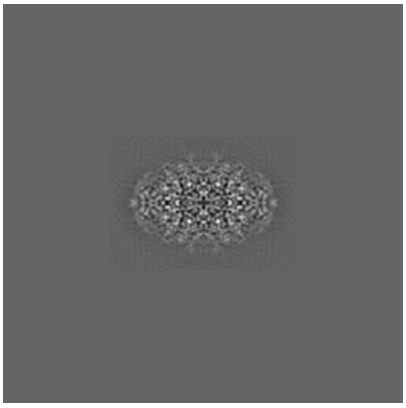
6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-23831. These allow visual inspection of the internal detail of the map and identification of artifacts.

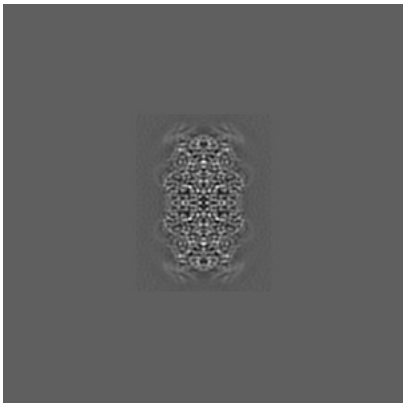
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

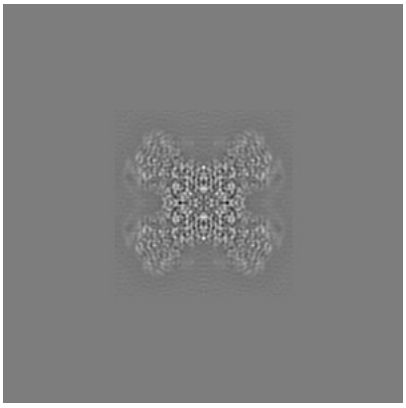
6.1.1 Primary map



X



Y

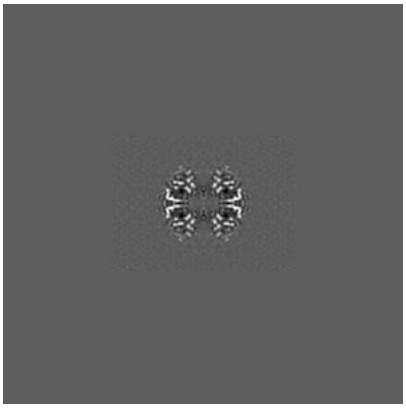


Z

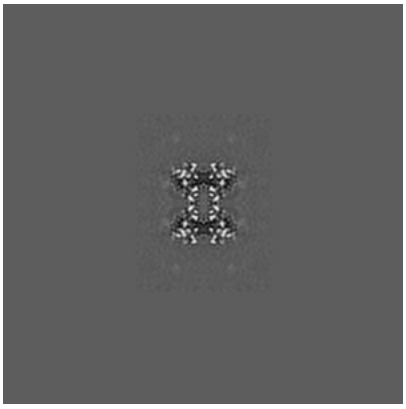
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

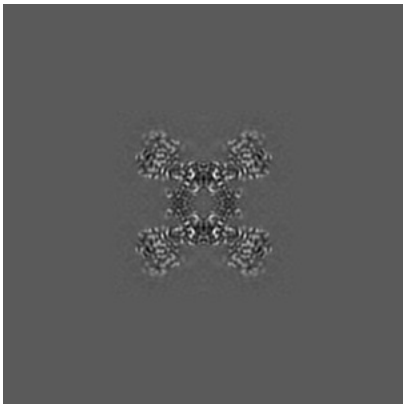
6.2.1 Primary map



X Index: 150



Y Index: 150

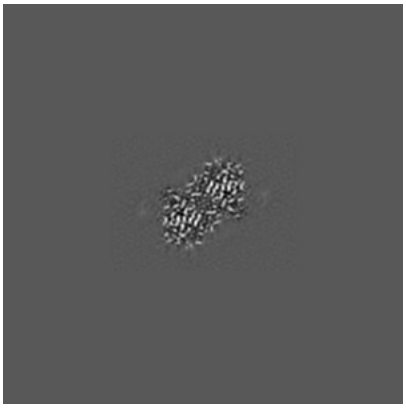


Z Index: 150

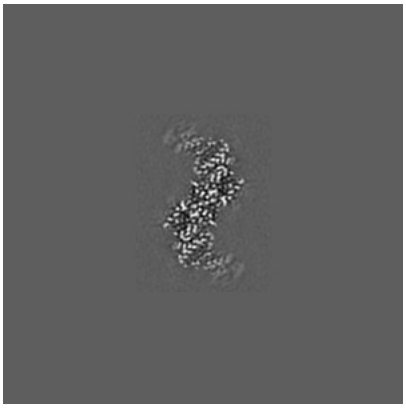
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

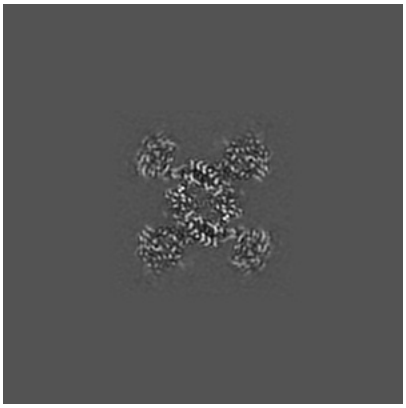
6.3.1 Primary map



X Index: 137



Y Index: 128

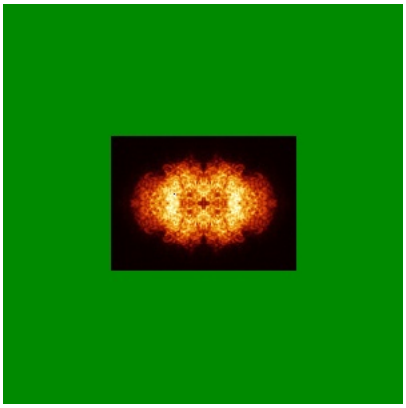


Z Index: 146

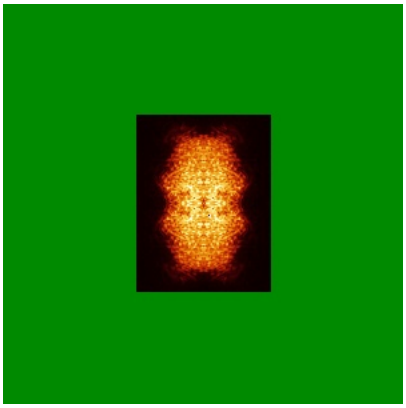
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

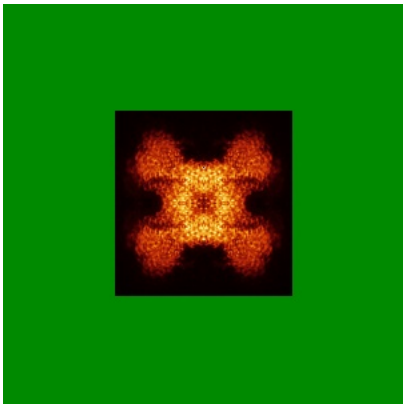
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

6.5.1 Primary map

X Y Z

The images above show the 3D surface view of the map at the recommended contour level 1.21. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

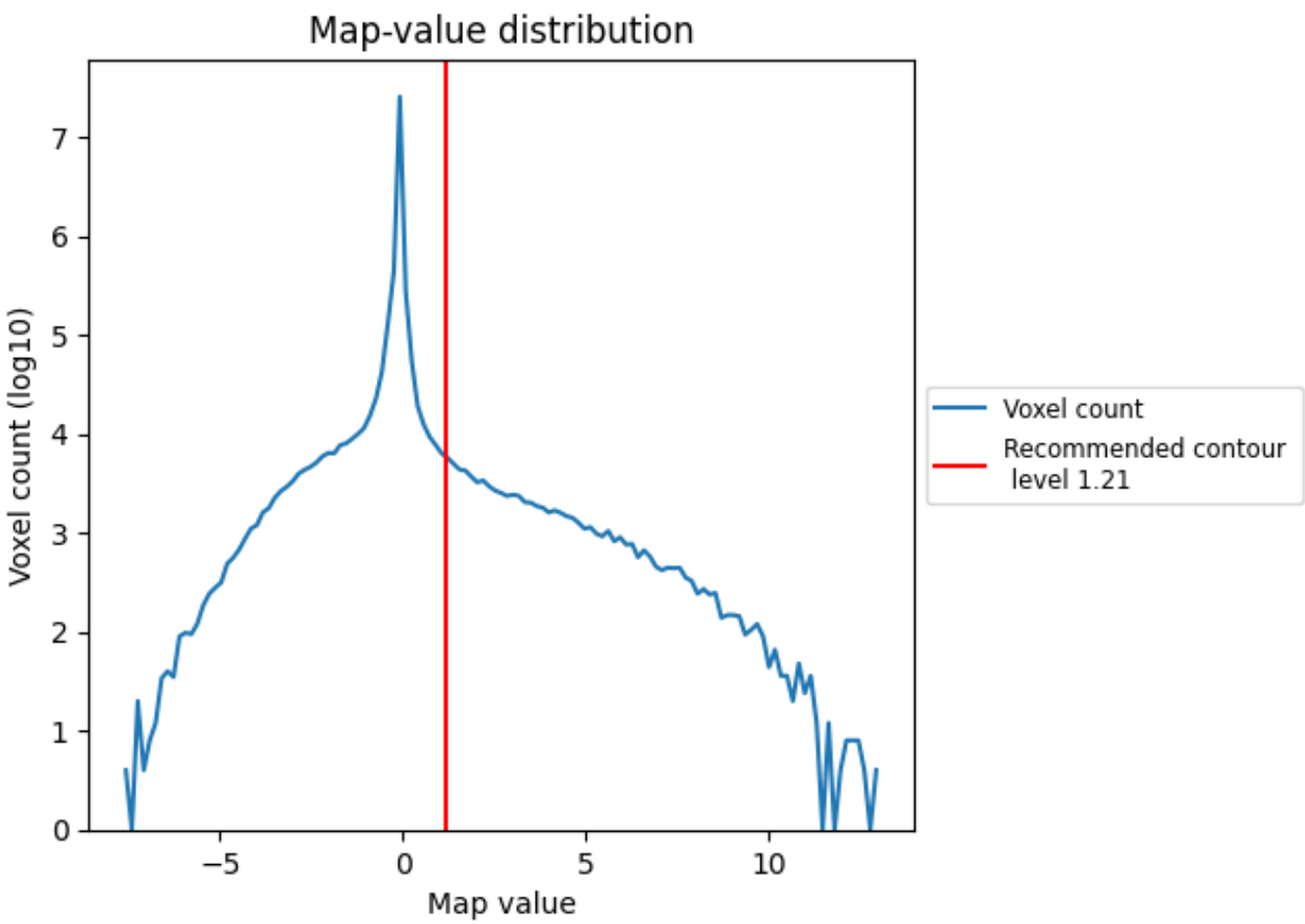
6.6 Mask visualisation (i)

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

7 Map analysis (i)

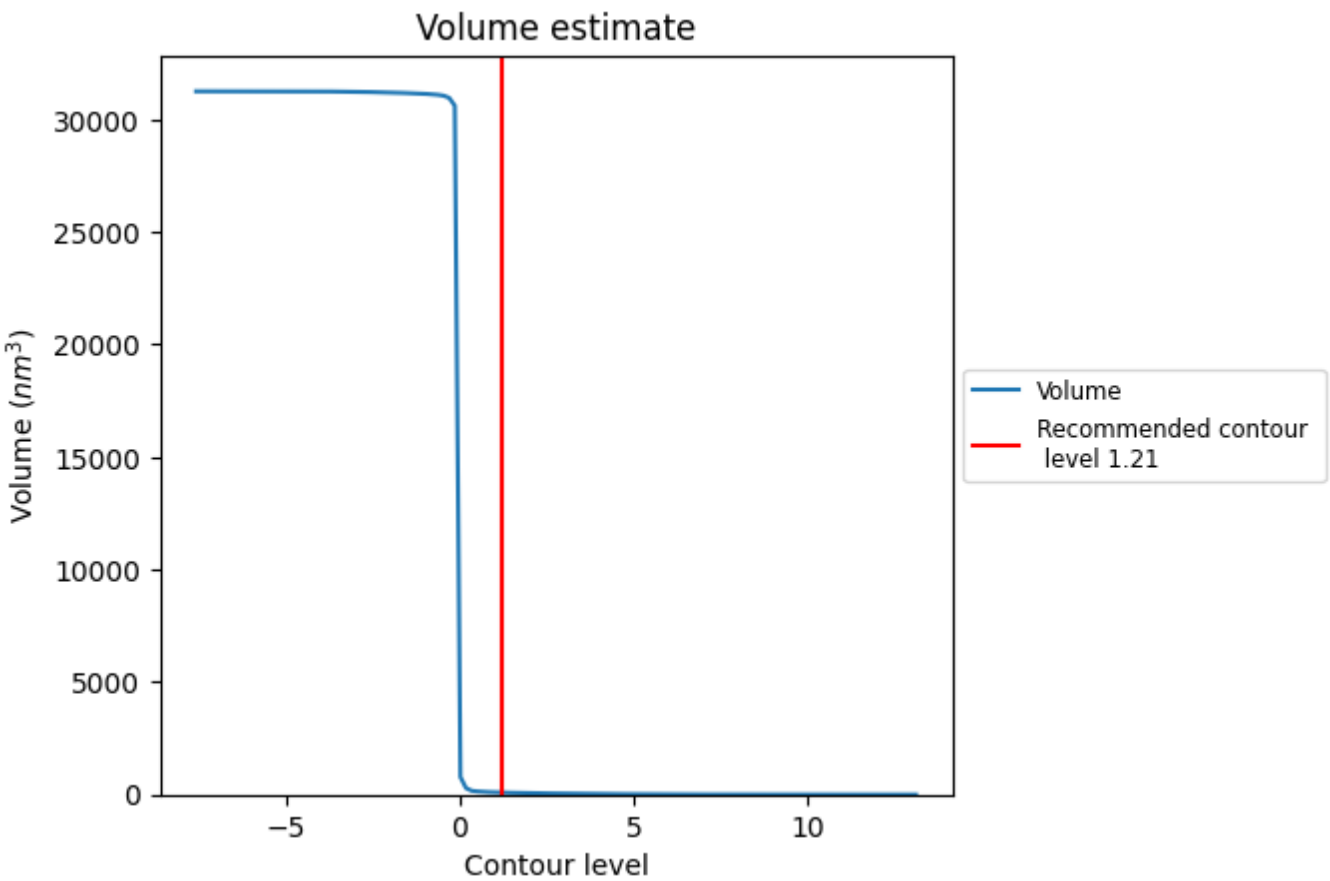
This section contains the results of statistical analysis of the map.

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.

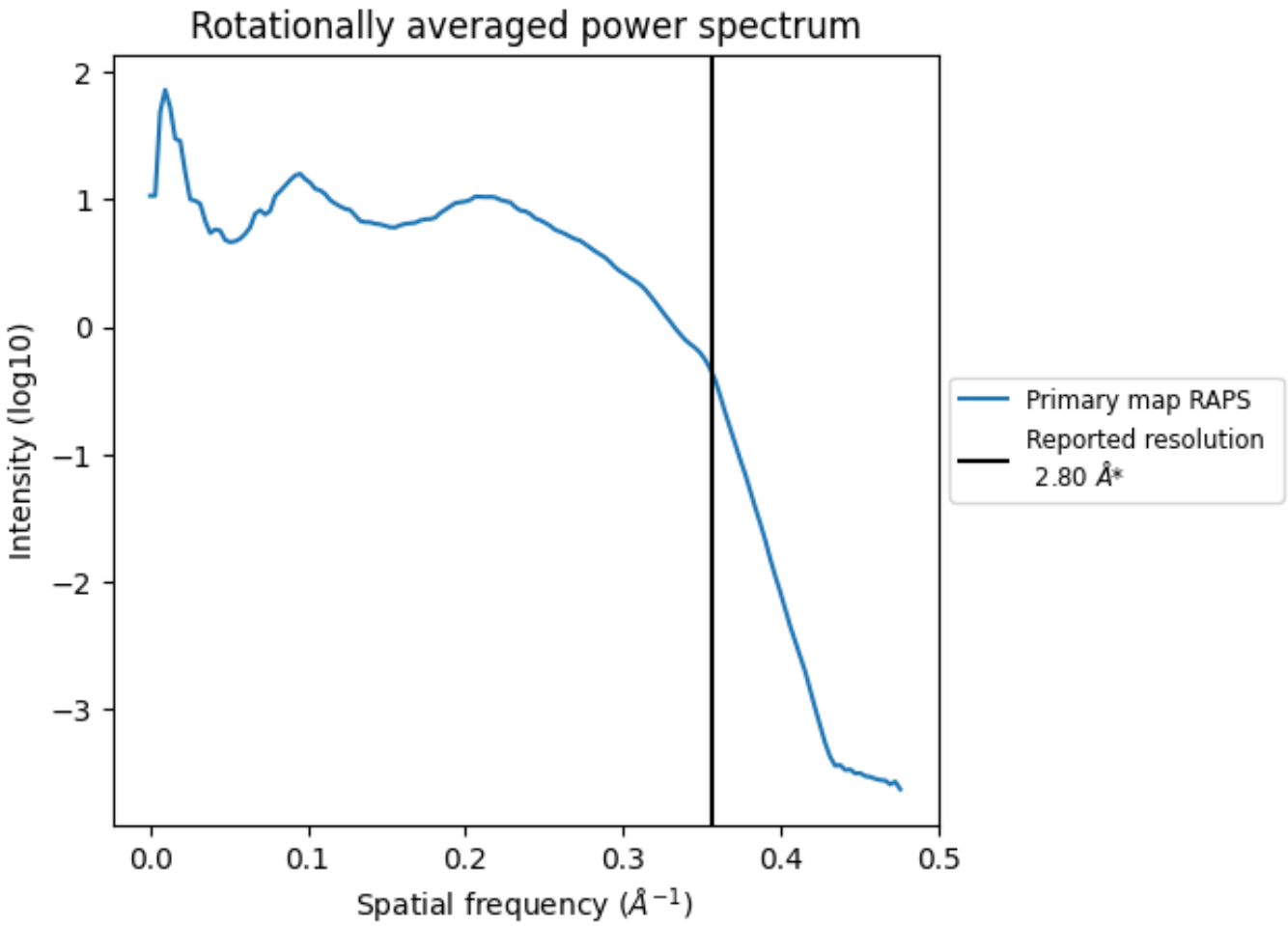
7.2 Volume estimate (i)



The volume at the recommended contour level is 91 nm^3; this corresponds to an approximate mass of 82 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)



*Reported resolution corresponds to spatial frequency of 0.357 Å^{-1}

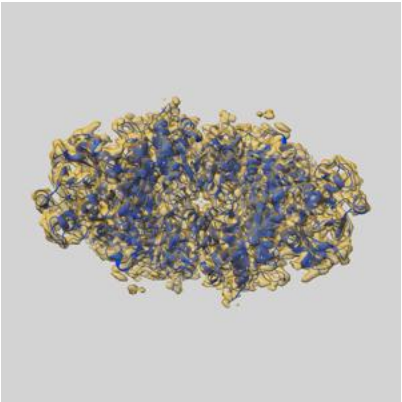
8 Fourier-Shell correlation (i)

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

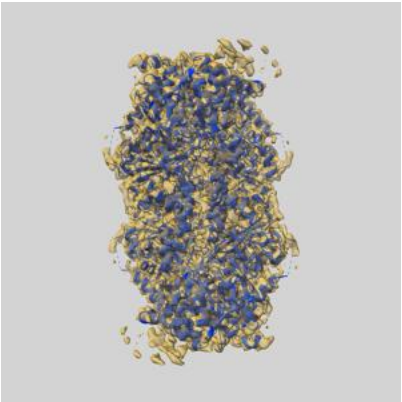
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-23831 and PDB model 7MGZ. Per-residue inclusion information can be found in section 3 on page 6.

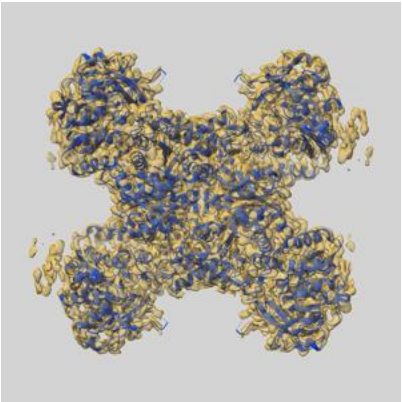
9.1 Map-model overlay (i)



X



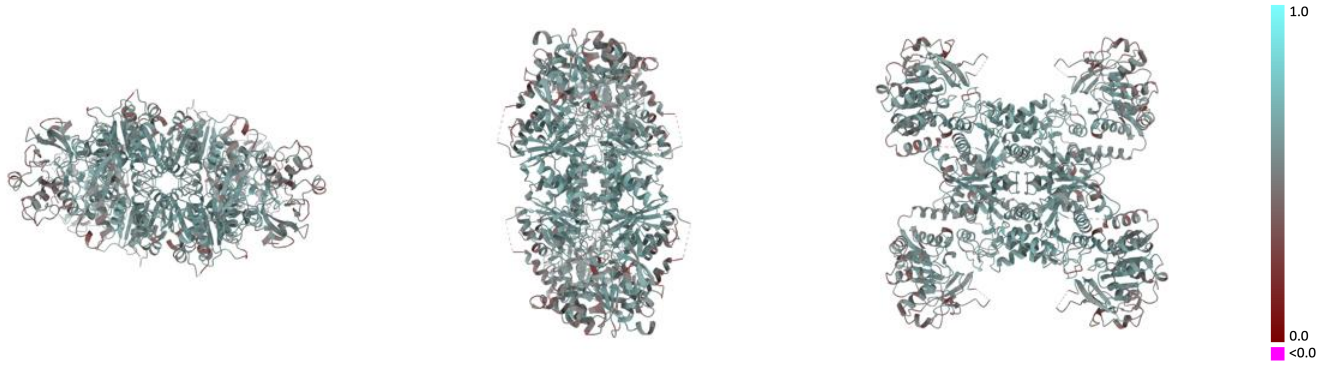
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 1.21 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.

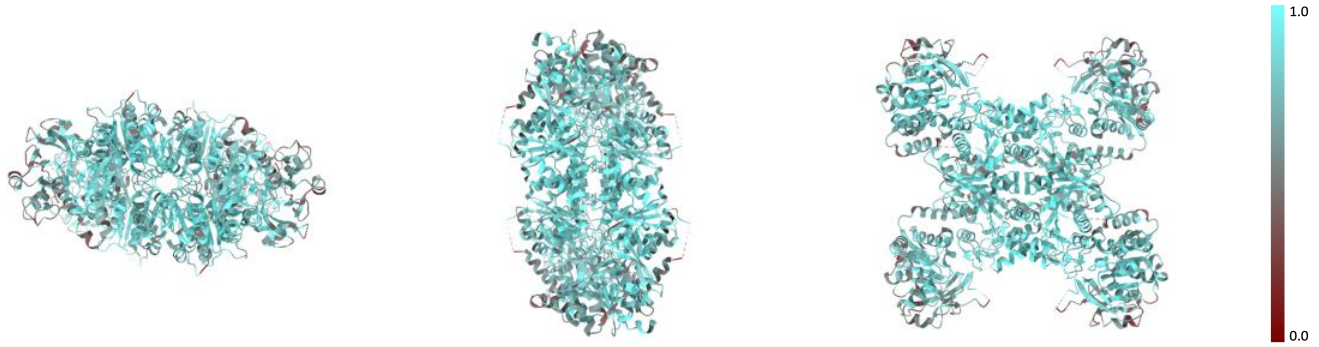
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

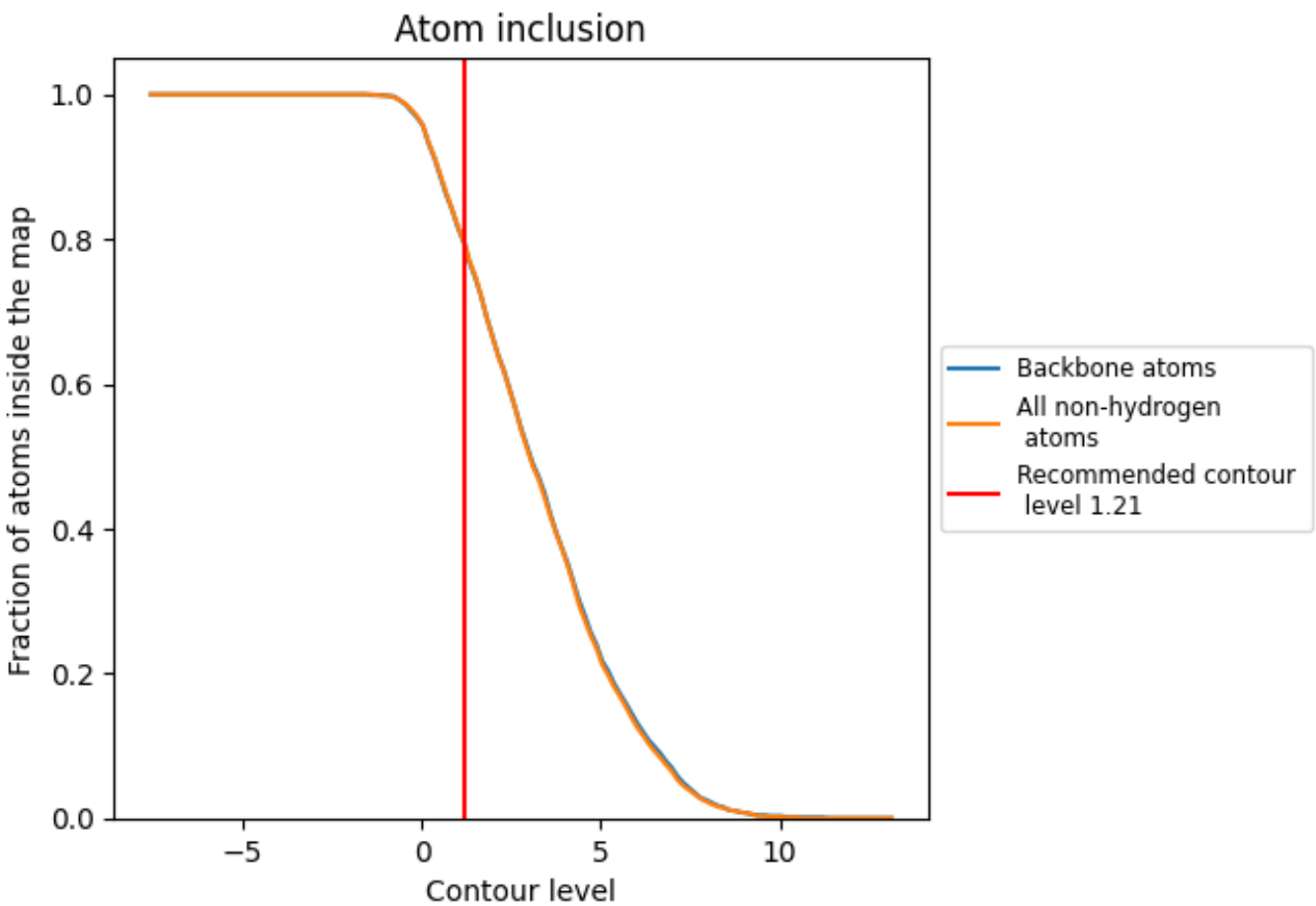
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (1.21).

9.4 Atom inclusion (i)



At the recommended contour level, 79% of all backbone atoms, 79% 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 (1.21) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7910	0.5500
F	0.7980	0.5490
O	0.7970	0.5510
P	0.7980	0.5500
Q	0.7960	0.5500