



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 04:08 PM UTC

PDB ID : 7RMC / pdb_00007rmc
EMDB ID : EMD-24560
Title : Yeast CTP Synthase (Ura7) filament bound to CTP at low pH
Authors : Hansen, J.M.; Lynch, E.M.; Farrell, D.P.; DiMaio, F.; Quispe, J.; Kollman, J.M.
Deposited on : 2021-07-27
Resolution : 3.50 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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

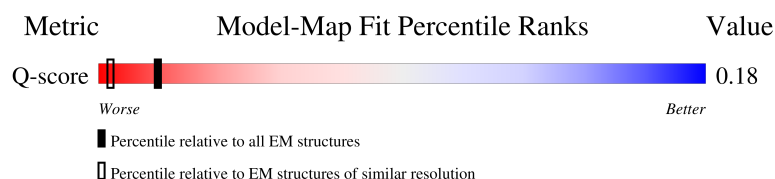
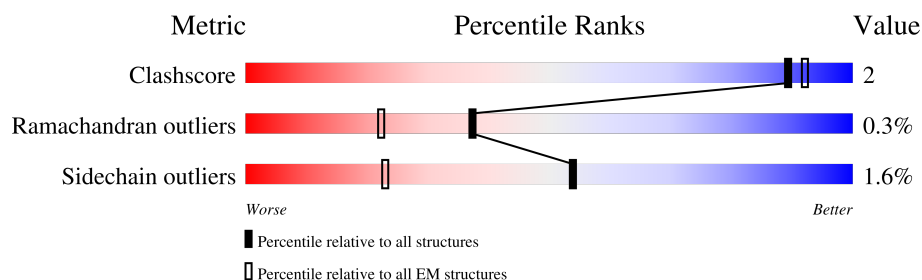
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13950 (3.00 - 4.00)

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 $\leq 5\%$. 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	D	561	100% 95% 5%
1	E	561	82% 95% 5%
1	F	561	82% 94% 6%
1	Q	561	84% 94% 6%

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Mol	Chain	Length	Quality of chain
1	R	561	 15% 93% 6%
1	S	561	 100% 94% 6%
1	T	561	 15% 94% 6%
1	U	561	 100% 94% 6%
1	V	561	 100% 94% 6%
1	W	561	 15% 93% 6%
1	g	561	 81% 93% 6%
1	h	561	 15% 93% 6%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 106824 atoms, of which 53244 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
1	V	561	Total	C	H	N	O	S	0	0
			8844	2804	4437	746	833	24		
1	D	561	Total	C	H	N	O	S	0	0
			8844	2804	4437	746	833	24		
1	E	561	Total	C	H	N	O	S	0	0
			8844	2804	4437	746	833	24		
1	F	561	Total	C	H	N	O	S	0	0
			8844	2804	4437	746	833	24		
1	g	561	Total	C	H	N	O	S	0	0
			8844	2804	4437	746	833	24		
1	Q	561	Total	C	H	N	O	S	0	0
			8844	2804	4437	746	833	24		
1	S	561	Total	C	H	N	O	S	0	0
			8844	2804	4437	746	833	24		
1	U	561	Total	C	H	N	O	S	0	0
			8844	2804	4437	746	833	24		
1	h	561	Total	C	H	N	O	S	0	0
			8844	2804	4437	746	833	24		
1	R	561	Total	C	H	N	O	S	0	0
			8844	2804	4437	746	833	24		
1	T	561	Total	C	H	N	O	S	0	0
			8844	2804	4437	746	833	24		
1	W	561	Total	C	H	N	O	S	0	0
			8844	2804	4437	746	833	24		

There are 132 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	?	-	PRO	deletion	UNP P28274
V	?	-	GLU	deletion	UNP P28274
V	?	-	ILE	deletion	UNP P28274
V	?	-	ASP	deletion	UNP P28274
V	?	-	LYS	deletion	UNP P28274
V	?	-	GLU	deletion	UNP P28274

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Chain	Residue	Modelled	Actual	Comment	Reference
V	?	-	THR	deletion	UNP P28274
V	?	-	MET	deletion	UNP P28274
V	?	-	GLY	deletion	UNP P28274
V	?	-	GLY	deletion	UNP P28274
V	?	-	SER	deletion	UNP P28274
D	?	-	PRO	deletion	UNP P28274
D	?	-	GLU	deletion	UNP P28274
D	?	-	ILE	deletion	UNP P28274
D	?	-	ASP	deletion	UNP P28274
D	?	-	LYS	deletion	UNP P28274
D	?	-	GLU	deletion	UNP P28274
D	?	-	THR	deletion	UNP P28274
D	?	-	MET	deletion	UNP P28274
D	?	-	GLY	deletion	UNP P28274
D	?	-	GLY	deletion	UNP P28274
D	?	-	SER	deletion	UNP P28274
E	?	-	PRO	deletion	UNP P28274
E	?	-	GLU	deletion	UNP P28274
E	?	-	ILE	deletion	UNP P28274
E	?	-	ASP	deletion	UNP P28274
E	?	-	LYS	deletion	UNP P28274
E	?	-	GLU	deletion	UNP P28274
E	?	-	THR	deletion	UNP P28274
E	?	-	MET	deletion	UNP P28274
E	?	-	GLY	deletion	UNP P28274
E	?	-	GLY	deletion	UNP P28274
E	?	-	SER	deletion	UNP P28274
F	?	-	PRO	deletion	UNP P28274
F	?	-	GLU	deletion	UNP P28274
F	?	-	ILE	deletion	UNP P28274
F	?	-	ASP	deletion	UNP P28274
F	?	-	LYS	deletion	UNP P28274
F	?	-	GLU	deletion	UNP P28274
F	?	-	THR	deletion	UNP P28274
F	?	-	MET	deletion	UNP P28274
F	?	-	GLY	deletion	UNP P28274
F	?	-	GLY	deletion	UNP P28274
F	?	-	SER	deletion	UNP P28274
g	?	-	PRO	deletion	UNP P28274
g	?	-	GLU	deletion	UNP P28274
g	?	-	ILE	deletion	UNP P28274
g	?	-	ASP	deletion	UNP P28274

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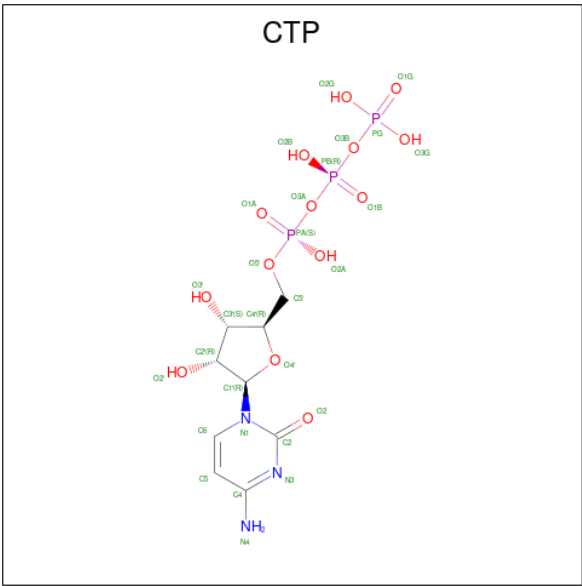
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g	?	-	GLU	deletion	UNP P28274
g	?	-	THR	deletion	UNP P28274
g	?	-	MET	deletion	UNP P28274
g	?	-	GLY	deletion	UNP P28274
g	?	-	GLY	deletion	UNP P28274
g	?	-	SER	deletion	UNP P28274
Q	?	-	PRO	deletion	UNP P28274
Q	?	-	GLU	deletion	UNP P28274
Q	?	-	ILE	deletion	UNP P28274
Q	?	-	ASP	deletion	UNP P28274
Q	?	-	LYS	deletion	UNP P28274
Q	?	-	GLU	deletion	UNP P28274
Q	?	-	THR	deletion	UNP P28274
Q	?	-	MET	deletion	UNP P28274
Q	?	-	GLY	deletion	UNP P28274
Q	?	-	GLY	deletion	UNP P28274
Q	?	-	SER	deletion	UNP P28274
S	?	-	PRO	deletion	UNP P28274
S	?	-	GLU	deletion	UNP P28274
S	?	-	ILE	deletion	UNP P28274
S	?	-	ASP	deletion	UNP P28274
S	?	-	LYS	deletion	UNP P28274
S	?	-	GLU	deletion	UNP P28274
S	?	-	THR	deletion	UNP P28274
S	?	-	MET	deletion	UNP P28274
S	?	-	GLY	deletion	UNP P28274
S	?	-	GLY	deletion	UNP P28274
S	?	-	SER	deletion	UNP P28274
U	?	-	PRO	deletion	UNP P28274
U	?	-	GLU	deletion	UNP P28274
U	?	-	ILE	deletion	UNP P28274
U	?	-	ASP	deletion	UNP P28274
U	?	-	LYS	deletion	UNP P28274
U	?	-	GLU	deletion	UNP P28274
U	?	-	THR	deletion	UNP P28274
U	?	-	MET	deletion	UNP P28274
U	?	-	GLY	deletion	UNP P28274
U	?	-	GLY	deletion	UNP P28274
U	?	-	SER	deletion	UNP P28274
h	?	-	PRO	deletion	UNP P28274
h	?	-	GLU	deletion	UNP P28274

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Chain	Residue	Modelled	Actual	Comment	Reference
h	?	-	ILE	deletion	UNP P28274
h	?	-	ASP	deletion	UNP P28274
h	?	-	LYS	deletion	UNP P28274
h	?	-	GLU	deletion	UNP P28274
h	?	-	THR	deletion	UNP P28274
h	?	-	MET	deletion	UNP P28274
h	?	-	GLY	deletion	UNP P28274
h	?	-	GLY	deletion	UNP P28274
h	?	-	SER	deletion	UNP P28274
R	?	-	PRO	deletion	UNP P28274
R	?	-	GLU	deletion	UNP P28274
R	?	-	ILE	deletion	UNP P28274
R	?	-	ASP	deletion	UNP P28274
R	?	-	LYS	deletion	UNP P28274
R	?	-	GLU	deletion	UNP P28274
R	?	-	THR	deletion	UNP P28274
R	?	-	MET	deletion	UNP P28274
R	?	-	GLY	deletion	UNP P28274
R	?	-	GLY	deletion	UNP P28274
R	?	-	SER	deletion	UNP P28274
T	?	-	PRO	deletion	UNP P28274
T	?	-	GLU	deletion	UNP P28274
T	?	-	ILE	deletion	UNP P28274
T	?	-	ASP	deletion	UNP P28274
T	?	-	LYS	deletion	UNP P28274
T	?	-	GLU	deletion	UNP P28274
T	?	-	THR	deletion	UNP P28274
T	?	-	MET	deletion	UNP P28274
T	?	-	GLY	deletion	UNP P28274
T	?	-	GLY	deletion	UNP P28274
T	?	-	SER	deletion	UNP P28274
W	?	-	PRO	deletion	UNP P28274
W	?	-	GLU	deletion	UNP P28274
W	?	-	ILE	deletion	UNP P28274
W	?	-	ASP	deletion	UNP P28274
W	?	-	LYS	deletion	UNP P28274
W	?	-	GLU	deletion	UNP P28274
W	?	-	THR	deletion	UNP P28274
W	?	-	MET	deletion	UNP P28274
W	?	-	GLY	deletion	UNP P28274
W	?	-	GLY	deletion	UNP P28274
W	?	-	SER	deletion	UNP P28274

- Molecule 2 is CYTIDINE-5'-TRIPHOSPHATE (CCD ID: CTP) (formula: C₉H₁₆N₃O₁₄P₃).



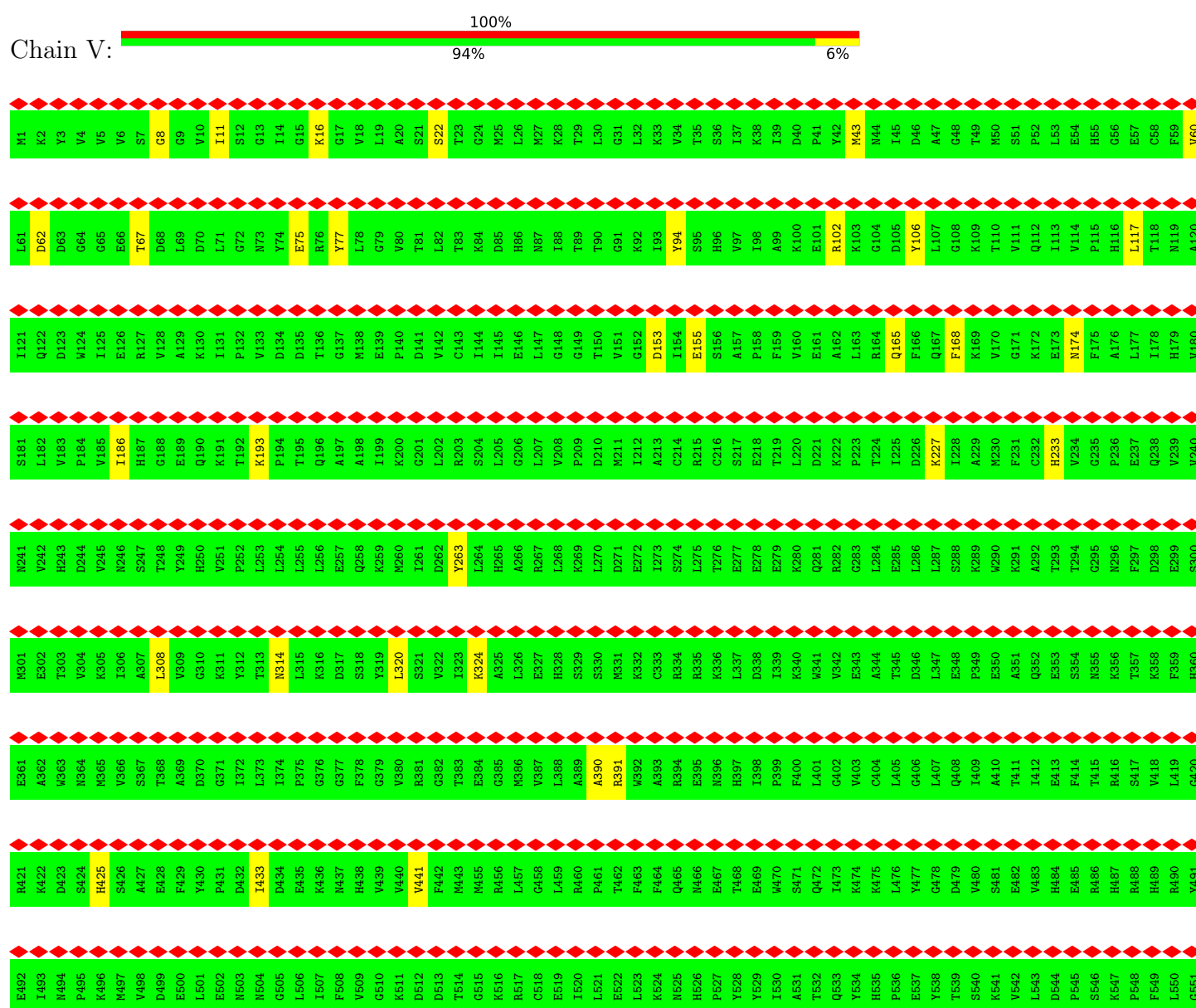
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Mol	Chain	Residues	Atoms					AltConf
2	S	1	Total 29	C 9	N 3	O 14	P 3	0
2	U	1	Total 29	C 9	N 3	O 14	P 3	0
2	U	1	Total 29	C 9	N 3	O 14	P 3	0
2	h	1	Total 29	C 9	N 3	O 14	P 3	0
2	h	1	Total 29	C 9	N 3	O 14	P 3	0
2	R	1	Total 29	C 9	N 3	O 14	P 3	0
2	R	1	Total 29	C 9	N 3	O 14	P 3	0
2	T	1	Total 29	C 9	N 3	O 14	P 3	0
2	T	1	Total 29	C 9	N 3	O 14	P 3	0
2	W	1	Total 29	C 9	N 3	O 14	P 3	0
2	W	1	Total 29	C 9	N 3	O 14	P 3	0

3 Residue-property plots

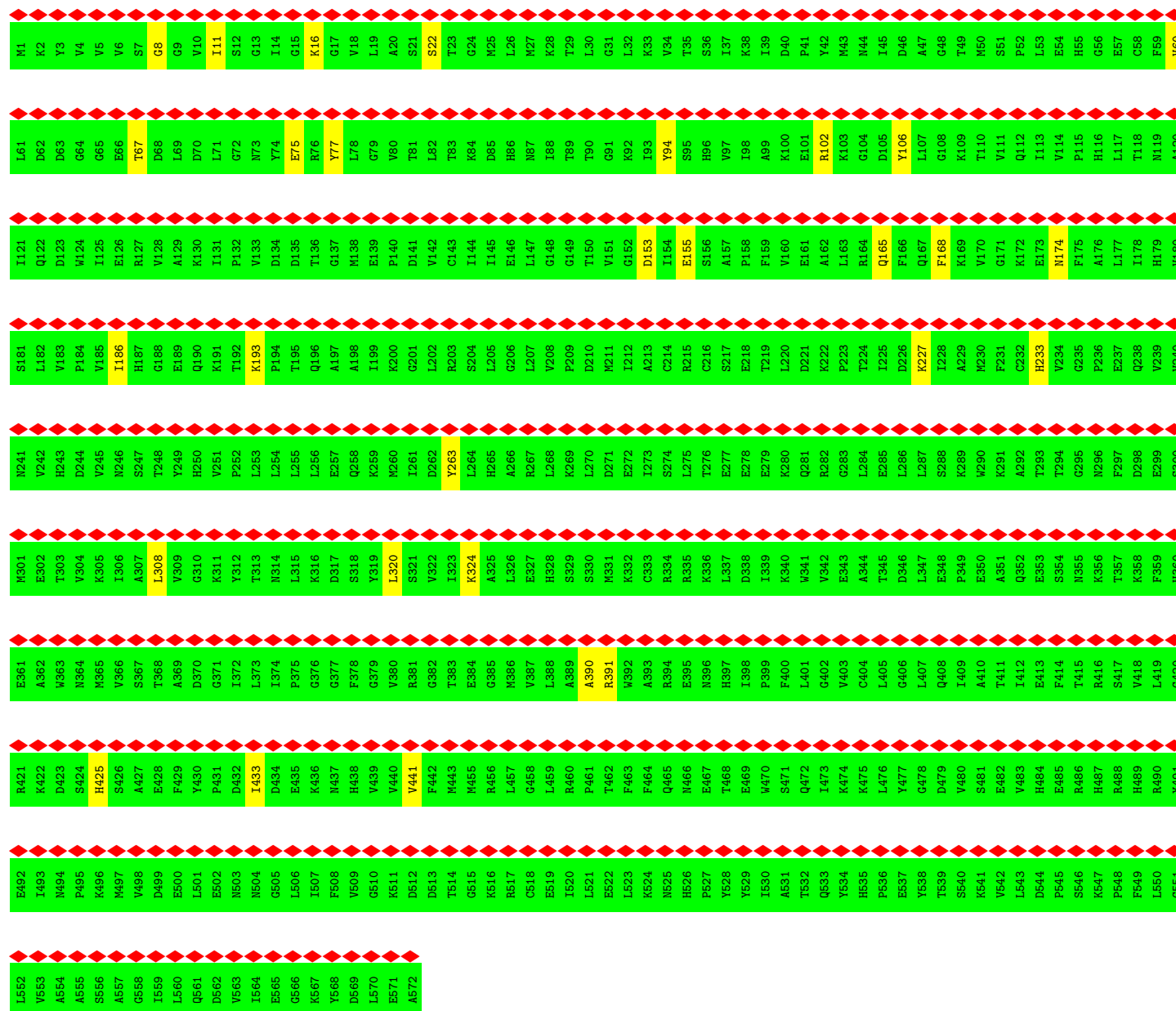
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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

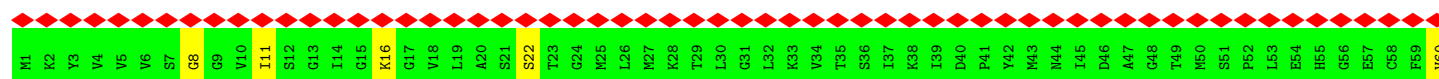
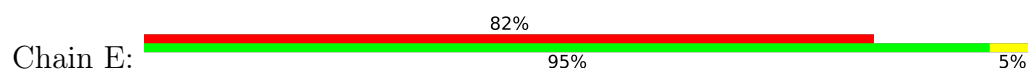


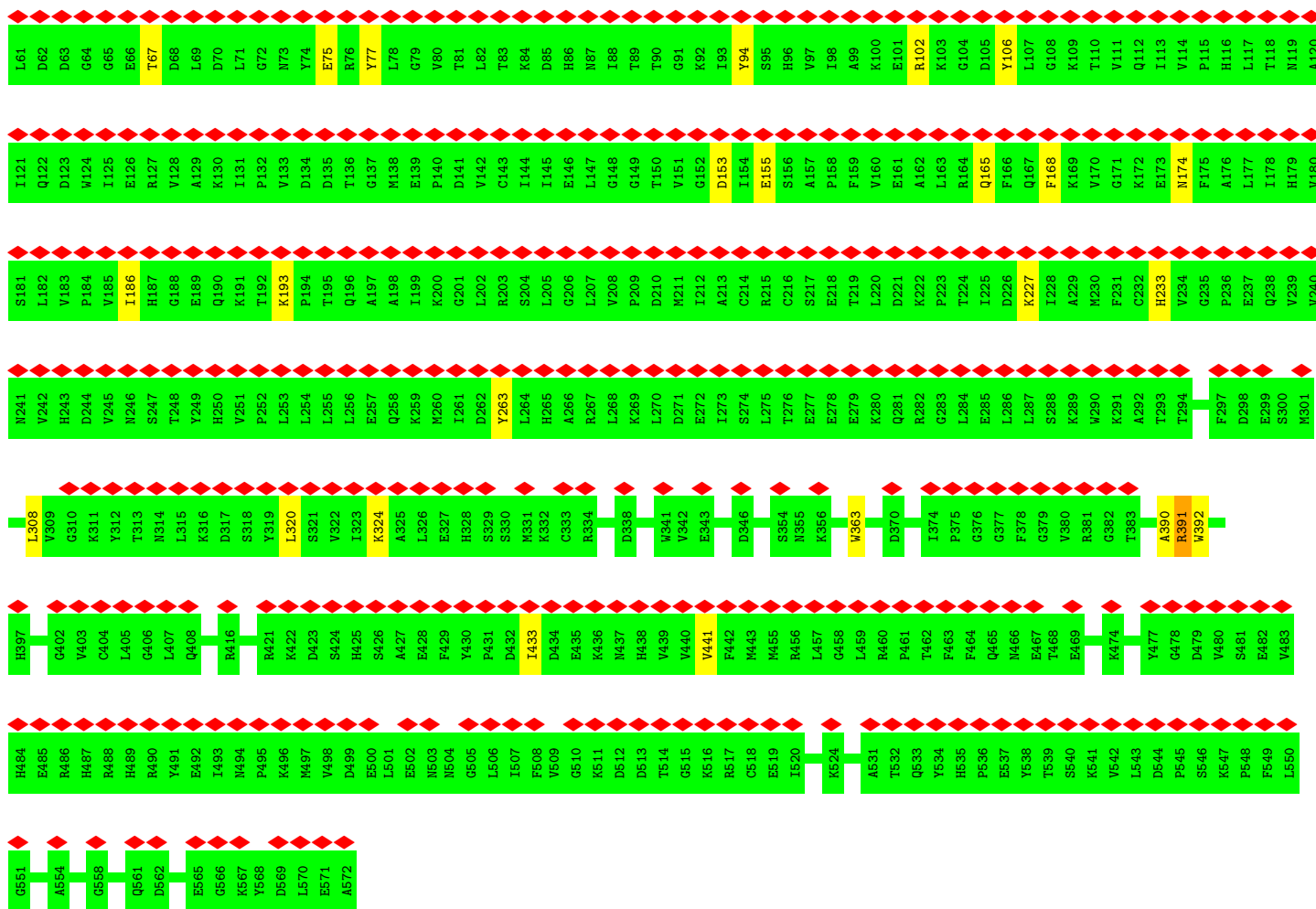


• Molecule 1: CTP synthase 1

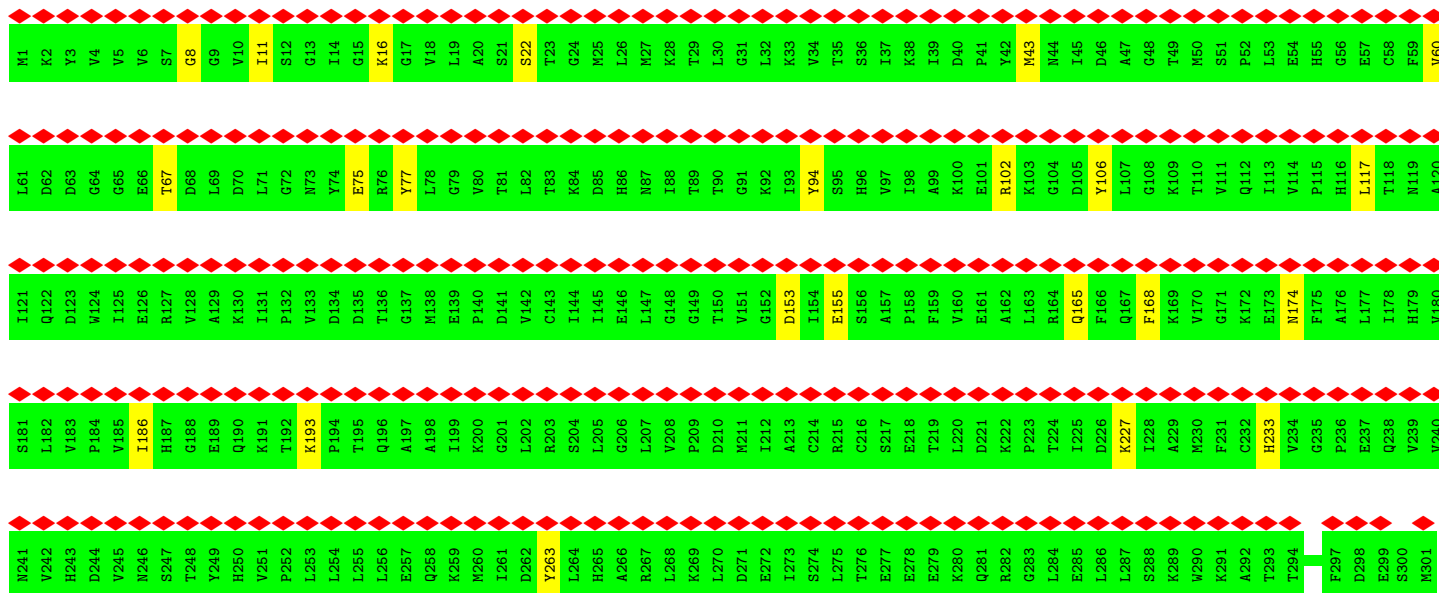
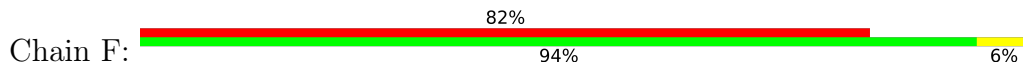


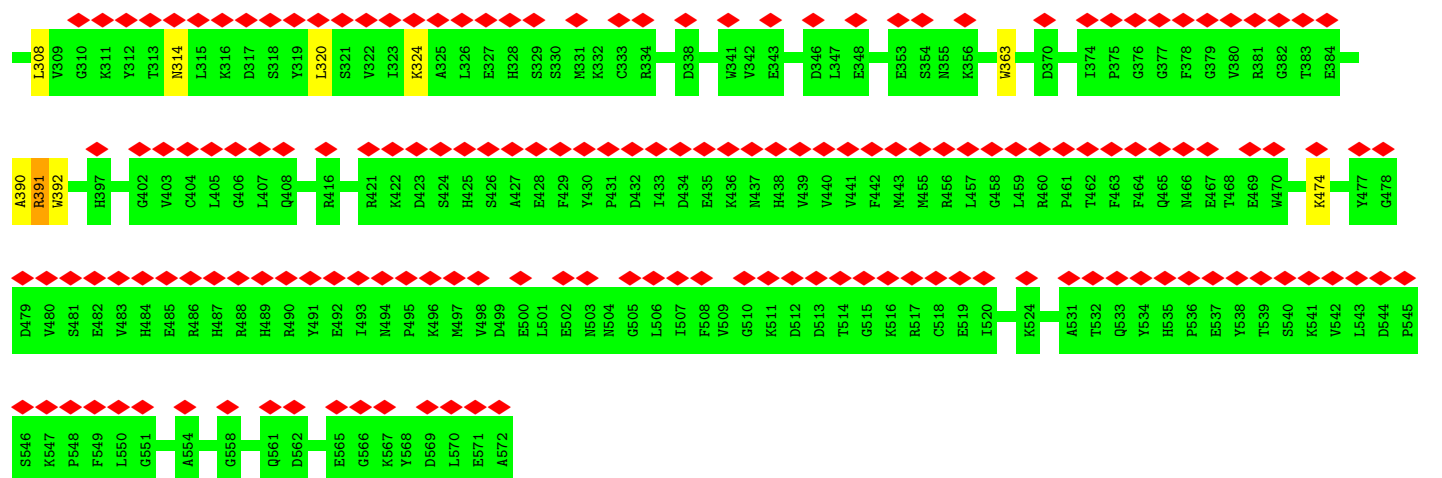
• Molecule 1: CTP synthase 1



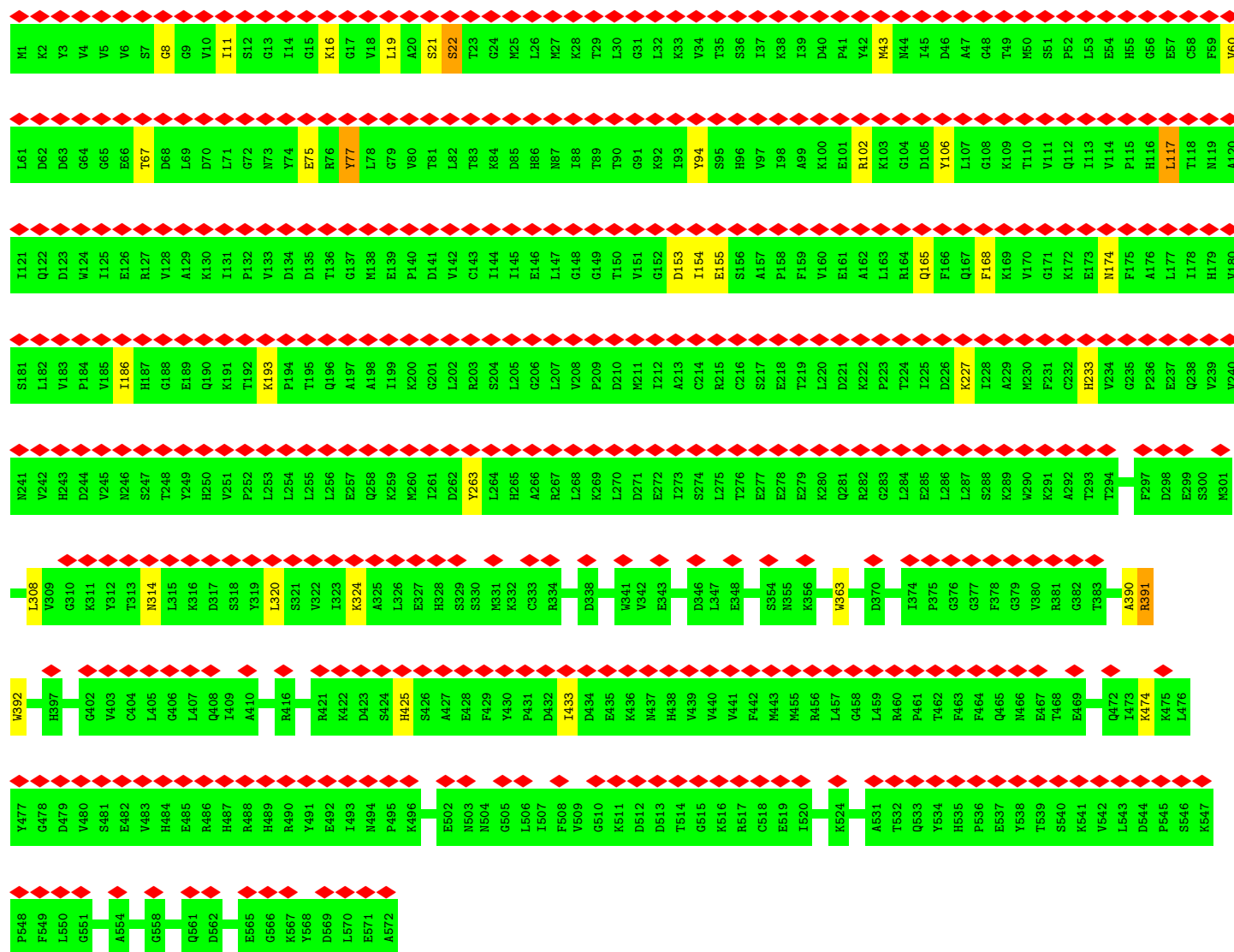
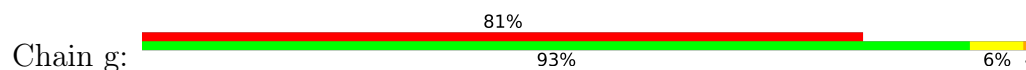


• Molecule 1: CTP synthase 1

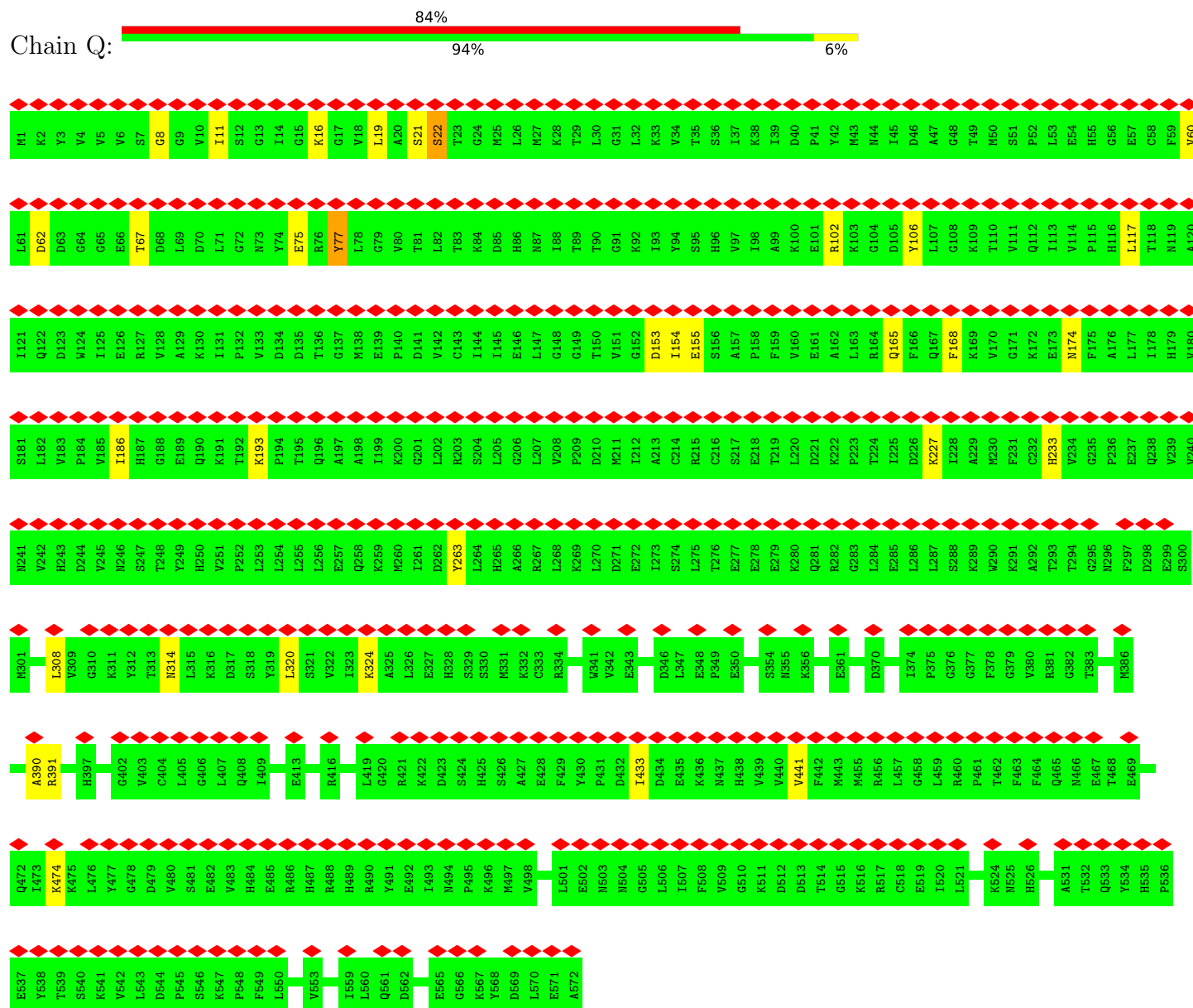




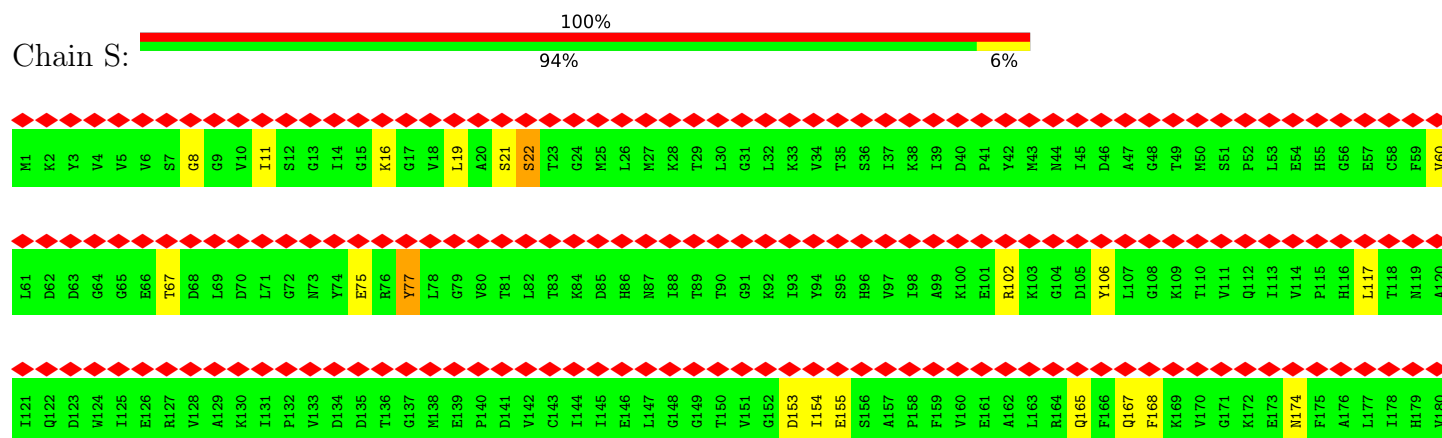
• Molecule 1: CTP synthase 1



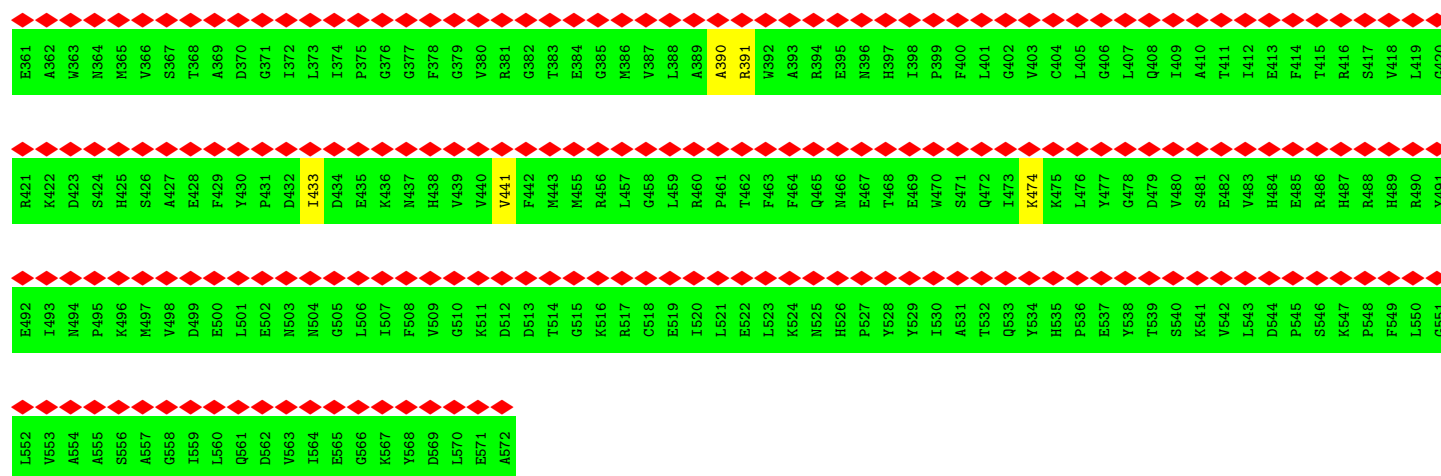
Chain Q:



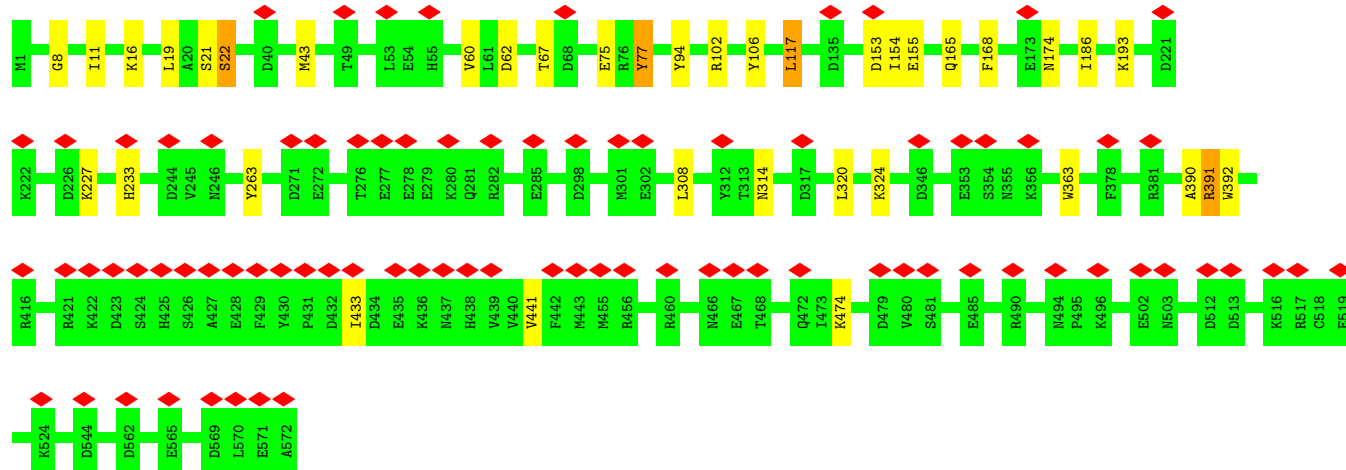
Chain S:



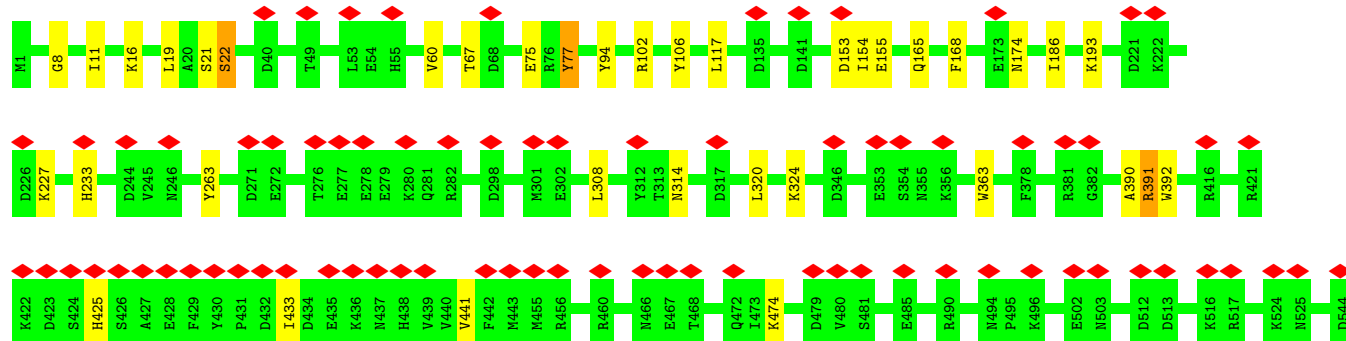
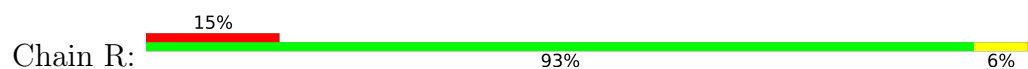
M301	M241	S181	I121	L61	M1
E302	V242	L182	Q122	D62	K2
H303	H243	P183	D123	D63	V3
V304	D244	P184	W124	G64	V4
K305	V245	V185	I125	G65	V5
I306	M246	T186	E126	E66	V6
A307	S247	H187	R127	T67	S7
L308	T248	G188	V128	D68	G8
V309	Y249	E189	A129	L69	G9
G310	H250	Q190	K130	D70	V10
K311	V251	K191	I131	D71	I11
Y312	P252	T192	P132	G72	S12
T313	L253	K193	V133	N73	G13
M314	L254	P194	D134	Y74	I14
L315	L255	T195	D135	E75	G15
K316	L256	Q196	T136	R76	K16
D317	E257	A197	G137	Y77	G17
S318	Q258	A198	M138	L78	V18
Y319	K259	I199	E139	G79	L19
L320	M260	K200	P140	V80	A20
S321	T261	G201	D141	T81	S21
V322	D262	L202	V142	L82	S22
K323	Y263	R203	C143	T83	T23
K324	L264	S204	I144	K84	G24
A325	H265	L205	I145	D85	M25
L326	A266	G206	E146	H86	L26
E327	R267	L207	L147	N87	M27
H328	L268	V208	G148	I88	K28
S329	K269	P209	G149	T89	T29
M330	L270	D210	T150	T90	L30
K331	D271	M211	V151	G91	G31
C332	E272	T212	G152	K92	L32
C333	T273	A213	D153	I93	K33
R334	S274	C214	I154	Y94	V34
R335	L275	R215	E155	S95	T35
K336	T276	C216	S156	H96	S36
L337	E277	S217	A157	V97	I37
D338	E278	E218	P158	I98	K38
I339	T279	T219	P159	A99	I39
K340	K280	L220	V160	K100	D40
W341	Q281	D221	E161	E101	P41
V342	R282	K222	A162	R102	Y42
E343	G283	T223	L163	K103	M43
A344	L284	T224	R164	G104	N44
T345	E285	L225	Q165	D105	I45
D346	L286	D226	F166	Y106	D46
L347	L287	K227	Q167	L107	A47
E348	S288	T228	F168	G108	G48
P349	K289	A229	K169	K109	T49
E350	W290	M230	V170	T110	M50
A351	K291	F231	G171	V111	S51
Q352	A292	C232	K172	Q112	P52
E353	T293	H233	E173	I113	L53
S354	T294	V234	N174	V114	E54
N355	G295	G235	P175	P115	H55
K356	M296	P236	A176	H116	G56
T357	T297	E237	L177	L117	E57
K358	D298	Q238	I178	T118	C58
F359	E299	V239	H179	N119	F59
C360	C300	V240	R180	A120	M60

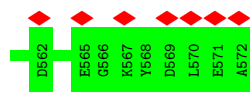


• Molecule 1: CTP synthase 1



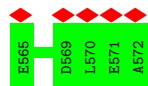
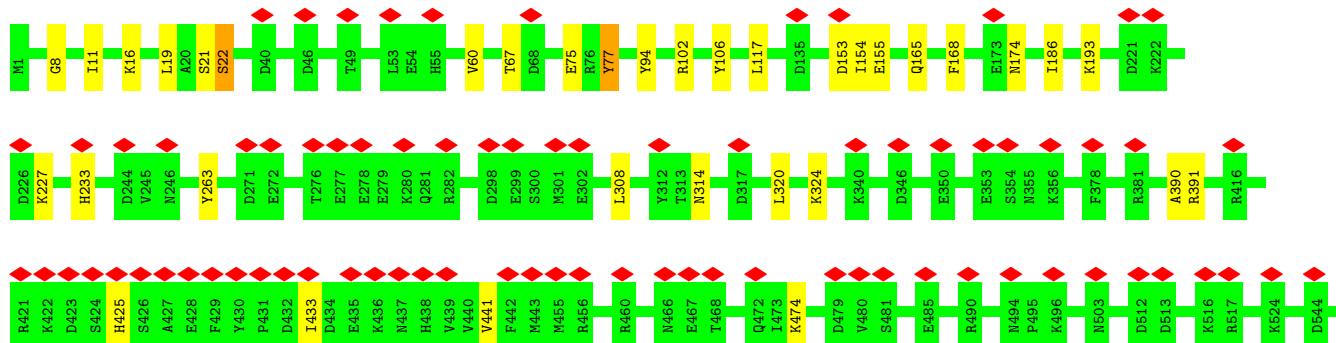
• Molecule 1: CTP synthase 1





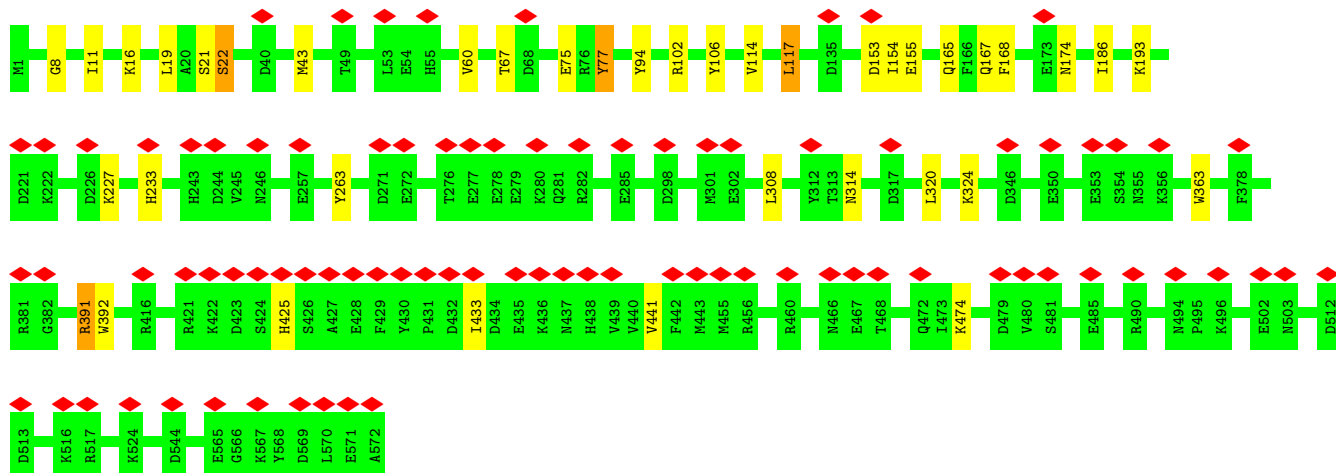
• Molecule 1: CTP synthase 1

Chain T: 15% 94% 6%



• Molecule 1: CTP synthase 1

Chain W: 15% 93% 6%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, D2	Depositor
Number of particles used	64010	Depositor
Resolution determination method	OTHER	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	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	10.548	Depositor
Minimum map value	-5.796	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.226	Depositor
Recommended contour level	1.5	Depositor
Map size (Å)	336.0, 336.0, 336.0	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.05, 1.05, 1.05	Depositor

5 Model quality

5.1 Standard geometry

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

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	D	0.79	0/4494	1.36	14/6076 (0.2%)
1	E	0.79	0/4494	1.36	13/6076 (0.2%)
1	F	0.79	0/4494	1.36	13/6076 (0.2%)
1	Q	0.79	0/4494	1.36	14/6076 (0.2%)
1	R	0.79	0/4494	1.36	14/6076 (0.2%)
1	S	0.79	0/4494	1.36	12/6076 (0.2%)
1	T	0.79	0/4494	1.36	14/6076 (0.2%)
1	U	0.79	0/4494	1.36	13/6076 (0.2%)
1	V	0.79	0/4494	1.36	15/6076 (0.2%)
1	W	0.79	0/4494	1.36	13/6076 (0.2%)
1	g	0.79	0/4494	1.36	14/6076 (0.2%)
1	h	0.79	0/4494	1.36	14/6076 (0.2%)
All	All	0.79	0/53928	1.36	163/72912 (0.2%)

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	D	2	4
1	E	2	4
1	F	2	4
1	Q	2	4
1	R	2	4
1	S	2	4
1	T	2	4
1	U	2	4
1	V	2	4
1	W	2	4
1	g	2	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	h	2	4
All	All	24	48

There are no bond length outliers.

The worst 5 of 163 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	S	67	THR	CA-CB-OG1	12.67	128.61	109.60
1	V	67	THR	CA-CB-OG1	12.65	128.58	109.60
1	U	67	THR	CA-CB-OG1	12.65	128.58	109.60
1	R	67	THR	CA-CB-OG1	12.64	128.57	109.60
1	E	67	THR	CA-CB-OG1	12.64	128.56	109.60

5 of 24 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	V	22	SER	CA
1	V	77	TYR	CA
1	D	22	SER	CA
1	D	77	TYR	CA
1	E	22	SER	CA

5 of 48 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	102	ARG	Sidechain
1	V	102	ARG	Sidechain
1	V	106	TYR	Sidechain
1	V	263	TYR	Sidechain
1	V	391	ARG	Sidechain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	4407	4437	4436	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	4407	4437	4436	27	0
1	F	4407	4437	4436	30	0
1	Q	4407	4437	4436	16	0
1	R	4407	4437	4436	28	0
1	S	4407	4437	4436	16	0
1	T	4407	4437	4436	18	0
1	U	4407	4437	4436	21	0
1	V	4407	4437	4436	20	0
1	W	4407	4437	4436	31	0
1	g	4407	4437	4436	30	0
1	h	4407	4437	4436	30	0
2	D	58	0	24	7	0
2	E	58	0	24	7	0
2	F	58	0	24	7	0
2	Q	58	0	24	7	0
2	R	58	0	24	7	0
2	S	58	0	24	7	0
2	T	58	0	24	7	0
2	U	58	0	24	7	0
2	V	58	0	24	7	0
2	W	58	0	24	7	0
2	g	58	0	24	8	0
2	h	58	0	24	8	0
All	All	53580	53244	53520	191	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 2.

The worst 5 of 191 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:324:LYS:HE3	2:F:602:CTP:O2	1.64	0.98
1:V:324:LYS:HE3	2:V:602:CTP:O2	1.64	0.98
1:Q:324:LYS:HE3	2:Q:602:CTP:O2	1.64	0.98
1:S:324:LYS:HE3	2:S:602:CTP:O2	1.64	0.97
1:g:324:LYS:HE3	2:g:602:CTP:O2	1.64	0.97

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	D	557/561 (99%)	530 (95%)	25 (4%)	2 (0%)	30	62
1	E	557/561 (99%)	530 (95%)	25 (4%)	2 (0%)	30	62
1	F	398/561 (71%)	381 (96%)	17 (4%)	0	100	100
1	Q	557/561 (99%)	530 (95%)	25 (4%)	2 (0%)	30	62
1	R	557/561 (99%)	529 (95%)	26 (5%)	2 (0%)	30	62
1	S	557/561 (99%)	530 (95%)	25 (4%)	2 (0%)	30	62
1	T	557/561 (99%)	530 (95%)	25 (4%)	2 (0%)	30	62
1	U	557/561 (99%)	530 (95%)	25 (4%)	2 (0%)	30	62
1	V	557/561 (99%)	529 (95%)	26 (5%)	2 (0%)	30	62
1	W	557/561 (99%)	529 (95%)	26 (5%)	2 (0%)	30	62
1	g	165/561 (29%)	153 (93%)	11 (7%)	1 (1%)	21	54
1	h	557/561 (99%)	529 (95%)	26 (5%)	2 (0%)	30	62
All	All	6133/6732 (91%)	5830 (95%)	282 (5%)	21 (0%)	37	67

5 of 21 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	V	433	ILE
1	D	433	ILE
1	E	433	ILE
1	g	433	ILE
1	Q	433	ILE

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	D	4/486 (1%)	4 (100%)	0	100	100
1	F	283/486 (58%)	281 (99%)	2 (1%)	76	78
1	Q	486/486 (100%)	478 (98%)	8 (2%)	55	70
1	R	486/486 (100%)	478 (98%)	8 (2%)	55	70
1	S	486/486 (100%)	478 (98%)	8 (2%)	55	70
1	T	486/486 (100%)	478 (98%)	8 (2%)	55	70
1	U	486/486 (100%)	478 (98%)	8 (2%)	55	70
1	V	68/486 (14%)	67 (98%)	1 (2%)	57	71
1	W	486/486 (100%)	478 (98%)	8 (2%)	55	70
1	g	486/486 (100%)	478 (98%)	8 (2%)	55	70
1	h	486/486 (100%)	478 (98%)	8 (2%)	55	70
All	All	4243/5346 (79%)	4176 (98%)	67 (2%)	54	70

5 of 67 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	T	314	ASN
1	W	19	LEU
1	W	314	ASN
1	S	154	ILE
1	S	117	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 55 such sidechains are listed below:

Mol	Chain	Res	Type
1	U	408	GLN
1	h	533	GLN
1	W	533	GLN
1	W	233	HIS
1	U	533	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

24 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	CTP	E	602	-	29,30,30	1.43	6 (20%)	43,47,47	1.41	6 (13%)
2	CTP	V	602	-	29,30,30	1.46	7 (24%)	43,47,47	1.45	7 (16%)
2	CTP	S	602	-	29,30,30	1.44	6 (20%)	43,47,47	1.41	6 (13%)
2	CTP	R	602	-	29,30,30	1.43	5 (17%)	43,47,47	1.41	6 (13%)
2	CTP	D	602	-	29,30,30	1.45	6 (20%)	43,47,47	1.41	6 (13%)
2	CTP	W	602	-	29,30,30	1.47	7 (24%)	43,47,47	1.45	7 (16%)
2	CTP	T	601	-	29,30,30	1.86	5 (17%)	43,47,47	1.35	6 (13%)
2	CTP	W	601	-	29,30,30	1.87	6 (20%)	43,47,47	1.33	4 (9%)
2	CTP	g	601	-	29,30,30	1.88	7 (24%)	43,47,47	1.32	4 (9%)
2	CTP	g	602	-	29,30,30	1.46	7 (24%)	43,47,47	1.45	7 (16%)
2	CTP	U	601	-	29,30,30	1.88	6 (20%)	43,47,47	1.32	4 (9%)
2	CTP	R	601	-	29,30,30	1.86	5 (17%)	43,47,47	1.34	6 (13%)
2	CTP	F	601	-	29,30,30	1.87	6 (20%)	43,47,47	1.32	4 (9%)
2	CTP	F	602	-	29,30,30	1.47	6 (20%)	43,47,47	1.46	7 (16%)
2	CTP	Q	601	-	29,30,30	1.87	5 (17%)	43,47,47	1.34	6 (13%)
2	CTP	Q	602	-	29,30,30	1.45	6 (20%)	43,47,47	1.41	6 (13%)
2	CTP	V	601	-	29,30,30	1.87	6 (20%)	43,47,47	1.33	4 (9%)
2	CTP	S	601	-	29,30,30	1.87	6 (20%)	43,47,47	1.33	6 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	CTP	D	601	-	29,30,30	1.86	5 (17%)	43,47,47	1.34	6 (13%)
2	CTP	h	601	-	29,30,30	1.87	6 (20%)	43,47,47	1.33	4 (9%)
2	CTP	T	602	-	29,30,30	1.44	5 (17%)	43,47,47	1.41	6 (13%)
2	CTP	h	602	-	29,30,30	1.47	7 (24%)	43,47,47	1.45	7 (16%)
2	CTP	E	601	-	29,30,30	1.87	6 (20%)	43,47,47	1.34	6 (13%)
2	CTP	U	602	-	29,30,30	1.47	6 (20%)	43,47,47	1.45	7 (16%)

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
2	CTP	E	602	-	-	7/22/38/38	0/2/2/2
2	CTP	V	602	-	-	7/22/38/38	0/2/2/2
2	CTP	S	602	-	-	7/22/38/38	0/2/2/2
2	CTP	R	602	-	-	7/22/38/38	0/2/2/2
2	CTP	D	602	-	-	7/22/38/38	0/2/2/2
2	CTP	W	602	-	-	7/22/38/38	0/2/2/2
2	CTP	T	601	-	-	8/22/38/38	0/2/2/2
2	CTP	W	601	-	-	10/22/38/38	0/2/2/2
2	CTP	g	601	-	-	10/22/38/38	0/2/2/2
2	CTP	g	602	-	-	7/22/38/38	0/2/2/2
2	CTP	U	601	-	-	10/22/38/38	0/2/2/2
2	CTP	R	601	-	-	8/22/38/38	0/2/2/2
2	CTP	F	601	-	-	10/22/38/38	0/2/2/2
2	CTP	F	602	-	-	7/22/38/38	0/2/2/2
2	CTP	Q	601	-	-	8/22/38/38	0/2/2/2
2	CTP	Q	602	-	-	7/22/38/38	0/2/2/2
2	CTP	V	601	-	-	10/22/38/38	0/2/2/2
2	CTP	S	601	-	-	8/22/38/38	0/2/2/2
2	CTP	D	601	-	-	8/22/38/38	0/2/2/2
2	CTP	h	601	-	-	10/22/38/38	0/2/2/2
2	CTP	T	602	-	-	7/22/38/38	0/2/2/2
2	CTP	h	602	-	-	7/22/38/38	0/2/2/2
2	CTP	E	601	-	-	8/22/38/38	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CTP	U	602	-	-	7/22/38/38	0/2/2/2

The worst 5 of 143 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	601	CTP	PB-O3B	-5.63	1.53	1.59
2	U	601	CTP	PB-O3B	-5.62	1.53	1.59
2	g	601	CTP	PB-O3B	-5.61	1.53	1.59
2	E	601	CTP	PB-O3B	-5.61	1.53	1.59
2	T	601	CTP	PB-O3B	-5.61	1.53	1.59

The worst 5 of 138 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	601	CTP	O2'-C2'-C1'	-3.08	99.50	110.10
2	F	602	CTP	O4'-C1'-N1	3.07	115.31	108.36
2	F	601	CTP	O2'-C2'-C1'	-3.07	99.53	110.10
2	R	601	CTP	O2'-C2'-C1'	-3.07	99.54	110.10
2	U	602	CTP	O4'-C1'-N1	3.06	115.30	108.36

There are no chirality outliers.

5 of 192 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	V	601	CTP	C2'-C1'-N1-C6
2	V	601	CTP	C5'-O5'-PA-O1A
2	V	601	CTP	C5'-O5'-PA-O2A
2	V	601	CTP	C5'-O5'-PA-O3A
2	V	602	CTP	C5'-O5'-PA-O1A

There are no ring outliers.

24 monomers are involved in 86 short contacts:

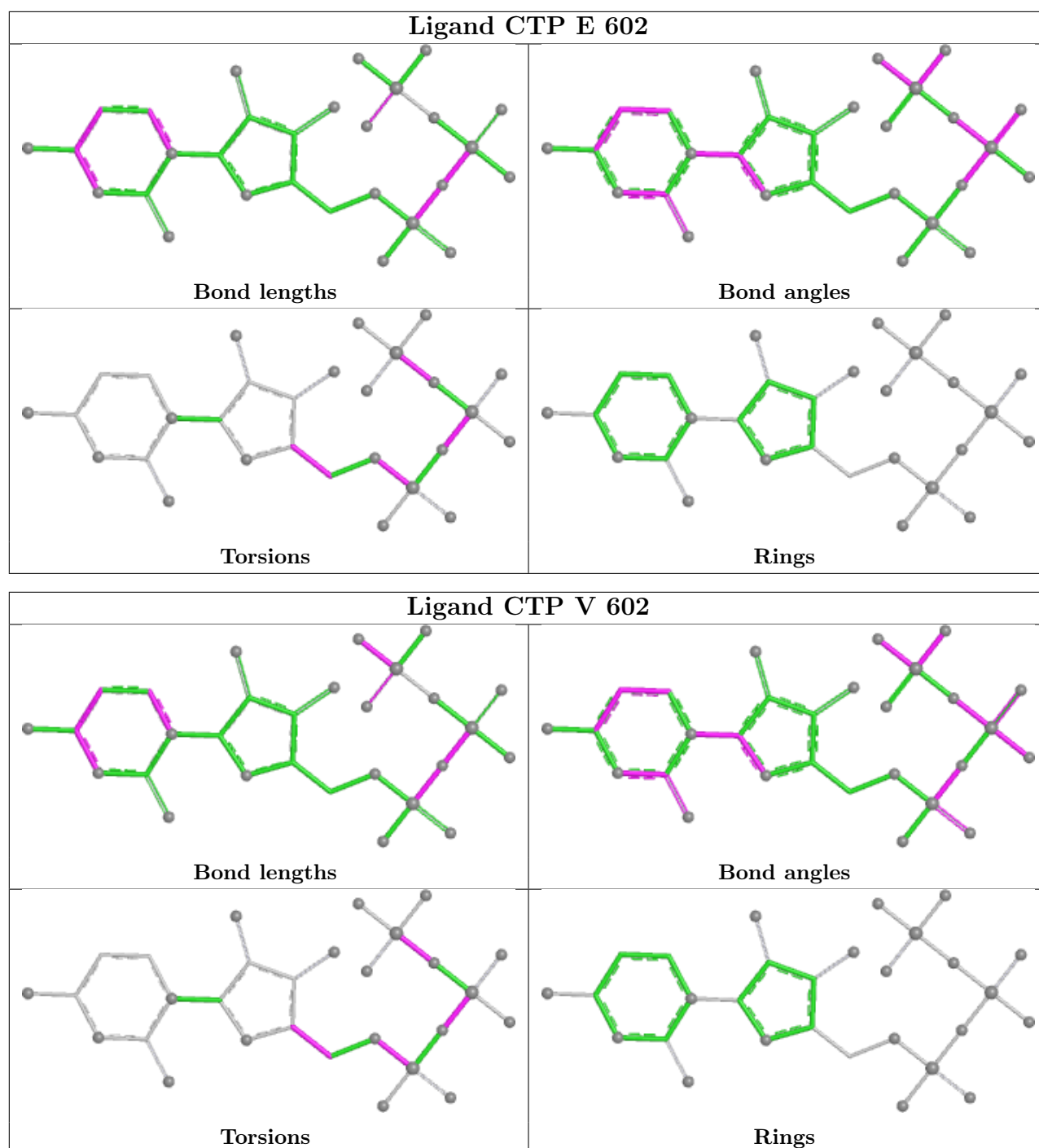
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	E	602	CTP	4	0
2	V	602	CTP	4	0
2	S	602	CTP	4	0
2	R	602	CTP	4	0
2	D	602	CTP	4	0
2	W	602	CTP	4	0
2	T	601	CTP	3	0

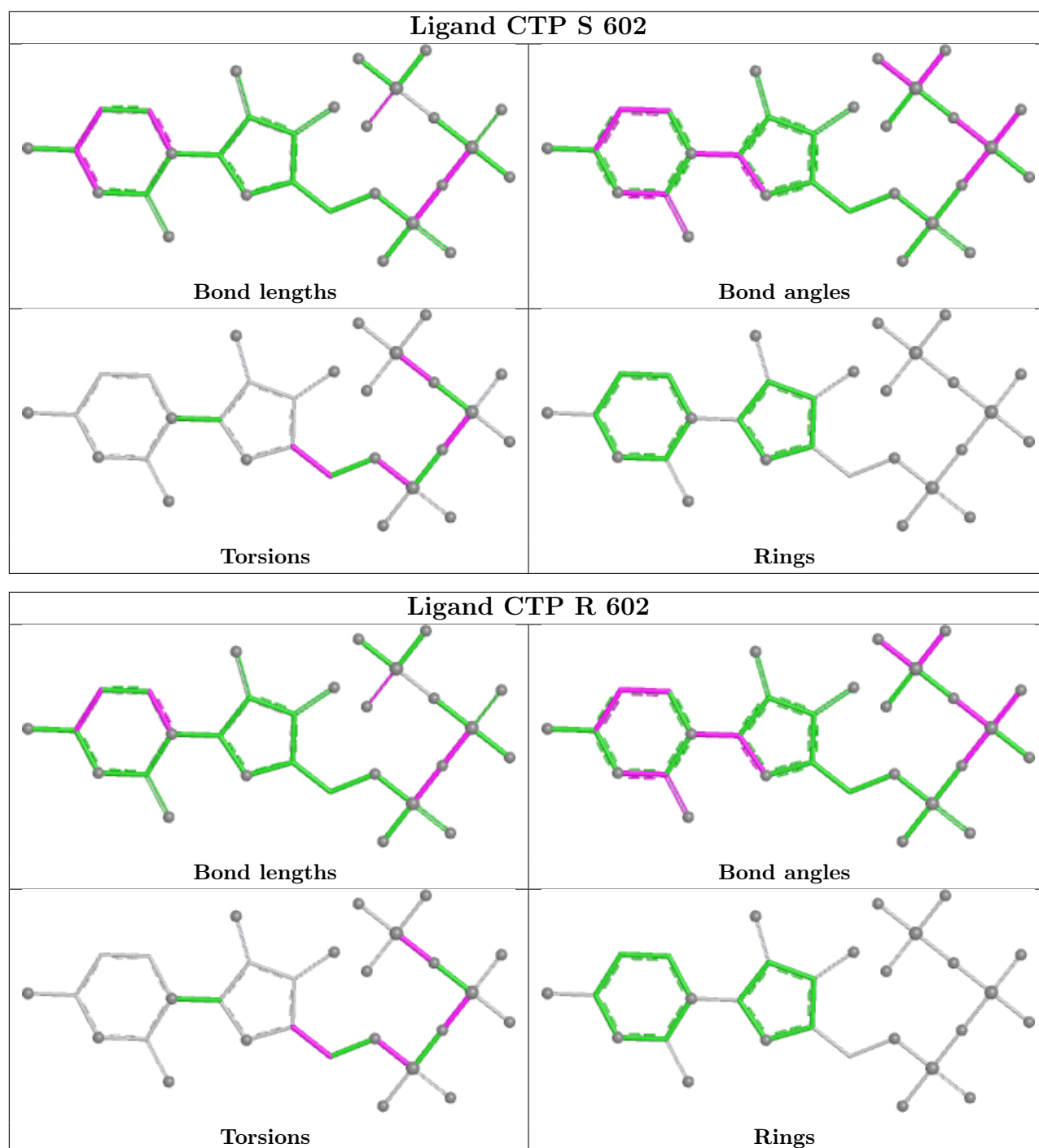
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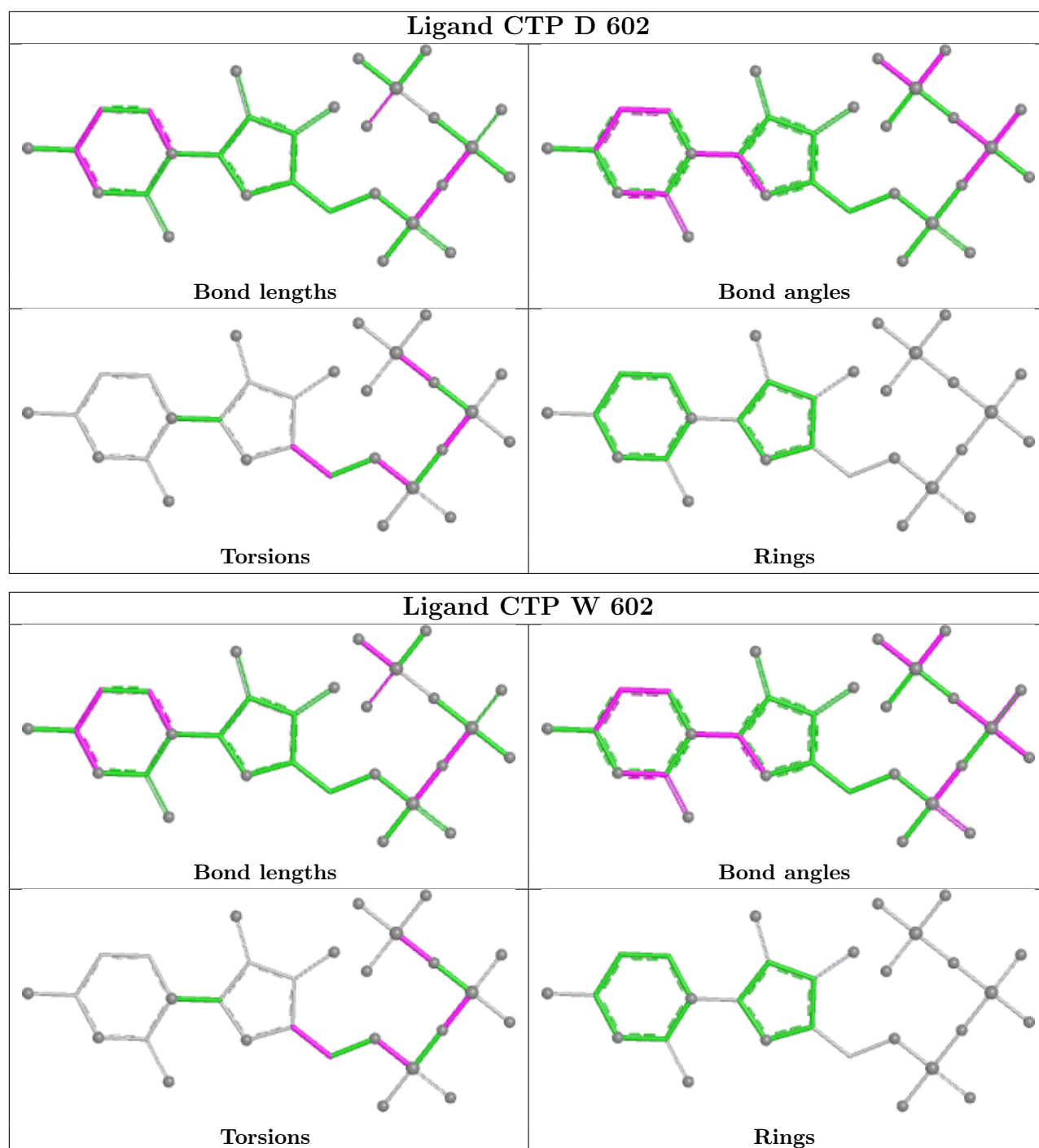
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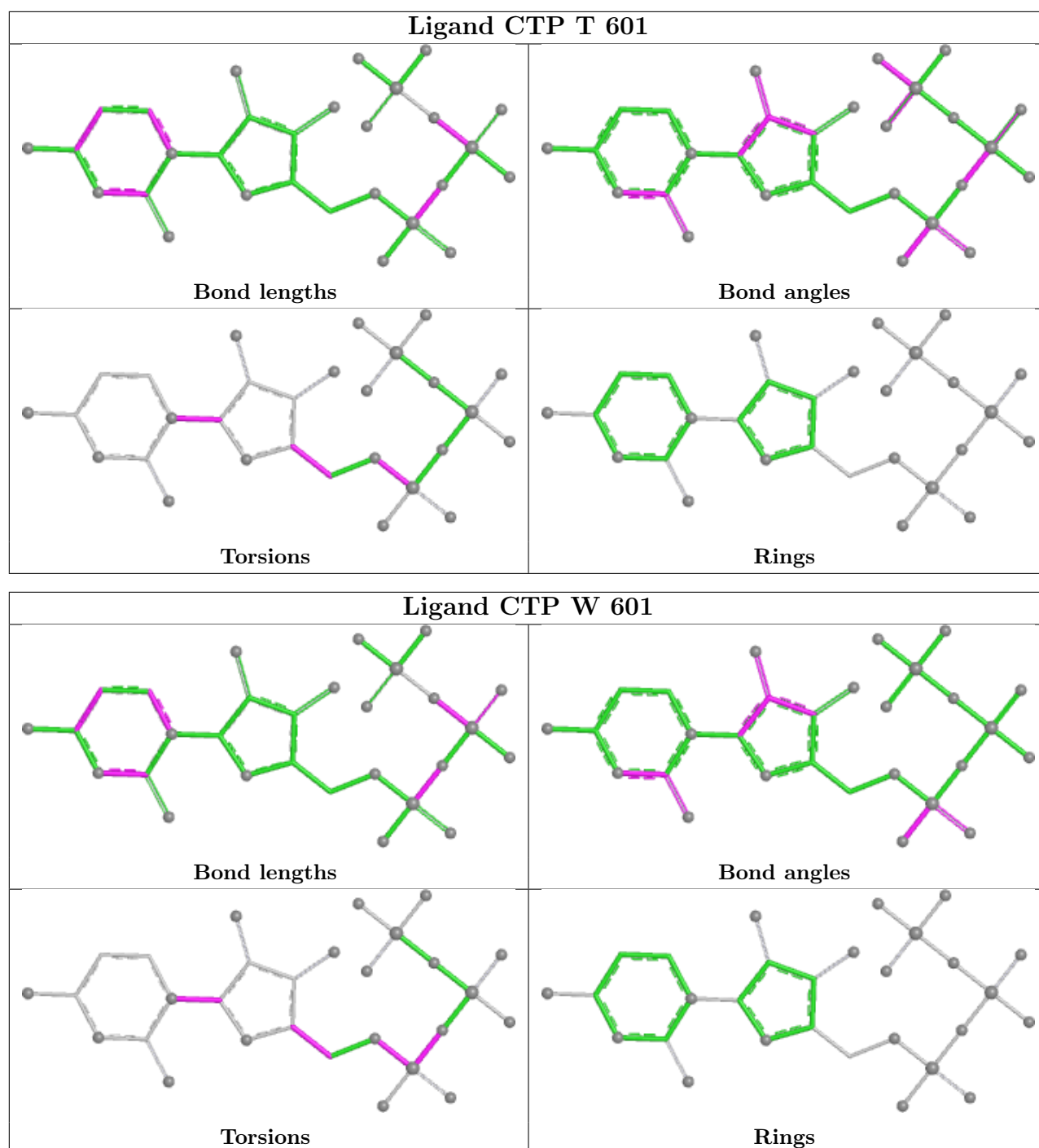
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	W	601	CTP	3	0
2	g	601	CTP	4	0
2	g	602	CTP	4	0
2	U	601	CTP	3	0
2	R	601	CTP	3	0
2	F	601	CTP	3	0
2	F	602	CTP	4	0
2	Q	601	CTP	3	0
2	Q	602	CTP	4	0
2	V	601	CTP	3	0
2	S	601	CTP	3	0
2	D	601	CTP	3	0
2	h	601	CTP	4	0
2	T	602	CTP	4	0
2	h	602	CTP	4	0
2	E	601	CTP	3	0
2	U	602	CTP	4	0

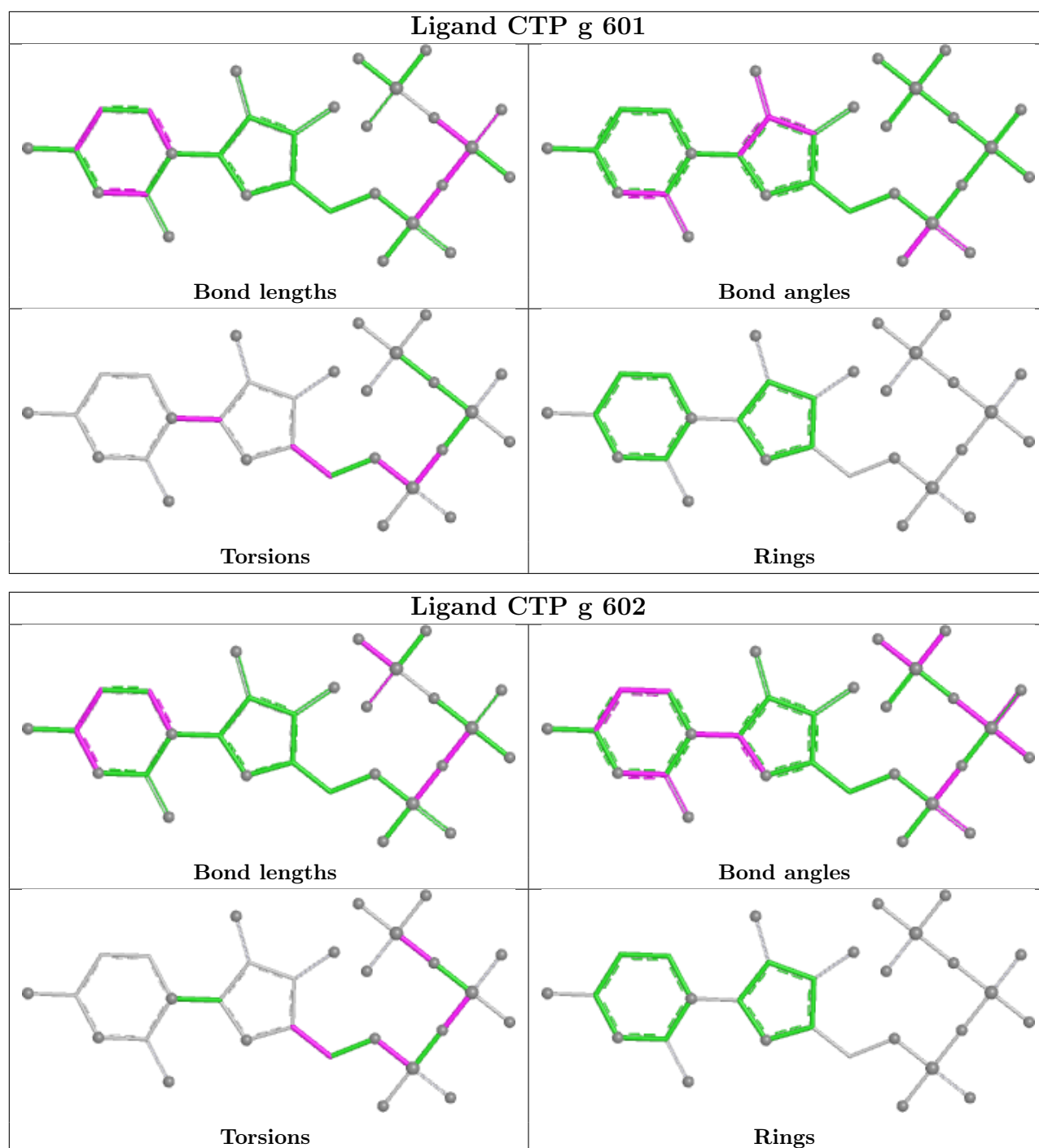
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

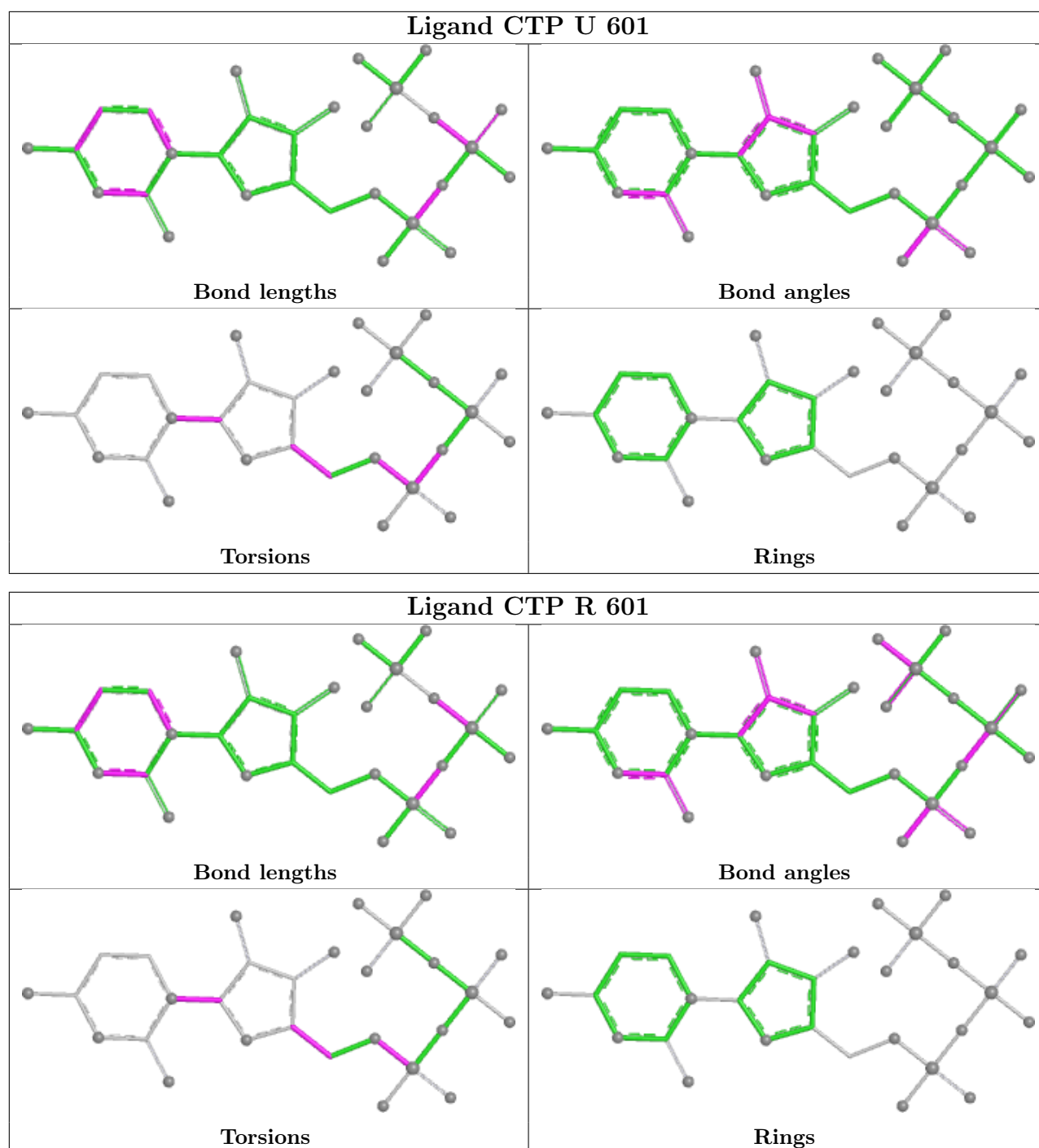


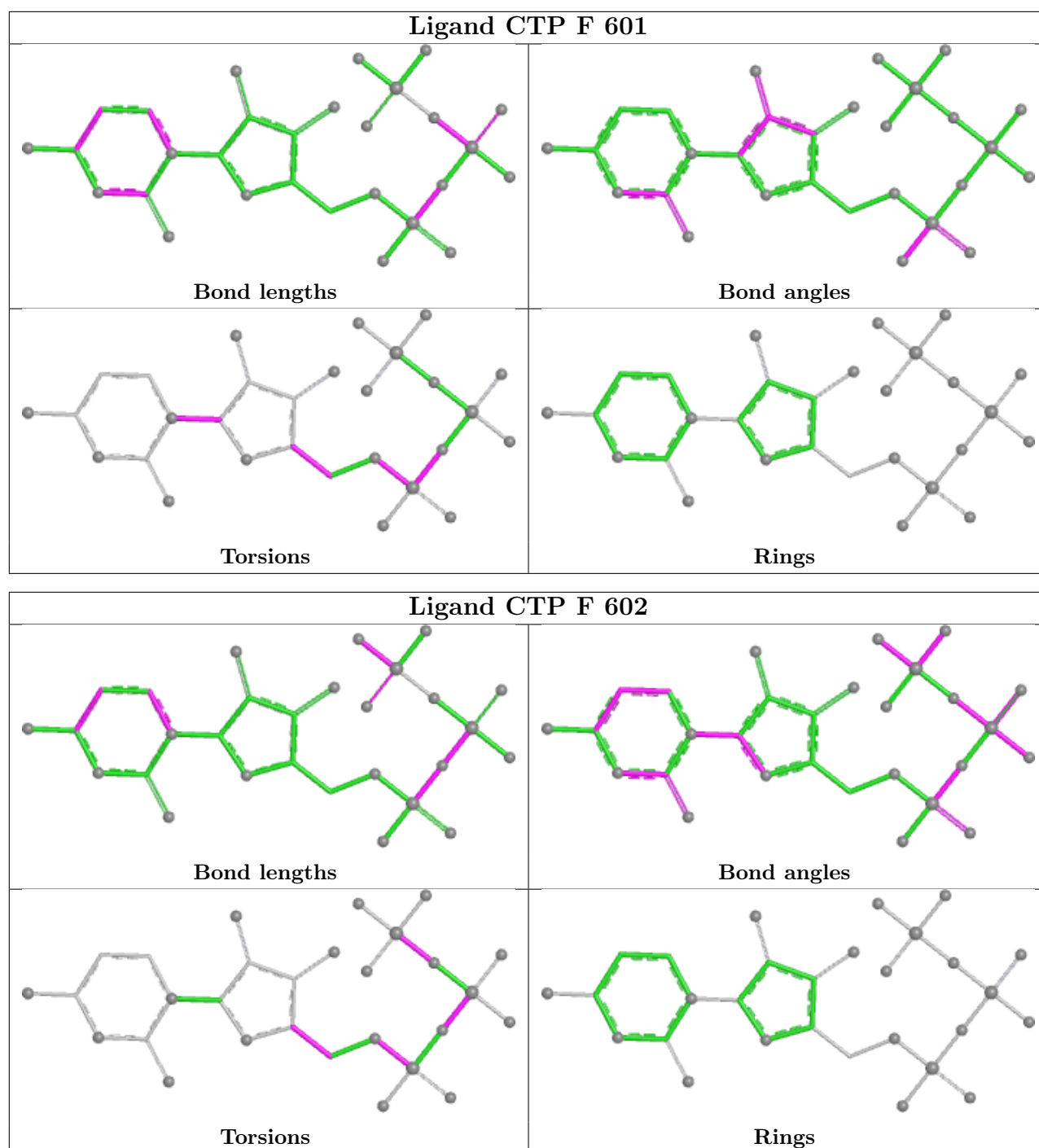


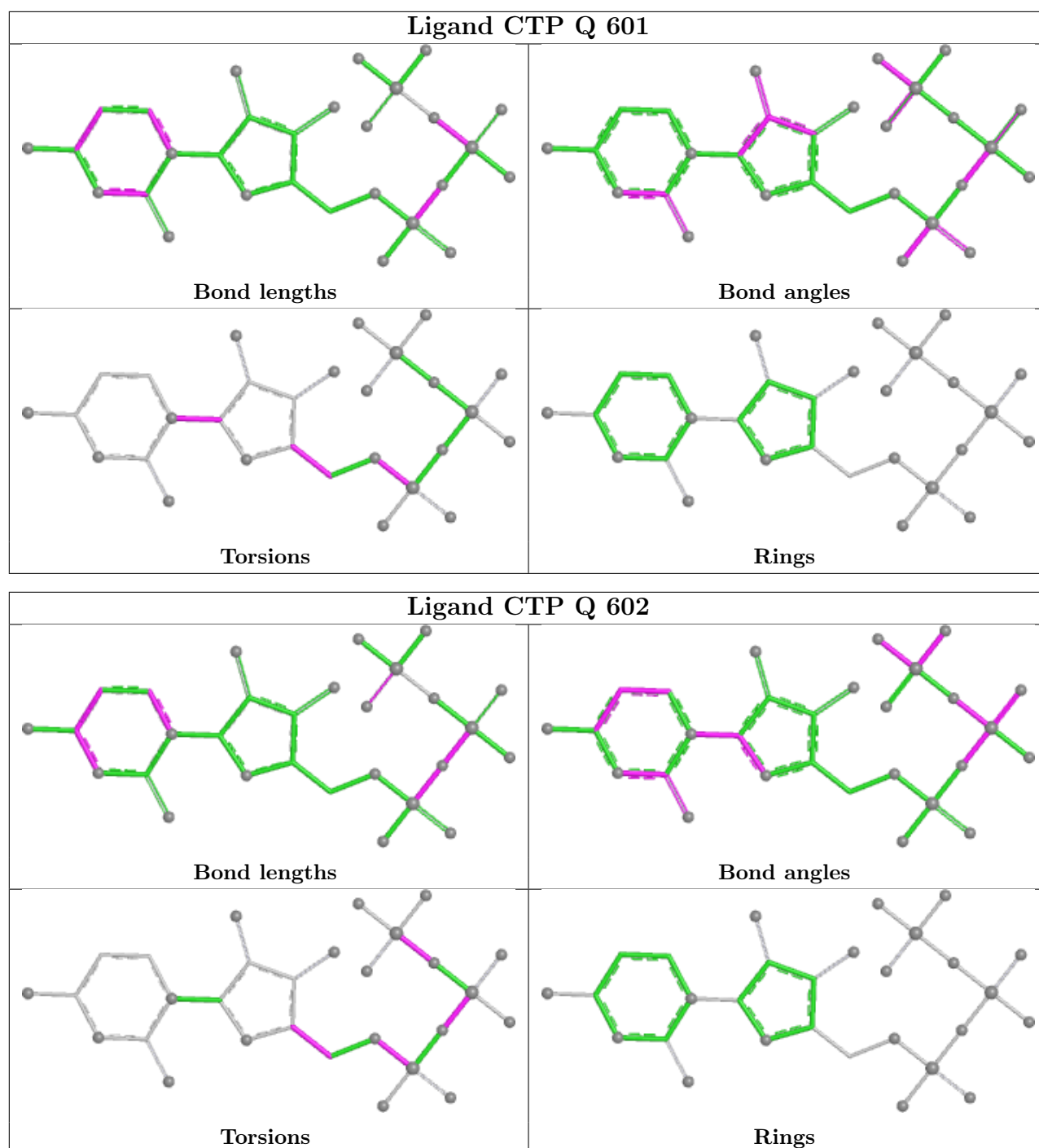


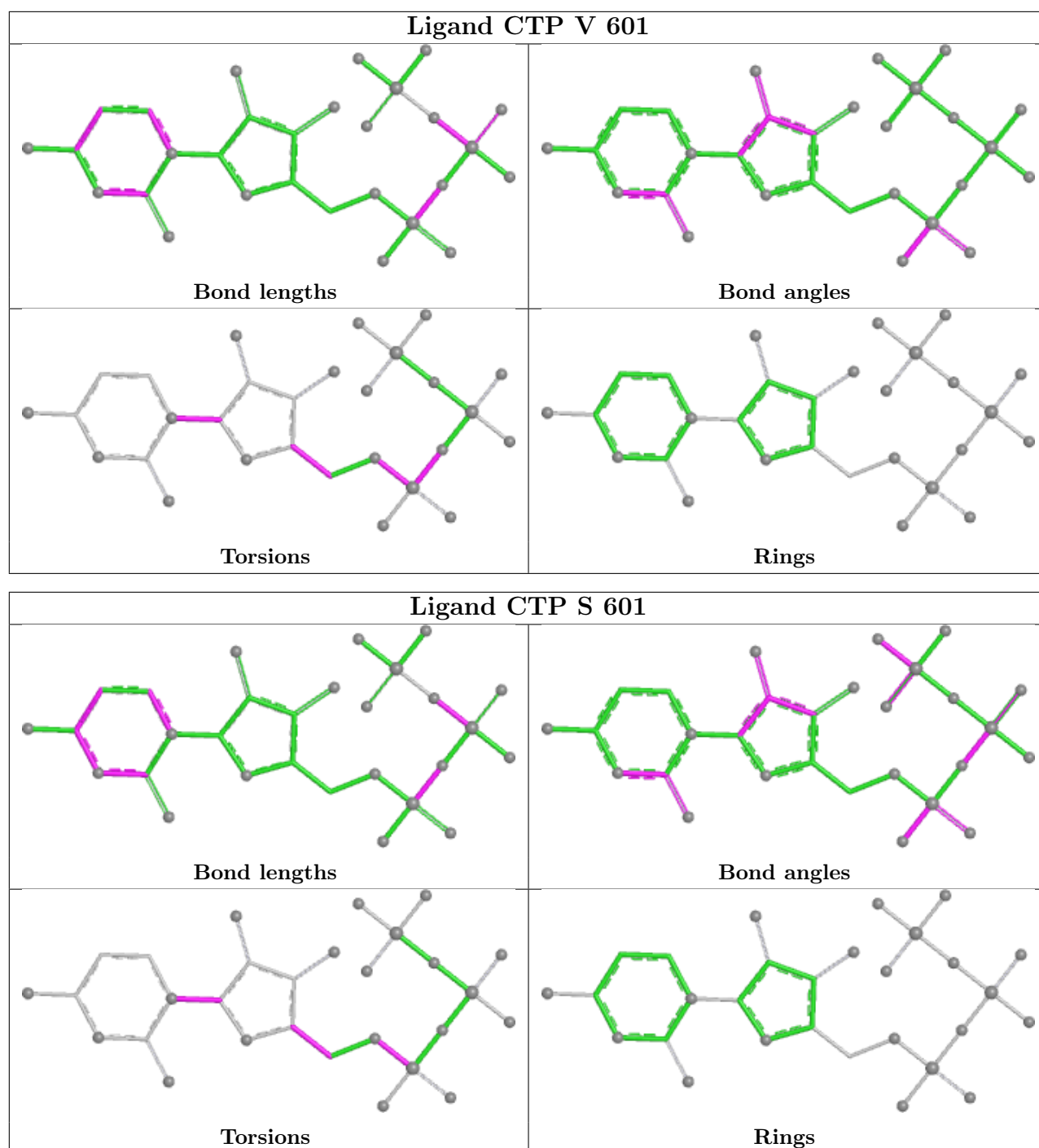


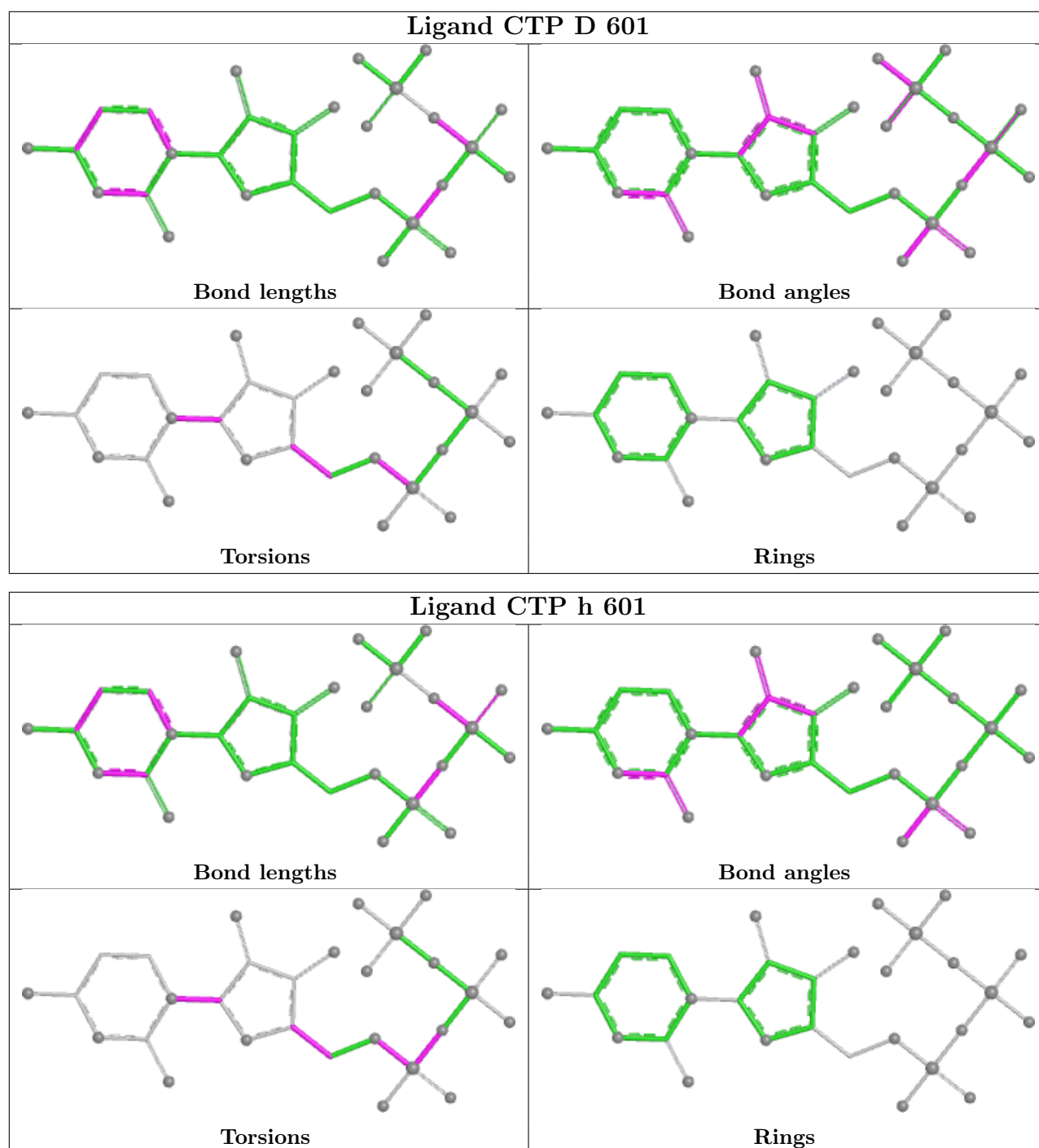


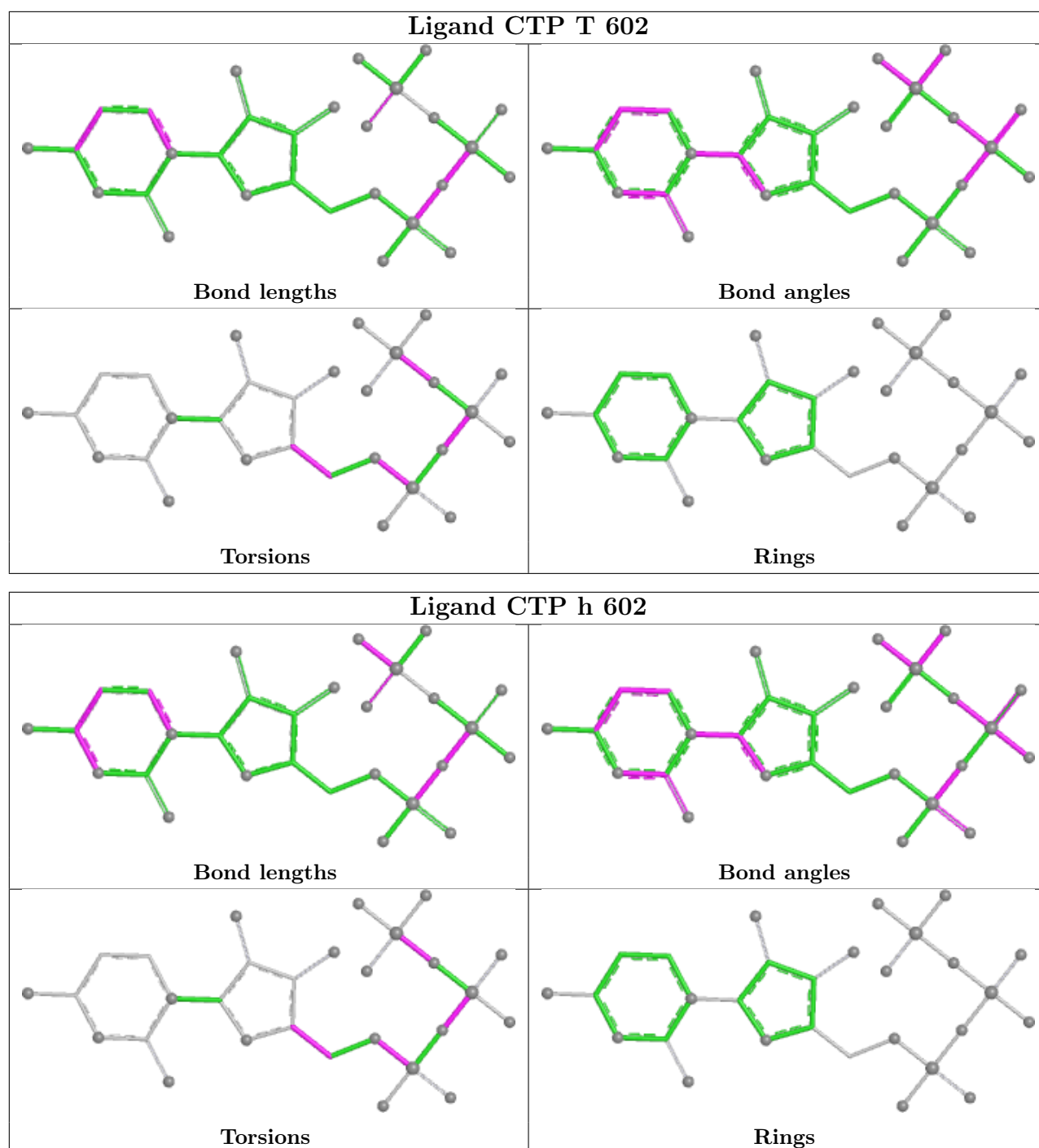


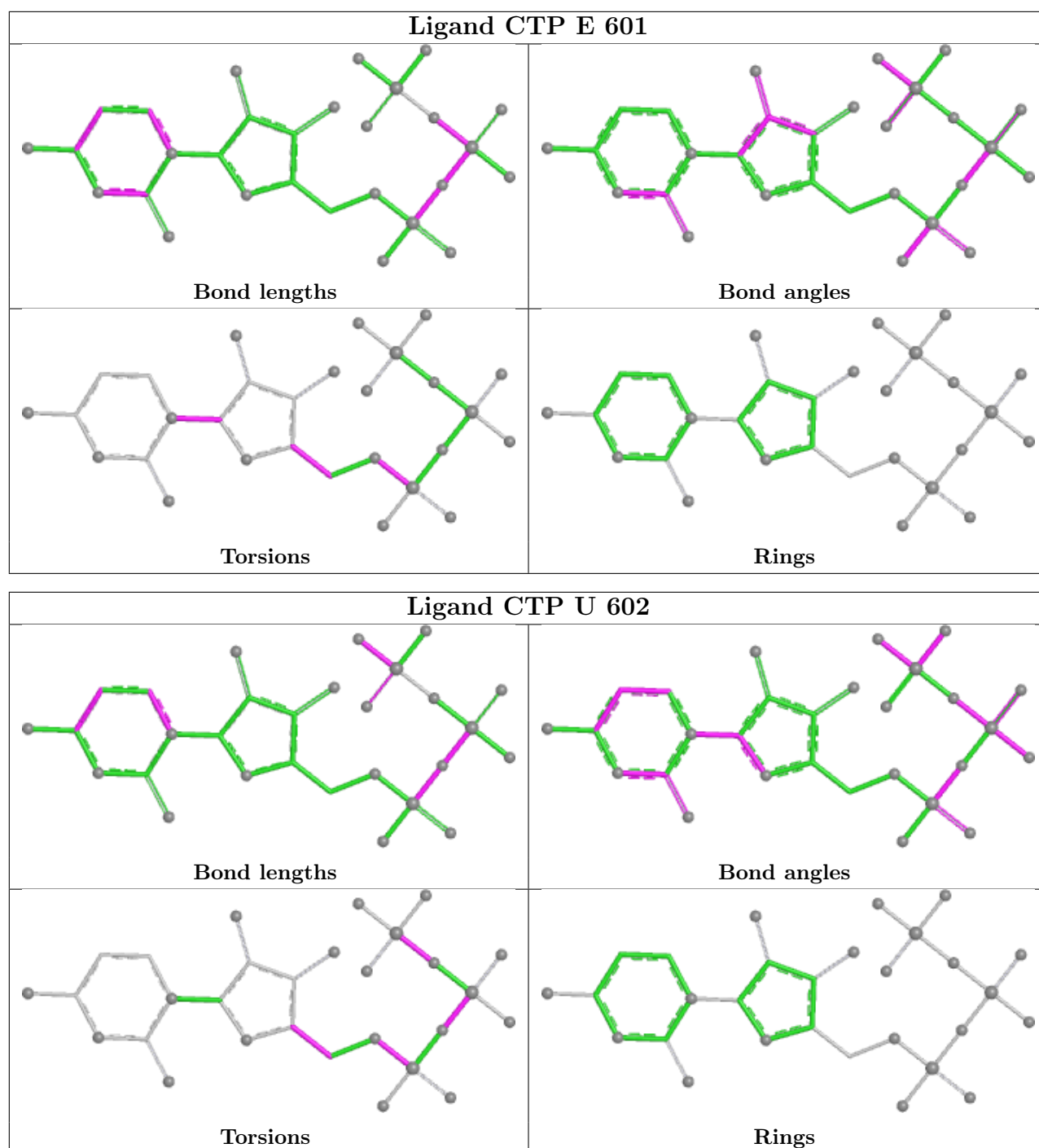












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	V	1
1	D	1
1	E	1
1	F	1
1	g	1
1	Q	1
1	S	1
1	U	1
1	h	1
1	R	1
1	T	1
1	W	1

The worst 5 of 12 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	V	443:MET	C	455:MET	N	5.62
1	D	443:MET	C	455:MET	N	5.62
1	E	443:MET	C	455:MET	N	5.62
1	F	443:MET	C	455:MET	N	5.62
1	g	443:MET	C	455:MET	N	5.62

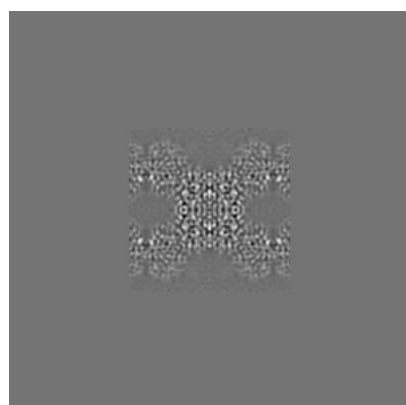
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24560. These allow visual inspection of the internal detail of the map and identification of artifacts.

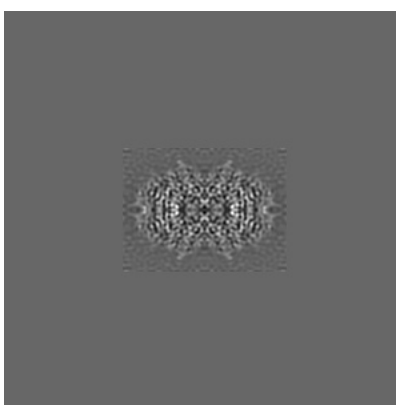
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

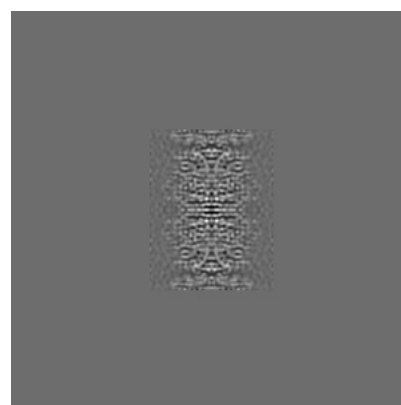
6.1.1 Primary map



X



Y

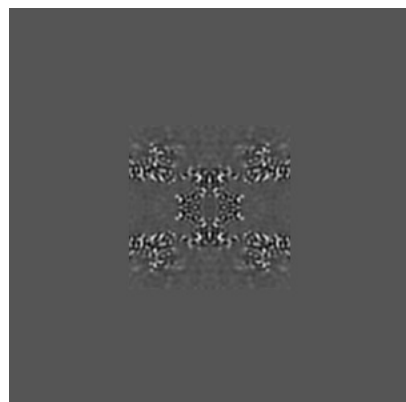


Z

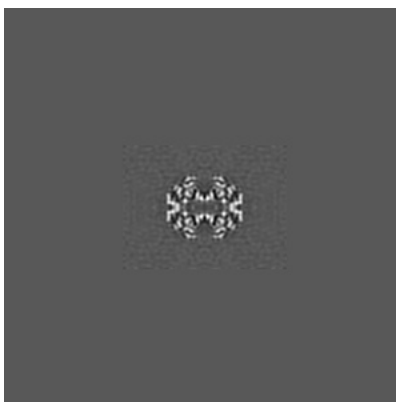
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

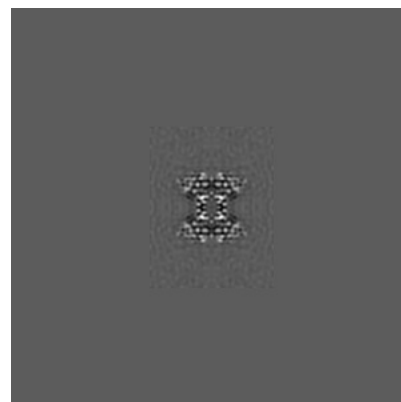
6.2.1 Primary map



X Index: 160



Y Index: 160

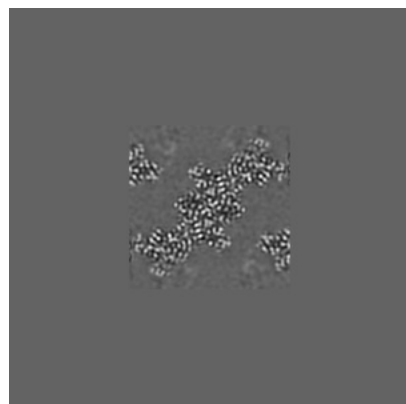


Z Index: 160

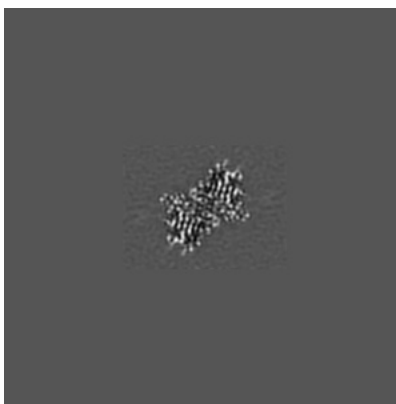
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

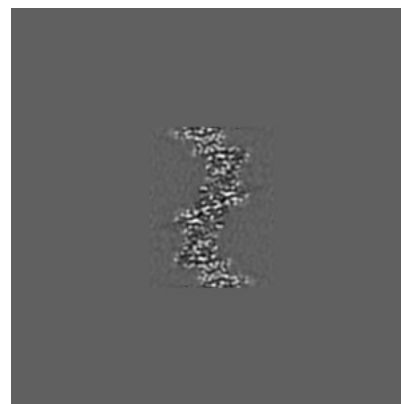
6.3.1 Primary map



X Index: 151



Y Index: 150

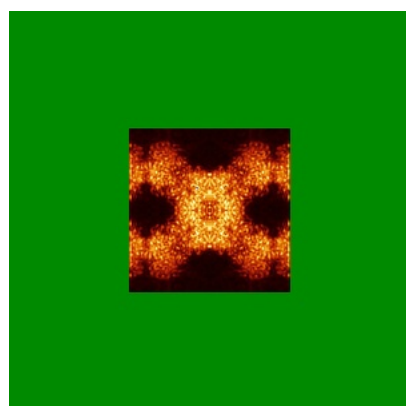


Z Index: 135

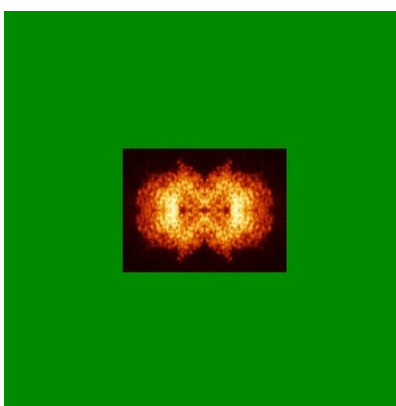
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

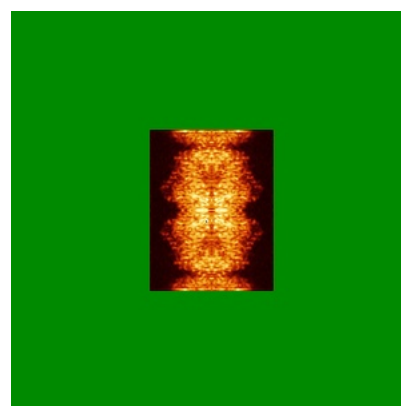
6.4.1 Primary map



X



Y

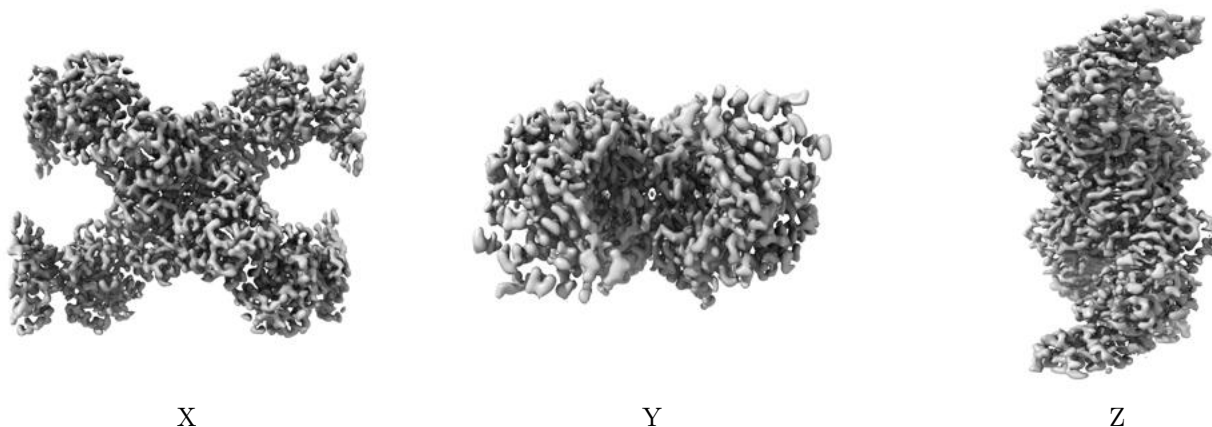


Z

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



The images above show the 3D surface view of the map at the recommended contour level 1.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

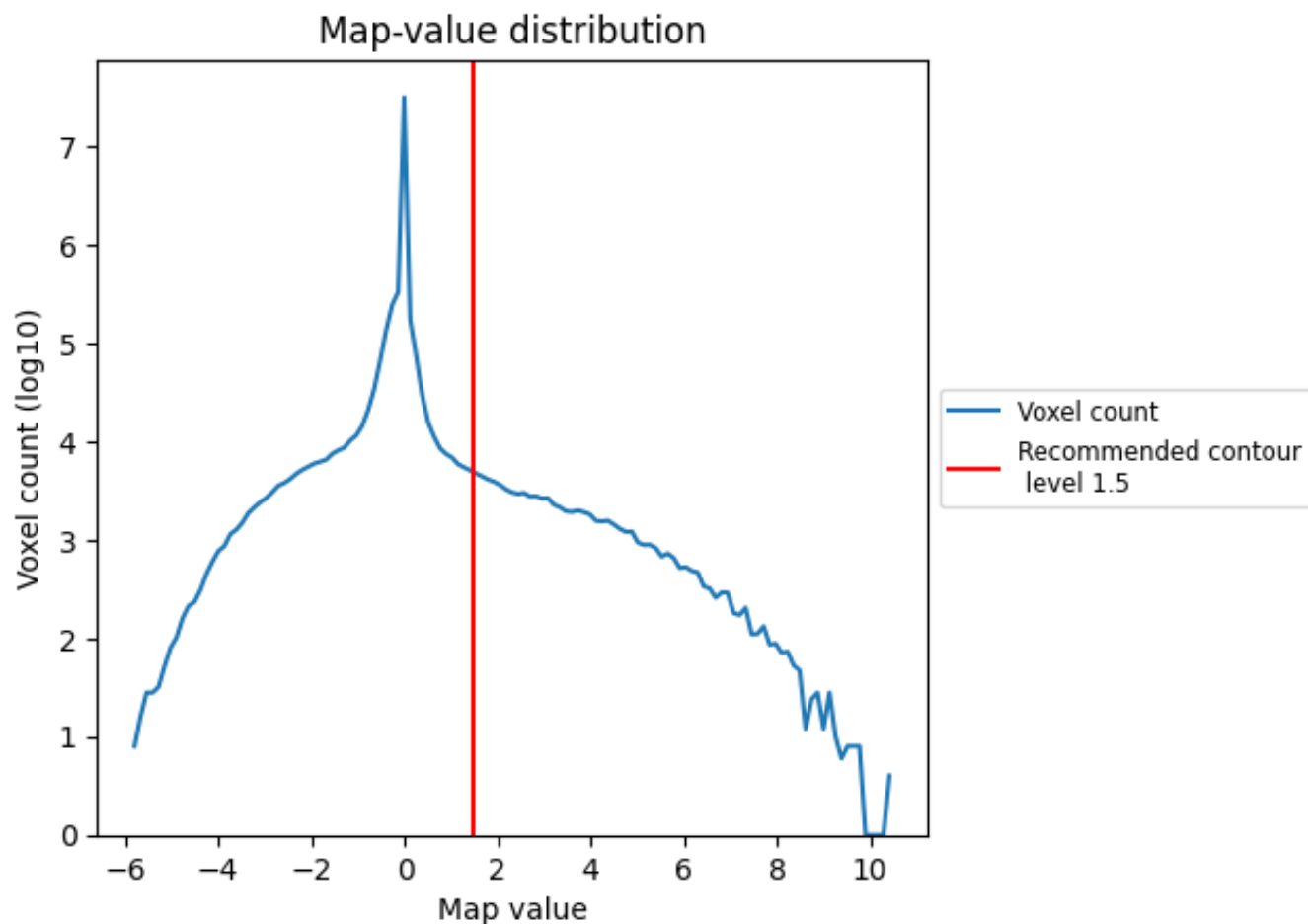
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

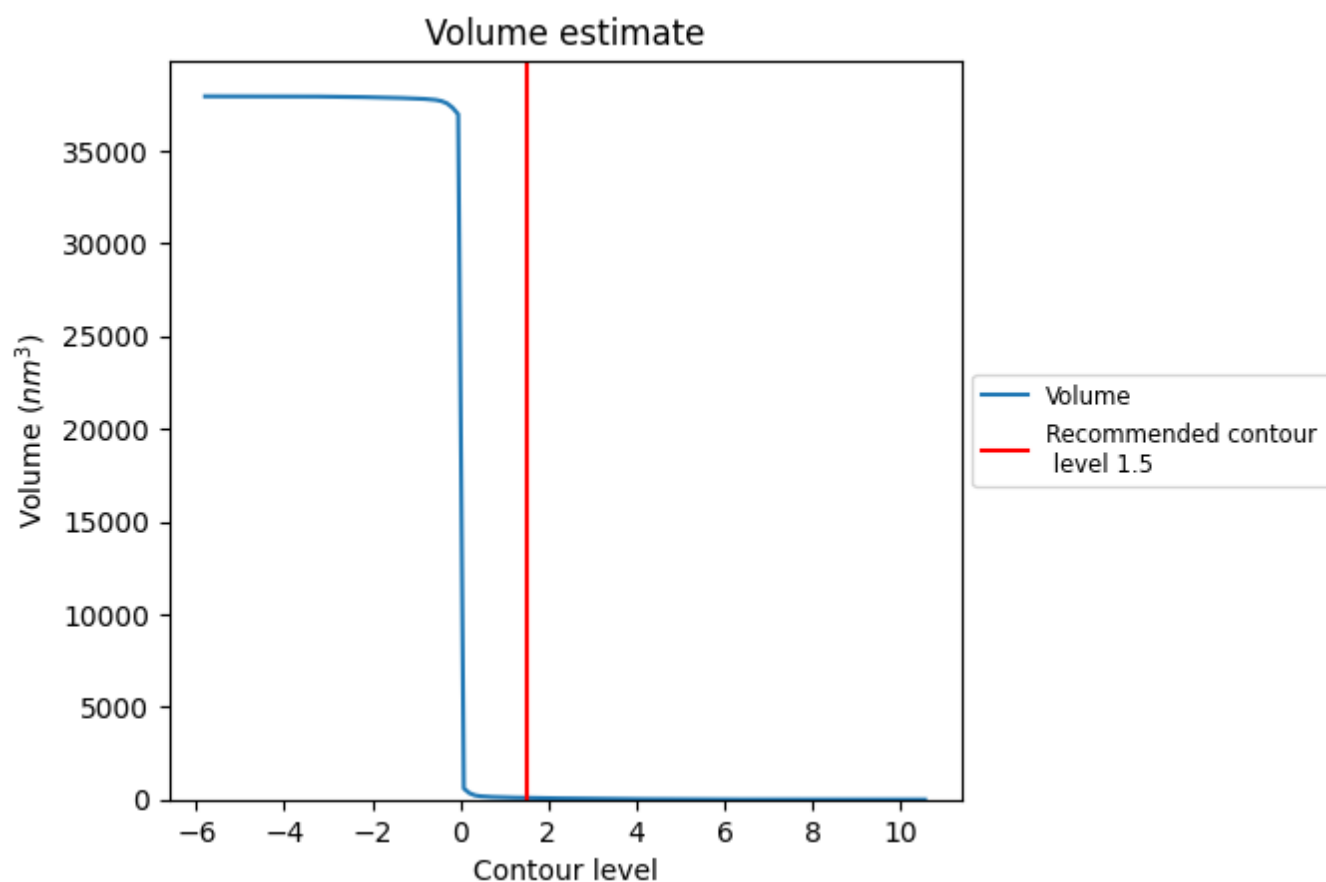
This section contains the results of statistical analysis of the map.

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.

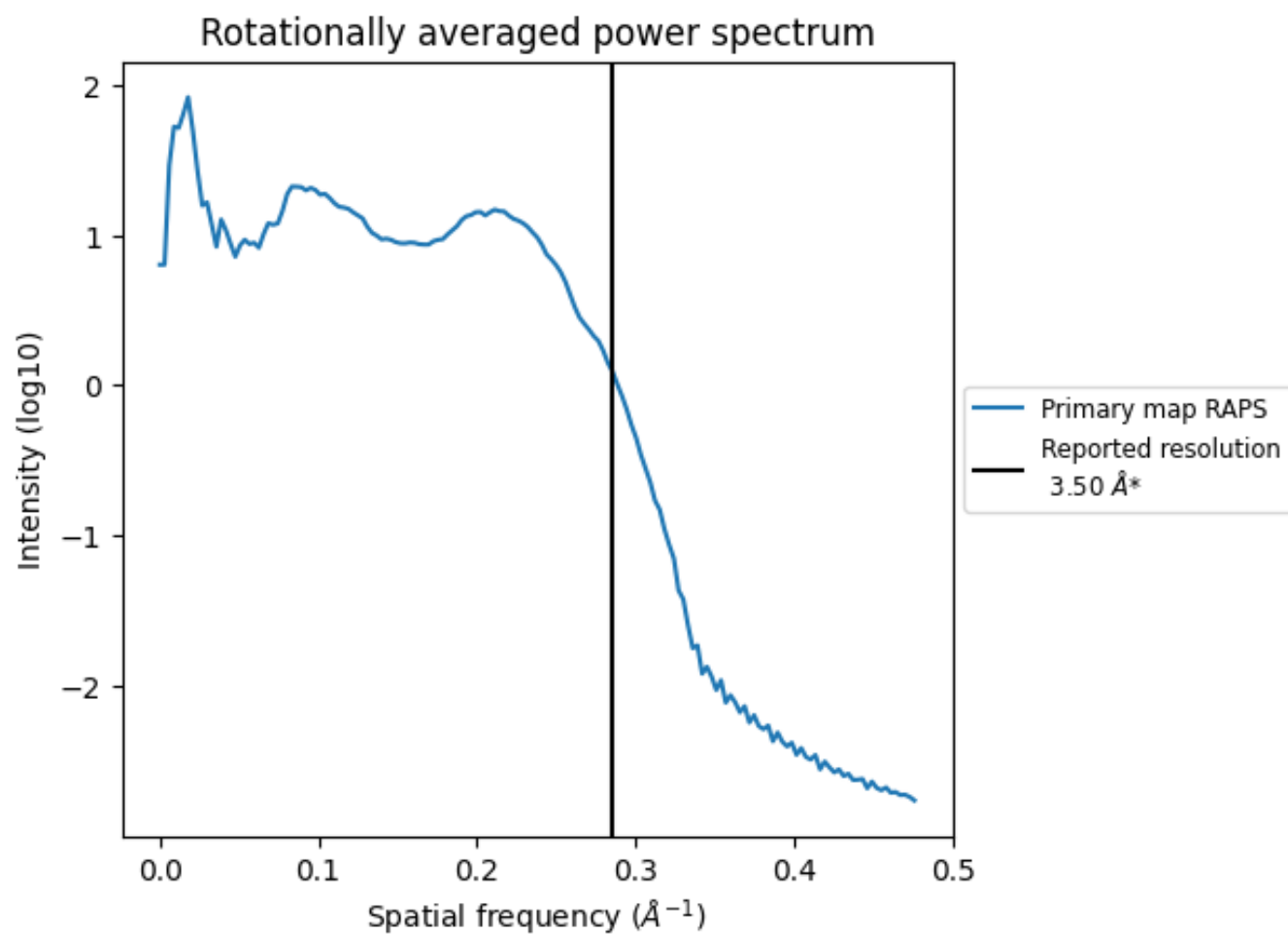
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 92 nm^3 ; this corresponds to an approximate mass of 83 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 ⓘ



*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

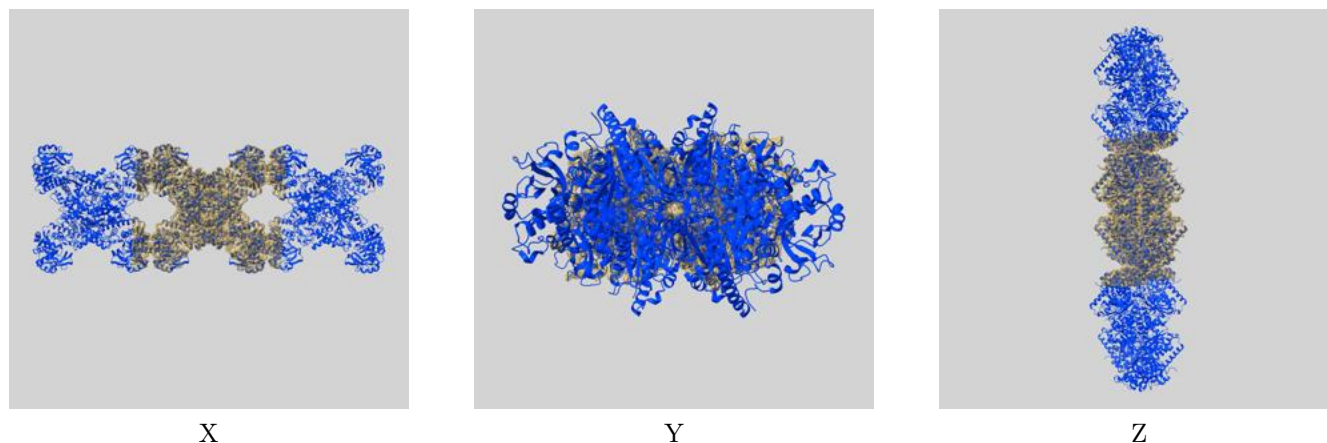
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

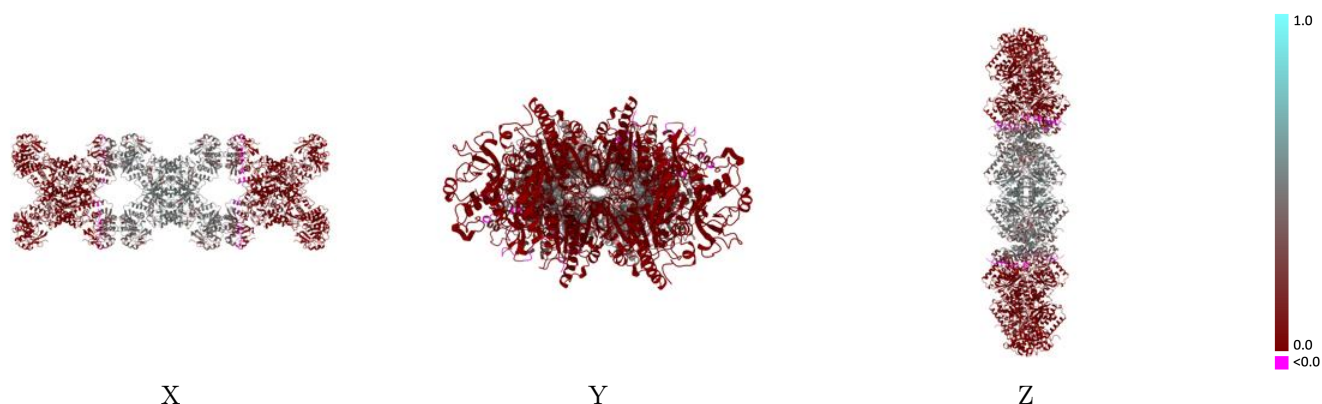
This section contains information regarding the fit between EMDB map EMD-24560 and PDB model 7RMC. Per-residue inclusion information can be found in section [3](#) on page [10](#).

9.1 Map-model overlay [i](#)



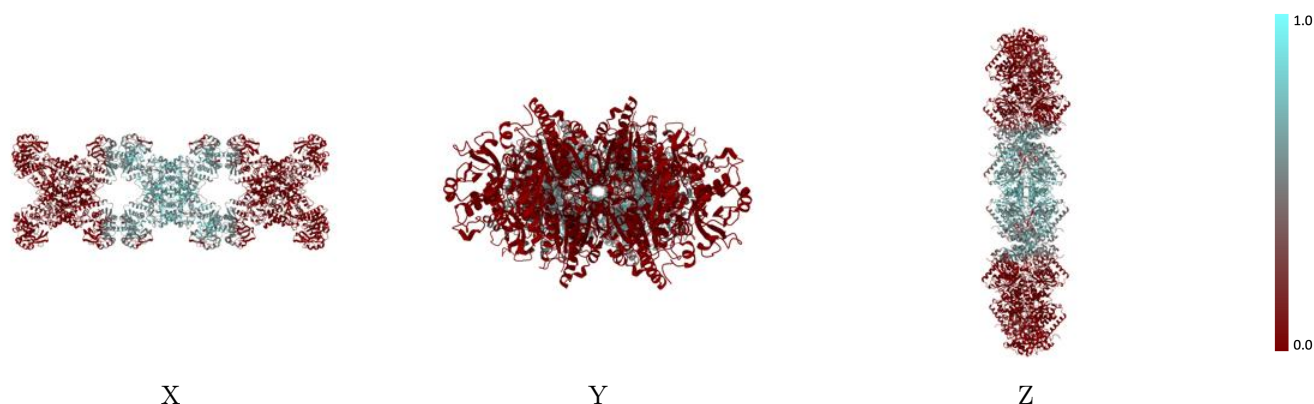
The images above show the 3D surface view of the map at the recommended contour level 1.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



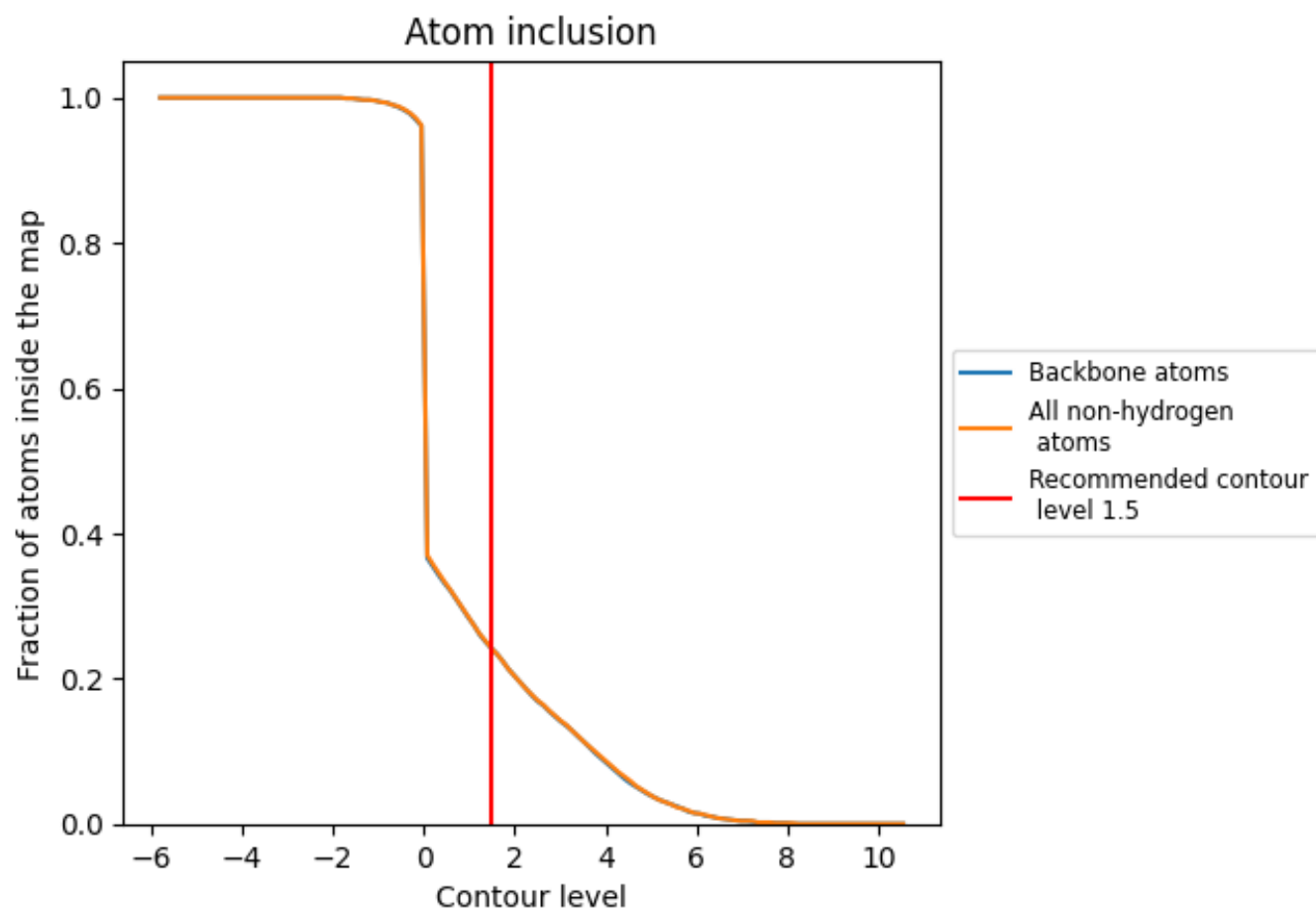
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.5).

9.4 Atom inclusion [i](#)



At the recommended contour level, 24% of all backbone atoms, 24% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (1.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.2410	0.1800
D	0.0000	0.0000
E	0.1290	0.0910
F	0.1270	0.0910
Q	0.1200	0.0790
R	0.6050	0.4520
S	0.0000	0.0000
T	0.6080	0.4530
U	0.0000	0.0000
V	0.0000	0.0000
W	0.6080	0.4520
g	0.1300	0.0900
h	0.6070	0.4530

1.0

0.0

<0.0