



## wwPDB EM Validation Summary Report ⓘ

Nov 21, 2023 – 12:29 PM EST

PDB ID : 8TFK  
EMDB ID : EMD-41232  
Title : Cryo-EM structure of the Methanosarcina mazei glutamine synthetase (GS) with Met-Sox-P and ADP  
Authors : Schumacher, M.A.  
Deposited on : 2023-07-11  
Resolution : 2.66 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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev70  
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 : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

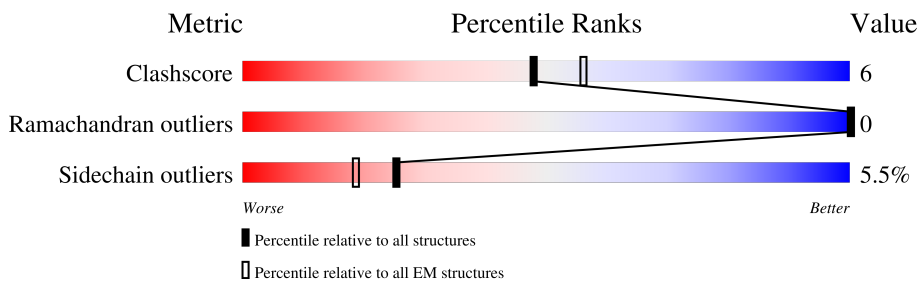
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 2.66 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  $\geq 3$ , 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	A	467	
1	B	467	
1	C	467	
1	D	467	
1	E	467	
1	F	467	
1	G	467	
1	H	467	

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Mol	Chain	Length	Quality of chain
1	I	467	<p>76% 77% 16% • 6%</p>
1	J	467	<p>61% 78% 16% • 6%</p>
1	K	467	<p>57% 77% 16% • 6%</p>
1	L	467	<p>70% 79% 13% • 6%</p>

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 81795 atoms, of which 39853 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 Glutamine synthetase.

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	H	N	O			S
1	A	440	6734	2213	3282	586	637	16	0	0
1	B	440	6750	2211	3299	585	640	15	0	0
1	C	440	6779	2215	3324	587	638	15	0	0
1	D	440	6752	2210	3303	586	638	15	0	0
1	E	440	6725	2207	3282	584	637	15	0	0
1	F	440	6755	2212	3304	586	638	15	0	0
1	G	440	6756	2211	3305	585	640	15	0	0
1	H	440	6750	2211	3302	586	636	15	0	0
1	I	440	6764	2216	3305	587	641	15	0	0
1	J	440	6755	2212	3304	586	638	15	0	0
1	K	440	6755	2212	3304	586	638	15	0	0
1	L	440	6728	2208	3287	586	632	15	0	0

There are 240 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP Q8PY99
A	-18	GLY	-	expression tag	UNP Q8PY99
A	-17	SER	-	expression tag	UNP Q8PY99
A	-16	SER	-	expression tag	UNP Q8PY99
A	-15	HIS	-	expression tag	UNP Q8PY99
A	-14	HIS	-	expression tag	UNP Q8PY99

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	HIS	-	expression tag	UNP Q8PY99
A	-12	HIS	-	expression tag	UNP Q8PY99
A	-11	HIS	-	expression tag	UNP Q8PY99
A	-10	HIS	-	expression tag	UNP Q8PY99
A	-9	SER	-	expression tag	UNP Q8PY99
A	-8	SER	-	expression tag	UNP Q8PY99
A	-7	GLY	-	expression tag	UNP Q8PY99
A	-6	LEU	-	expression tag	UNP Q8PY99
A	-5	VAL	-	expression tag	UNP Q8PY99
A	-4	PRO	-	expression tag	UNP Q8PY99
A	-3	ARG	-	expression tag	UNP Q8PY99
A	-2	GLY	-	expression tag	UNP Q8PY99
A	-1	SER	-	expression tag	UNP Q8PY99
A	0	HIS	-	expression tag	UNP Q8PY99
B	-19	MET	-	initiating methionine	UNP Q8PY99
B	-18	GLY	-	expression tag	UNP Q8PY99
B	-17	SER	-	expression tag	UNP Q8PY99
B	-16	SER	-	expression tag	UNP Q8PY99
B	-15	HIS	-	expression tag	UNP Q8PY99
B	-14	HIS	-	expression tag	UNP Q8PY99
B	-13	HIS	-	expression tag	UNP Q8PY99
B	-12	HIS	-	expression tag	UNP Q8PY99
B	-11	HIS	-	expression tag	UNP Q8PY99
B	-10	HIS	-	expression tag	UNP Q8PY99
B	-9	SER	-	expression tag	UNP Q8PY99
B	-8	SER	-	expression tag	UNP Q8PY99
B	-7	GLY	-	expression tag	UNP Q8PY99
B	-6	LEU	-	expression tag	UNP Q8PY99
B	-5	VAL	-	expression tag	UNP Q8PY99
B	-4	PRO	-	expression tag	UNP Q8PY99
B	-3	ARG	-	expression tag	UNP Q8PY99
B	-2	GLY	-	expression tag	UNP Q8PY99
B	-1	SER	-	expression tag	UNP Q8PY99
B	0	HIS	-	expression tag	UNP Q8PY99
C	-19	MET	-	initiating methionine	UNP Q8PY99
C	-18	GLY	-	expression tag	UNP Q8PY99
C	-17	SER	-	expression tag	UNP Q8PY99
C	-16	SER	-	expression tag	UNP Q8PY99
C	-15	HIS	-	expression tag	UNP Q8PY99
C	-14	HIS	-	expression tag	UNP Q8PY99
C	-13	HIS	-	expression tag	UNP Q8PY99
C	-12	HIS	-	expression tag	UNP Q8PY99

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-11	HIS	-	expression tag	UNP Q8PY99
C	-10	HIS	-	expression tag	UNP Q8PY99
C	-9	SER	-	expression tag	UNP Q8PY99
C	-8	SER	-	expression tag	UNP Q8PY99
C	-7	GLY	-	expression tag	UNP Q8PY99
C	-6	LEU	-	expression tag	UNP Q8PY99
C	-5	VAL	-	expression tag	UNP Q8PY99
C	-4	PRO	-	expression tag	UNP Q8PY99
C	-3	ARG	-	expression tag	UNP Q8PY99
C	-2	GLY	-	expression tag	UNP Q8PY99
C	-1	SER	-	expression tag	UNP Q8PY99
C	0	HIS	-	expression tag	UNP Q8PY99
D	-19	MET	-	initiating methionine	UNP Q8PY99
D	-18	GLY	-	expression tag	UNP Q8PY99
D	-17	SER	-	expression tag	UNP Q8PY99
D	-16	SER	-	expression tag	UNP Q8PY99
D	-15	HIS	-	expression tag	UNP Q8PY99
D	-14	HIS	-	expression tag	UNP Q8PY99
D	-13	HIS	-	expression tag	UNP Q8PY99
D	-12	HIS	-	expression tag	UNP Q8PY99
D	-11	HIS	-	expression tag	UNP Q8PY99
D	-10	HIS	-	expression tag	UNP Q8PY99
D	-9	SER	-	expression tag	UNP Q8PY99
D	-8	SER	-	expression tag	UNP Q8PY99
D	-7	GLY	-	expression tag	UNP Q8PY99
D	-6	LEU	-	expression tag	UNP Q8PY99
D	-5	VAL	-	expression tag	UNP Q8PY99
D	-4	PRO	-	expression tag	UNP Q8PY99
D	-3	ARG	-	expression tag	UNP Q8PY99
D	-2	GLY	-	expression tag	UNP Q8PY99
D	-1	SER	-	expression tag	UNP Q8PY99
D	0	HIS	-	expression tag	UNP Q8PY99
E	-19	MET	-	initiating methionine	UNP Q8PY99
E	-18	GLY	-	expression tag	UNP Q8PY99
E	-17	SER	-	expression tag	UNP Q8PY99
E	-16	SER	-	expression tag	UNP Q8PY99
E	-15	HIS	-	expression tag	UNP Q8PY99
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E	-13	HIS	-	expression tag	UNP Q8PY99
E	-12	HIS	-	expression tag	UNP Q8PY99
E	-11	HIS	-	expression tag	UNP Q8PY99
E	-10	HIS	-	expression tag	UNP Q8PY99

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-9	SER	-	expression tag	UNP Q8PY99
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E	-7	GLY	-	expression tag	UNP Q8PY99
E	-6	LEU	-	expression tag	UNP Q8PY99
E	-5	VAL	-	expression tag	UNP Q8PY99
E	-4	PRO	-	expression tag	UNP Q8PY99
E	-3	ARG	-	expression tag	UNP Q8PY99
E	-2	GLY	-	expression tag	UNP Q8PY99
E	-1	SER	-	expression tag	UNP Q8PY99
E	0	HIS	-	expression tag	UNP Q8PY99
F	-19	MET	-	initiating methionine	UNP Q8PY99
F	-18	GLY	-	expression tag	UNP Q8PY99
F	-17	SER	-	expression tag	UNP Q8PY99
F	-16	SER	-	expression tag	UNP Q8PY99
F	-15	HIS	-	expression tag	UNP Q8PY99
F	-14	HIS	-	expression tag	UNP Q8PY99
F	-13	HIS	-	expression tag	UNP Q8PY99
F	-12	HIS	-	expression tag	UNP Q8PY99
F	-11	HIS	-	expression tag	UNP Q8PY99
F	-10	HIS	-	expression tag	UNP Q8PY99
F	-9	SER	-	expression tag	UNP Q8PY99
F	-8	SER	-	expression tag	UNP Q8PY99
F	-7	GLY	-	expression tag	UNP Q8PY99
F	-6	LEU	-	expression tag	UNP Q8PY99
F	-5	VAL	-	expression tag	UNP Q8PY99
F	-4	PRO	-	expression tag	UNP Q8PY99
F	-3	ARG	-	expression tag	UNP Q8PY99
F	-2	GLY	-	expression tag	UNP Q8PY99
F	-1	SER	-	expression tag	UNP Q8PY99
F	0	HIS	-	expression tag	UNP Q8PY99
G	-19	MET	-	initiating methionine	UNP Q8PY99
G	-18	GLY	-	expression tag	UNP Q8PY99
G	-17	SER	-	expression tag	UNP Q8PY99
G	-16	SER	-	expression tag	UNP Q8PY99
G	-15	HIS	-	expression tag	UNP Q8PY99
G	-14	HIS	-	expression tag	UNP Q8PY99
G	-13	HIS	-	expression tag	UNP Q8PY99
G	-12	HIS	-	expression tag	UNP Q8PY99
G	-11	HIS	-	expression tag	UNP Q8PY99
G	-10	HIS	-	expression tag	UNP Q8PY99
G	-9	SER	-	expression tag	UNP Q8PY99
G	-8	SER	-	expression tag	UNP Q8PY99

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-7	GLY	-	expression tag	UNP Q8PY99
G	-6	LEU	-	expression tag	UNP Q8PY99
G	-5	VAL	-	expression tag	UNP Q8PY99
G	-4	PRO	-	expression tag	UNP Q8PY99
G	-3	ARG	-	expression tag	UNP Q8PY99
G	-2	GLY	-	expression tag	UNP Q8PY99
G	-1	SER	-	expression tag	UNP Q8PY99
G	0	HIS	-	expression tag	UNP Q8PY99
H	-19	MET	-	initiating methionine	UNP Q8PY99
H	-18	GLY	-	expression tag	UNP Q8PY99
H	-17	SER	-	expression tag	UNP Q8PY99
H	-16	SER	-	expression tag	UNP Q8PY99
H	-15	HIS	-	expression tag	UNP Q8PY99
H	-14	HIS	-	expression tag	UNP Q8PY99
H	-13	HIS	-	expression tag	UNP Q8PY99
H	-12	HIS	-	expression tag	UNP Q8PY99
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I	-8	SER	-	expression tag	UNP Q8PY99
I	-7	GLY	-	expression tag	UNP Q8PY99
I	-6	LEU	-	expression tag	UNP Q8PY99

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Chain	Residue	Modelled	Actual	Comment	Reference
I	-5	VAL	-	expression tag	UNP Q8PY99
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I	-3	ARG	-	expression tag	UNP Q8PY99
I	-2	GLY	-	expression tag	UNP Q8PY99
I	-1	SER	-	expression tag	UNP Q8PY99
I	0	HIS	-	expression tag	UNP Q8PY99
J	-19	MET	-	initiating methionine	UNP Q8PY99
J	-18	GLY	-	expression tag	UNP Q8PY99
J	-17	SER	-	expression tag	UNP Q8PY99
J	-16	SER	-	expression tag	UNP Q8PY99
J	-15	HIS	-	expression tag	UNP Q8PY99
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J	-13	HIS	-	expression tag	UNP Q8PY99
J	-12	HIS	-	expression tag	UNP Q8PY99
J	-11	HIS	-	expression tag	UNP Q8PY99
J	-10	HIS	-	expression tag	UNP Q8PY99
J	-9	SER	-	expression tag	UNP Q8PY99
J	-8	SER	-	expression tag	UNP Q8PY99
J	-7	GLY	-	expression tag	UNP Q8PY99
J	-6	LEU	-	expression tag	UNP Q8PY99
J	-5	VAL	-	expression tag	UNP Q8PY99
J	-4	PRO	-	expression tag	UNP Q8PY99
J	-3	ARG	-	expression tag	UNP Q8PY99
J	-2	GLY	-	expression tag	UNP Q8PY99
J	-1	SER	-	expression tag	UNP Q8PY99
J	0	HIS	-	expression tag	UNP Q8PY99
K	-19	MET	-	initiating methionine	UNP Q8PY99
K	-18	GLY	-	expression tag	UNP Q8PY99
K	-17	SER	-	expression tag	UNP Q8PY99
K	-16	SER	-	expression tag	UNP Q8PY99
K	-15	HIS	-	expression tag	UNP Q8PY99
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K	-12	HIS	-	expression tag	UNP Q8PY99
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K	-10	HIS	-	expression tag	UNP Q8PY99
K	-9	SER	-	expression tag	UNP Q8PY99
K	-8	SER	-	expression tag	UNP Q8PY99
K	-7	GLY	-	expression tag	UNP Q8PY99
K	-6	LEU	-	expression tag	UNP Q8PY99
K	-5	VAL	-	expression tag	UNP Q8PY99
K	-4	PRO	-	expression tag	UNP Q8PY99

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Chain	Residue	Modelled	Actual	Comment	Reference
K	-3	ARG	-	expression tag	UNP Q8PY99
K	-2	GLY	-	expression tag	UNP Q8PY99
K	-1	SER	-	expression tag	UNP Q8PY99
K	0	HIS	-	expression tag	UNP Q8PY99
L	-19	MET	-	initiating methionine	UNP Q8PY99
L	-18	GLY	-	expression tag	UNP Q8PY99
L	-17	SER	-	expression tag	UNP Q8PY99
L	-16	SER	-	expression tag	UNP Q8PY99
L	-15	HIS	-	expression tag	UNP Q8PY99
L	-14	HIS	-	expression tag	UNP Q8PY99
L	-13	HIS	-	expression tag	UNP Q8PY99
L	-12	HIS	-	expression tag	UNP Q8PY99
L	-11	HIS	-	expression tag	UNP Q8PY99
L	-10	HIS	-	expression tag	UNP Q8PY99
L	-9	SER	-	expression tag	UNP Q8PY99
L	-8	SER	-	expression tag	UNP Q8PY99
L	-7	GLY	-	expression tag	UNP Q8PY99
L	-6	LEU	-	expression tag	UNP Q8PY99
L	-5	VAL	-	expression tag	UNP Q8PY99
L	-4	PRO	-	expression tag	UNP Q8PY99
L	-3	ARG	-	expression tag	UNP Q8PY99
L	-2	GLY	-	expression tag	UNP Q8PY99
L	-1	SER	-	expression tag	UNP Q8PY99
L	0	HIS	-	expression tag	UNP Q8PY99

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

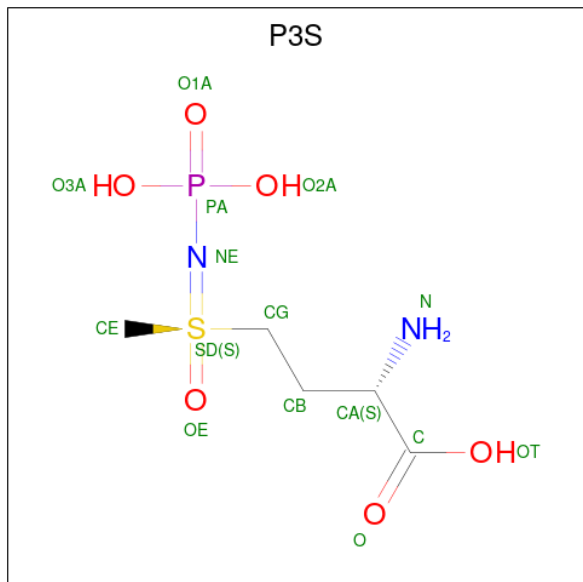
Mol	Chain	Residues	Atoms	AltConf
2	A	3	Total Mg 3 3	0
2	B	3	Total Mg 3 3	0
2	C	3	Total Mg 3 3	0
2	D	3	Total Mg 3 3	0
2	E	3	Total Mg 3 3	0
2	F	3	Total Mg 3 3	0
2	G	3	Total Mg 3 3	0

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Mol	Chain	Residues	Atoms		AltConf
2	H	3	Total 3	Mg 3	0
2	I	3	Total 3	Mg 3	0
2	J	3	Total 3	Mg 3	0
2	K	3	Total 3	Mg 3	0
2	L	3	Total 3	Mg 3	0

- Molecule 3 is L-METHIONINE-S-SULFOXIMINE PHOSPHATE (three-letter code: P3S) (formula:  $C_5H_{13}N_2O_6PS$ ) (labeled as "Ligand of Interest" by depositor).



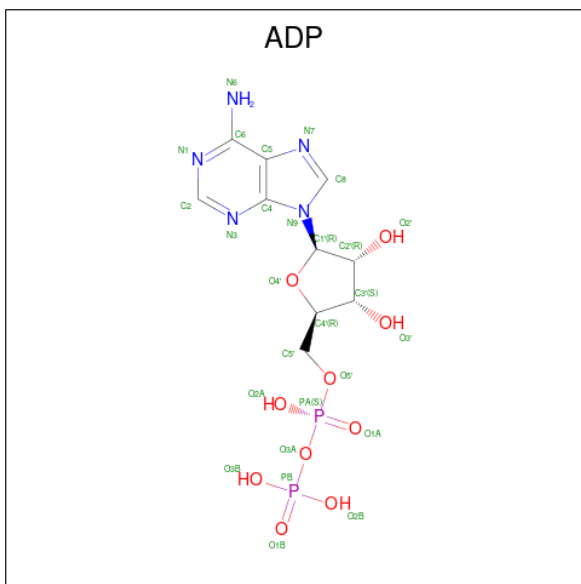
Mol	Chain	Residues	Atoms							AltConf
			Total	C	H	N	O	P	S	
3	A	1	Total 25	C 5	H 10	N 2	O 6	P 1	S 1	0
3	B	1	Total 25	C 5	H 10	N 2	O 6	P 1	S 1	0
3	C	1	Total 25	C 5	H 10	N 2	O 6	P 1	S 1	0
3	D	1	Total 25	C 5	H 10	N 2	O 6	P 1	S 1	0
3	E	1	Total 25	C 5	H 10	N 2	O 6	P 1	S 1	0
3	F	1	Total 25	C 5	H 10	N 2	O 6	P 1	S 1	0

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Mol	Chain	Residues	Atoms						AltConf	
			Total	C	H	N	O	P		S
3	G	1	Total	C	H	N	O	P	S	0
			25	5	10	2	6	1	1	
3	H	1	Total	C	H	N	O	P	S	0
			25	5	10	2	6	1	1	
3	I	1	Total	C	H	N	O	P	S	0
			25	5	10	2	6	1	1	
3	J	1	Total	C	H	N	O	P	S	0
			25	5	10	2	6	1	1	
3	K	1	Total	C	H	N	O	P	S	0
			25	5	10	2	6	1	1	
3	L	1	Total	C	H	N	O	P	S	0
			25	5	10	2	6	1	1	

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula:  $C_{10}H_{15}N_5O_{10}P_2$ ).



Mol	Chain	Residues	Atoms					AltConf	
			Total	C	H	N	O		P
4	A	1	Total	C	H	N	O	P	0
			38	10	11	5	10	2	
4	B	1	Total	C	H	N	O	P	0
			38	10	11	5	10	2	
4	C	1	Total	C	H	N	O	P	0
			38	10	11	5	10	2	
4	D	1	Total	C	H	N	O	P	0
			38	10	11	5	10	2	
4	E	1	Total	C	H	N	O	P	0
			38	10	11	5	10	2	

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Mol	Chain	Residues	Atoms					AltConf	
			Total	C	H	N	O		P
4	F	1	Total 38	10	11	5	10	2	0
4	G	1	Total 38	10	11	5	10	2	0
4	H	1	Total 38	10	11	5	10	2	0
4	I	1	Total 38	10	11	5	10	2	0
4	J	1	Total 38	10	11	5	10	2	0
4	K	1	Total 38	10	11	5	10	2	0
4	L	1	Total 38	10	11	5	10	2	0

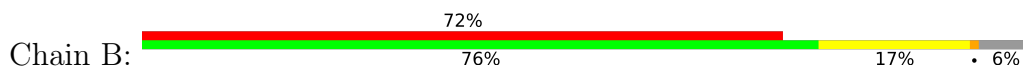
### 3 Residue-property plots [i](#)

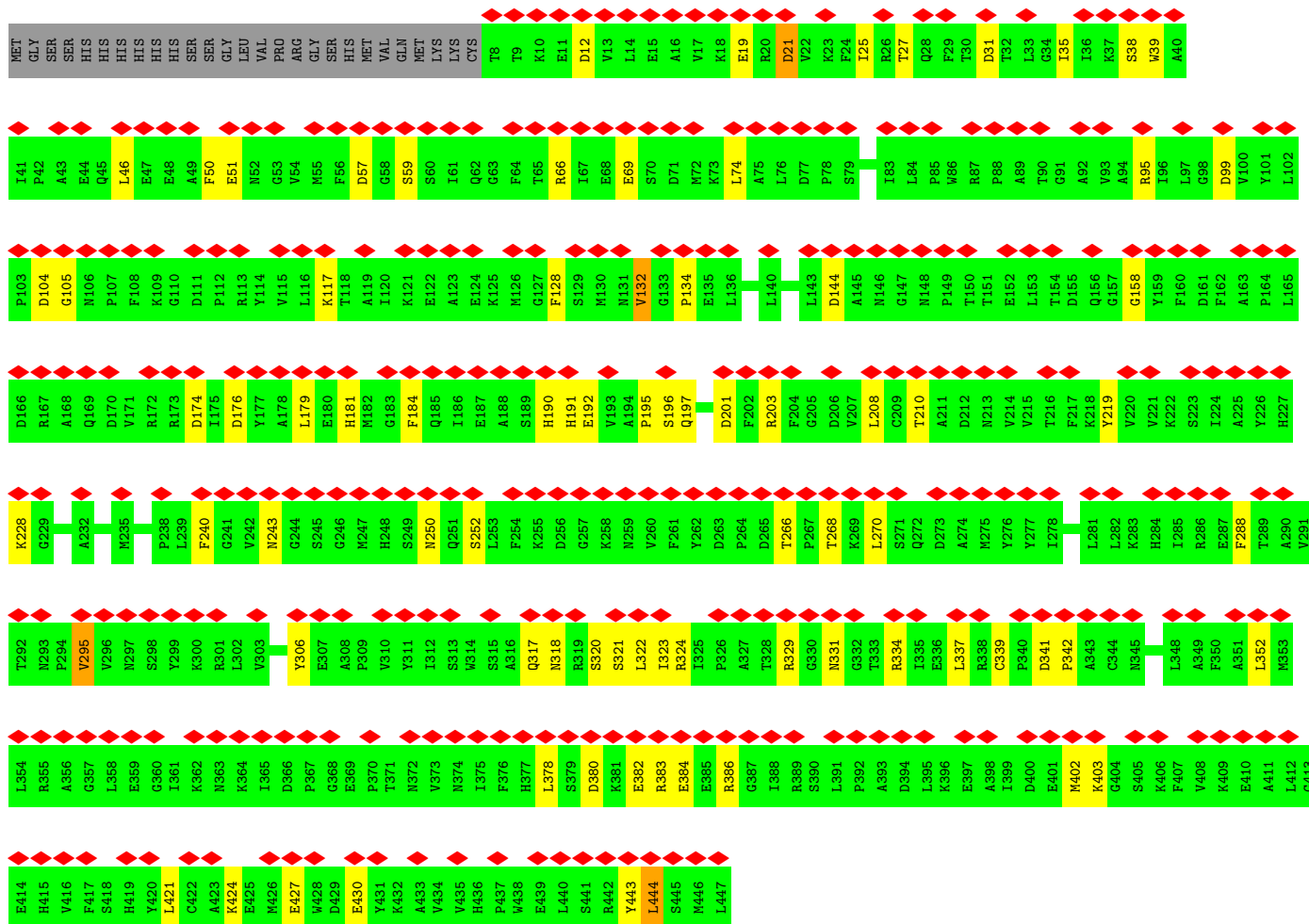
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

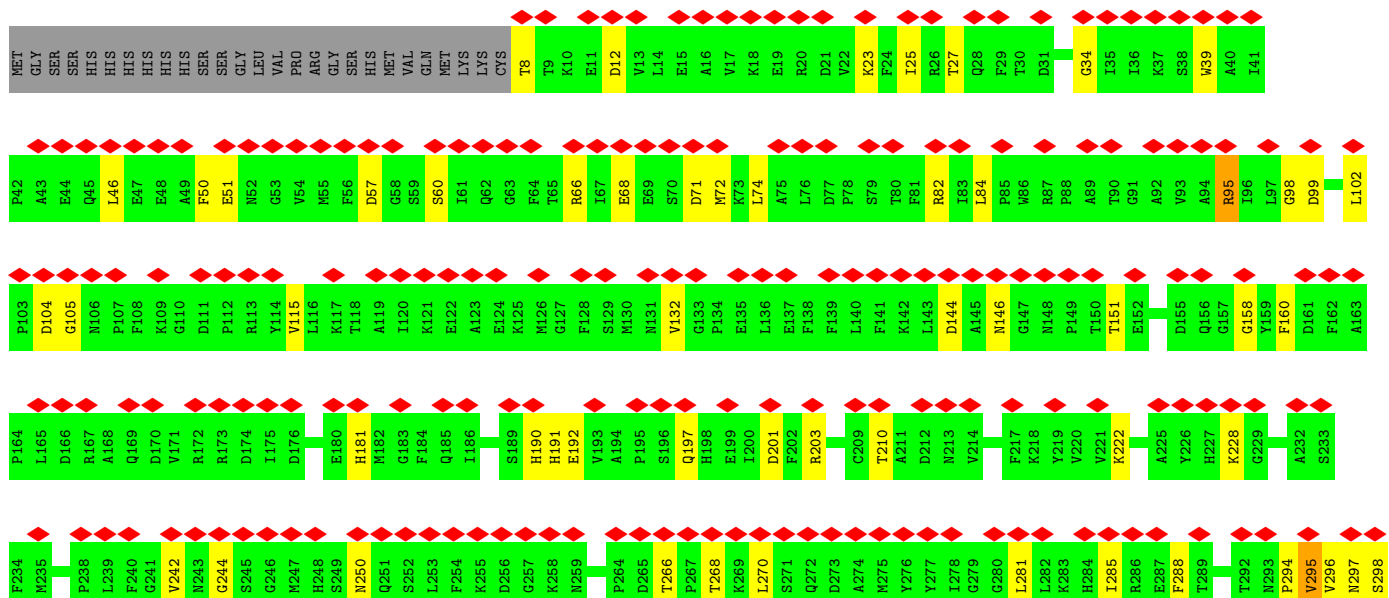
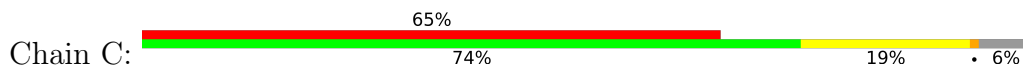


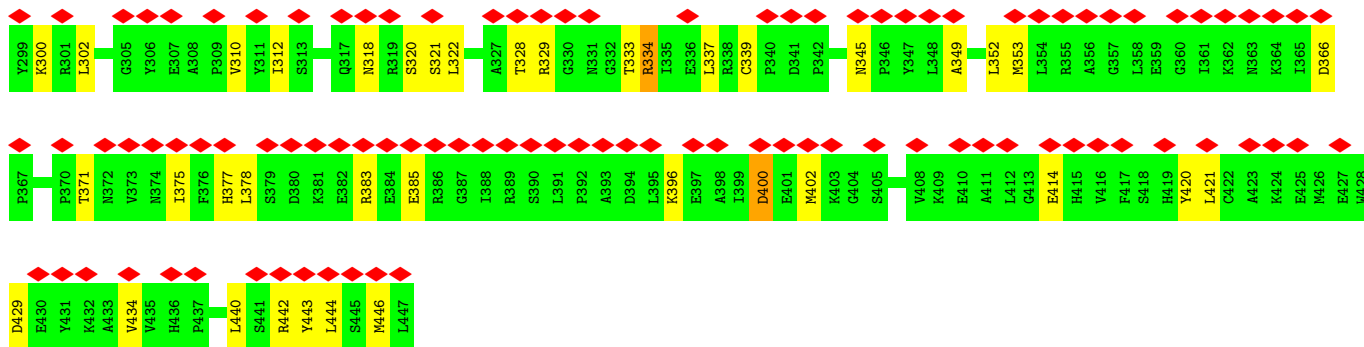
- Molecule 1: Glutamine synthetase



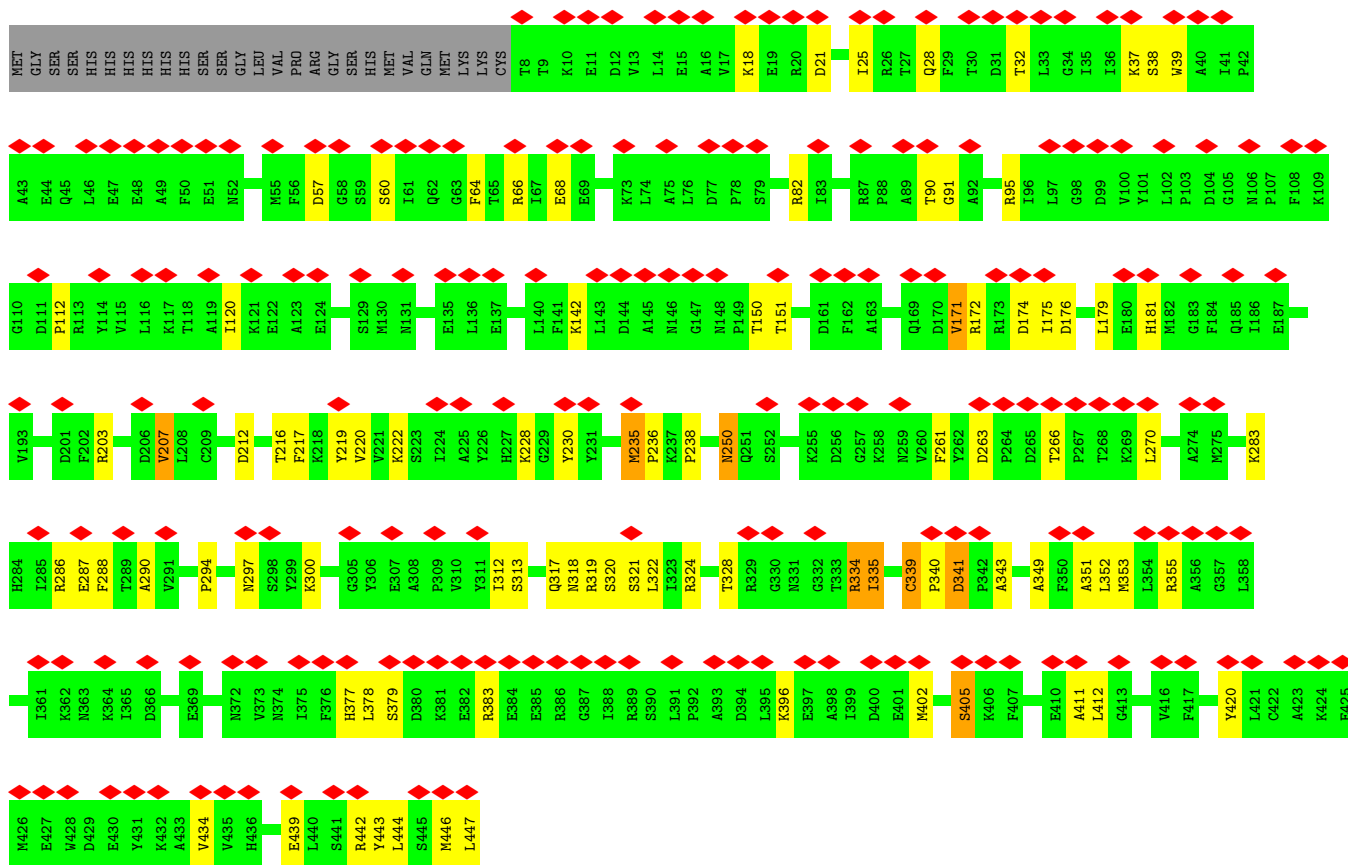
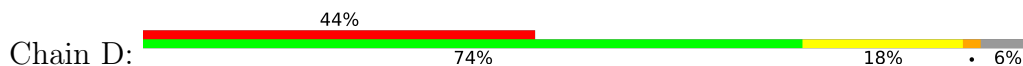


• Molecule 1: Glutamine synthetase

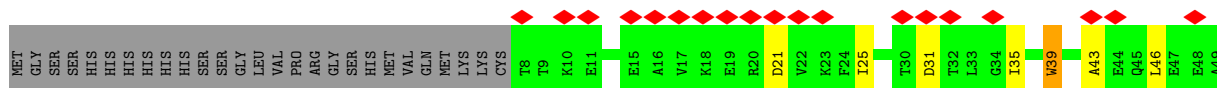
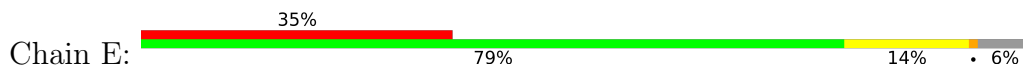




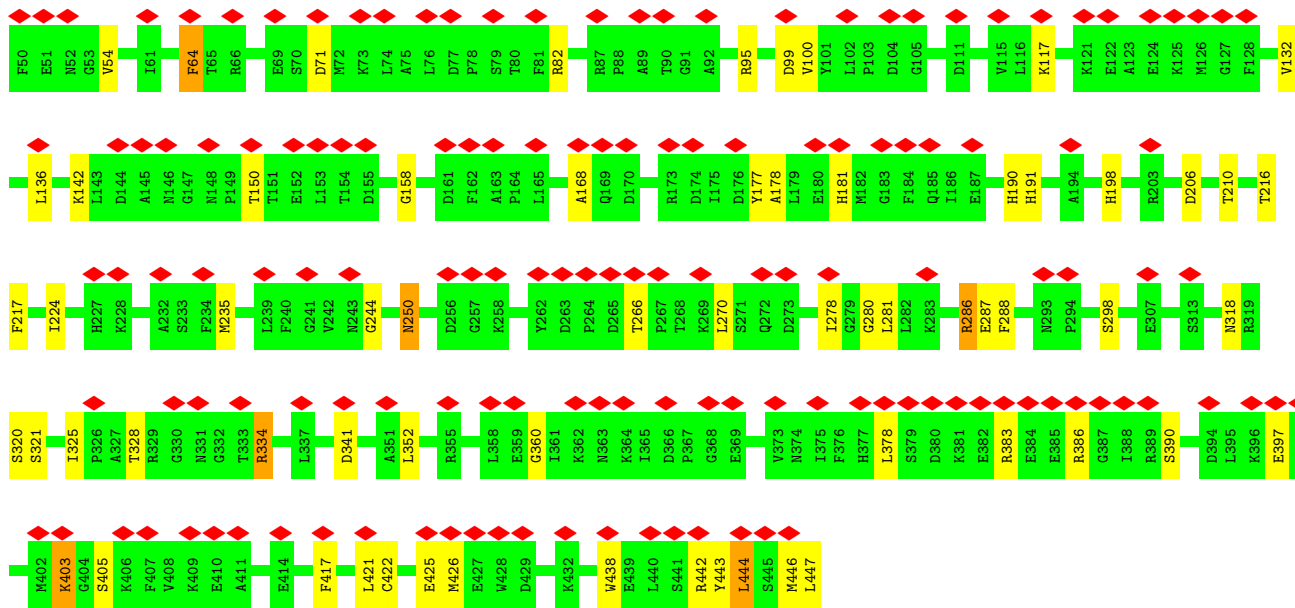
• Molecule 1: Glutamine synthetase



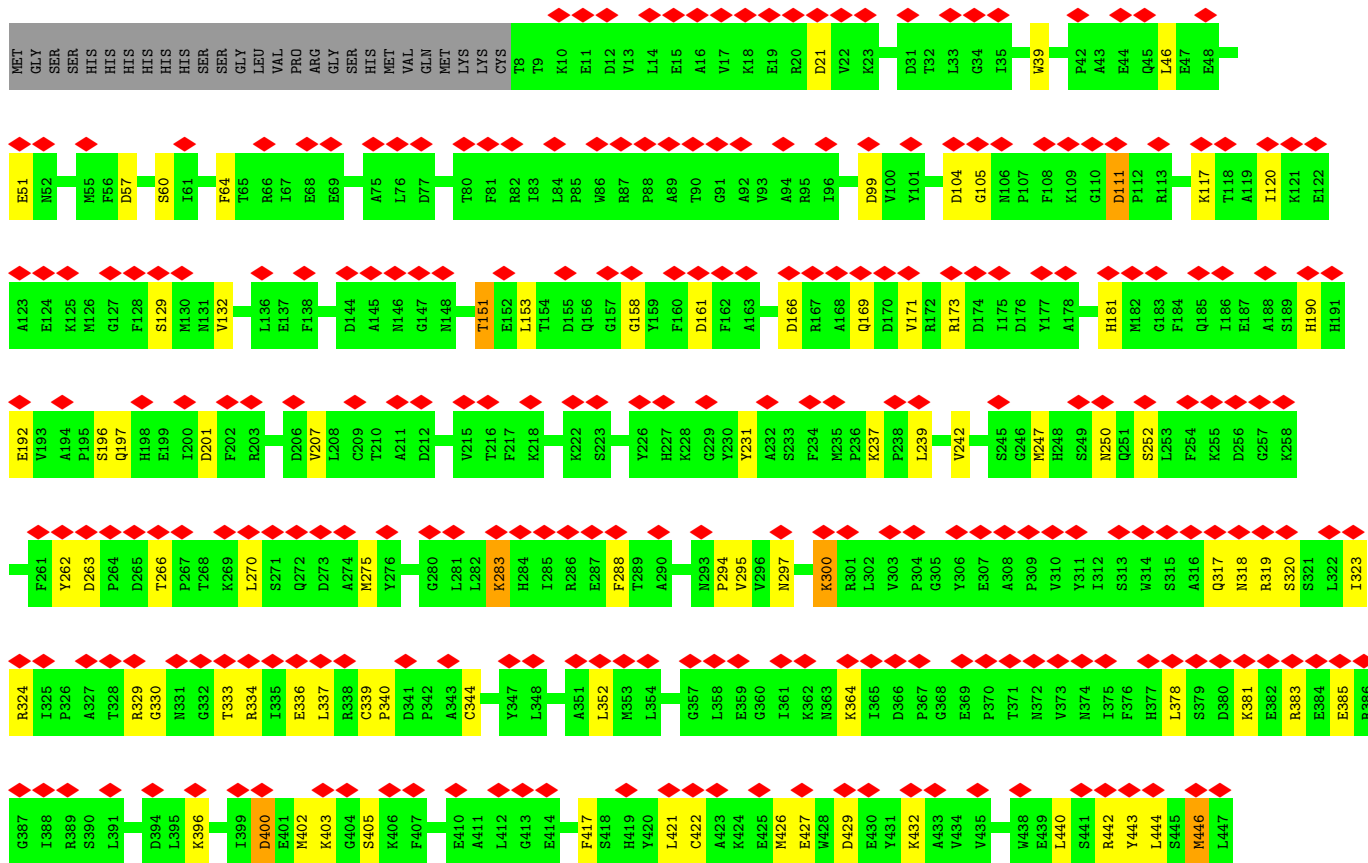
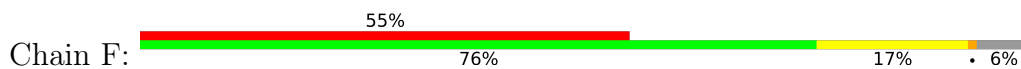
• Molecule 1: Glutamine synthetase



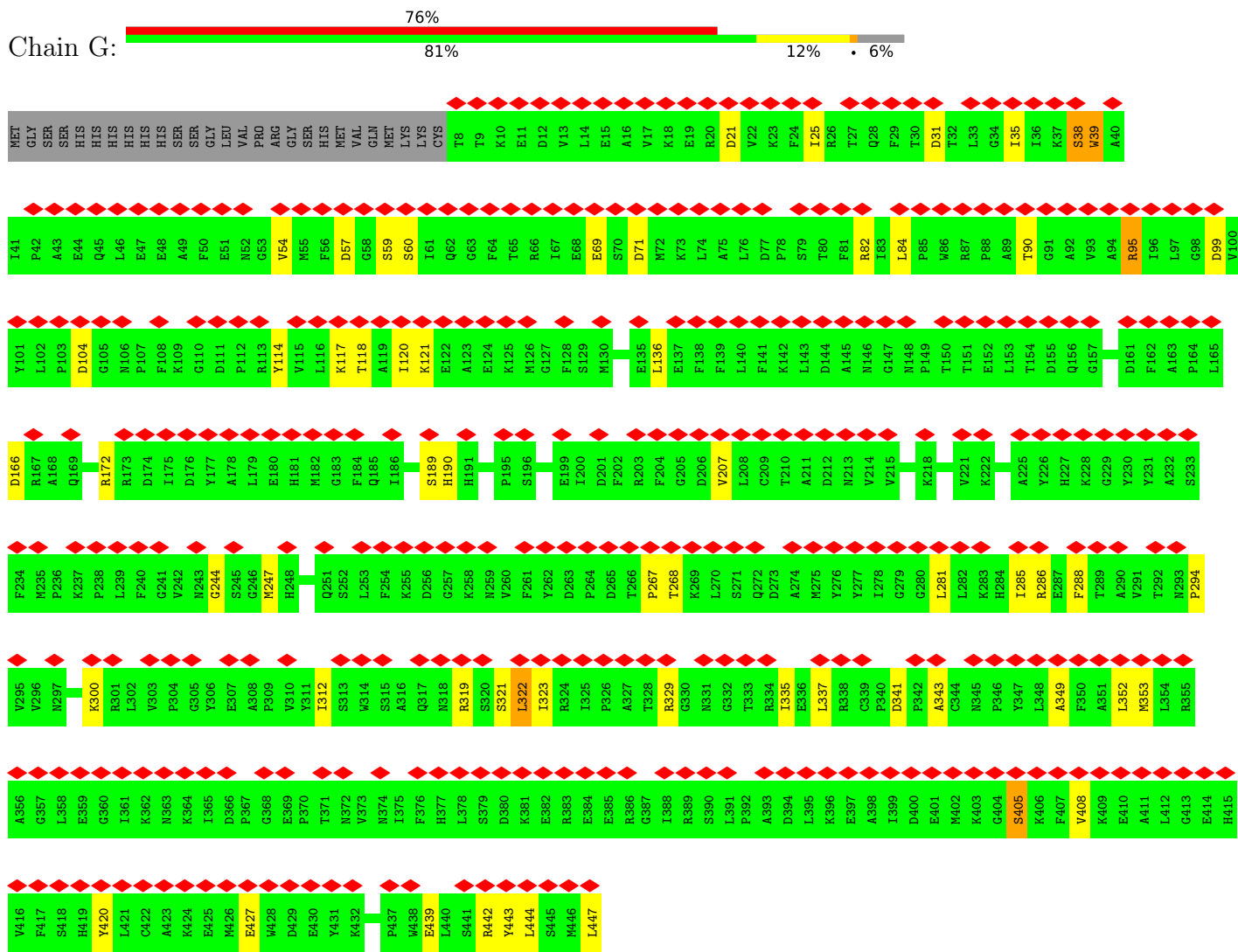




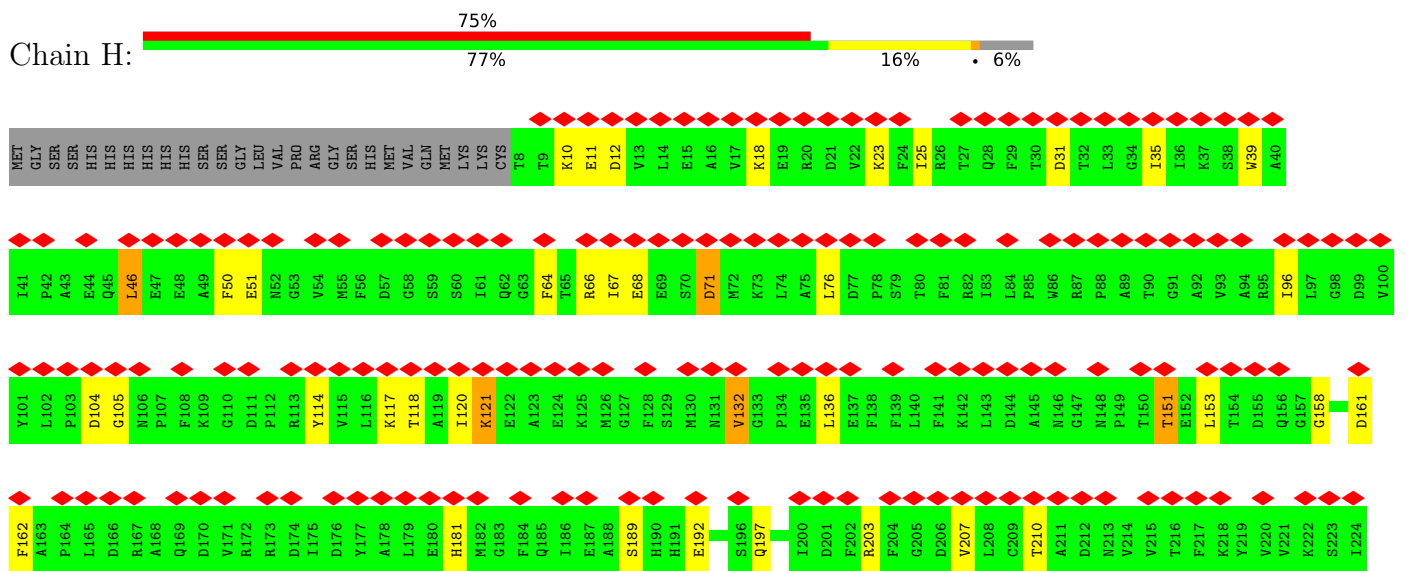
• Molecule 1: Glutamine synthetase

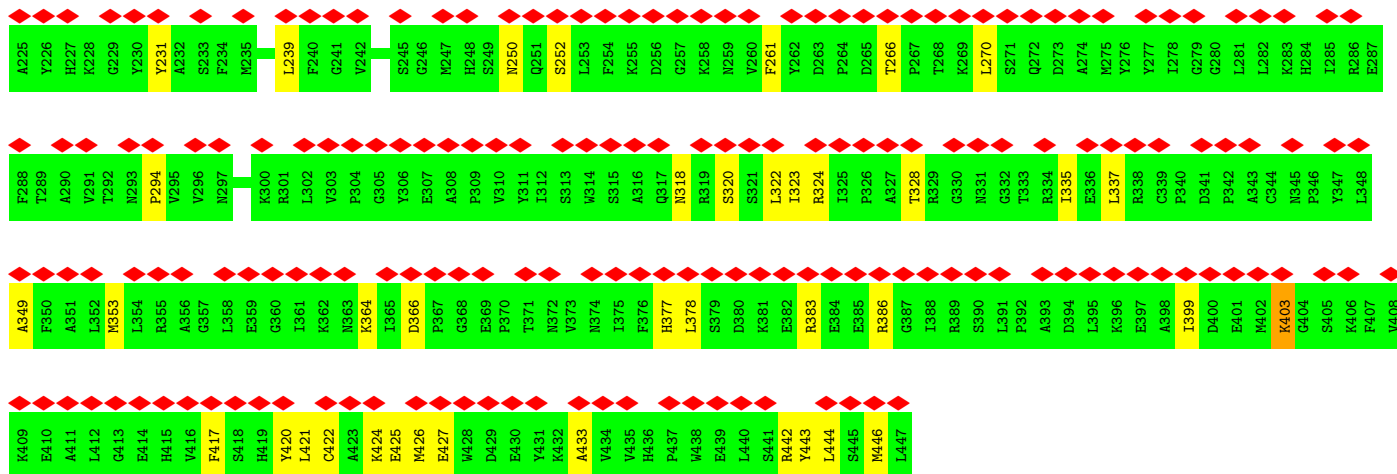


• Molecule 1: Glutamine synthetase

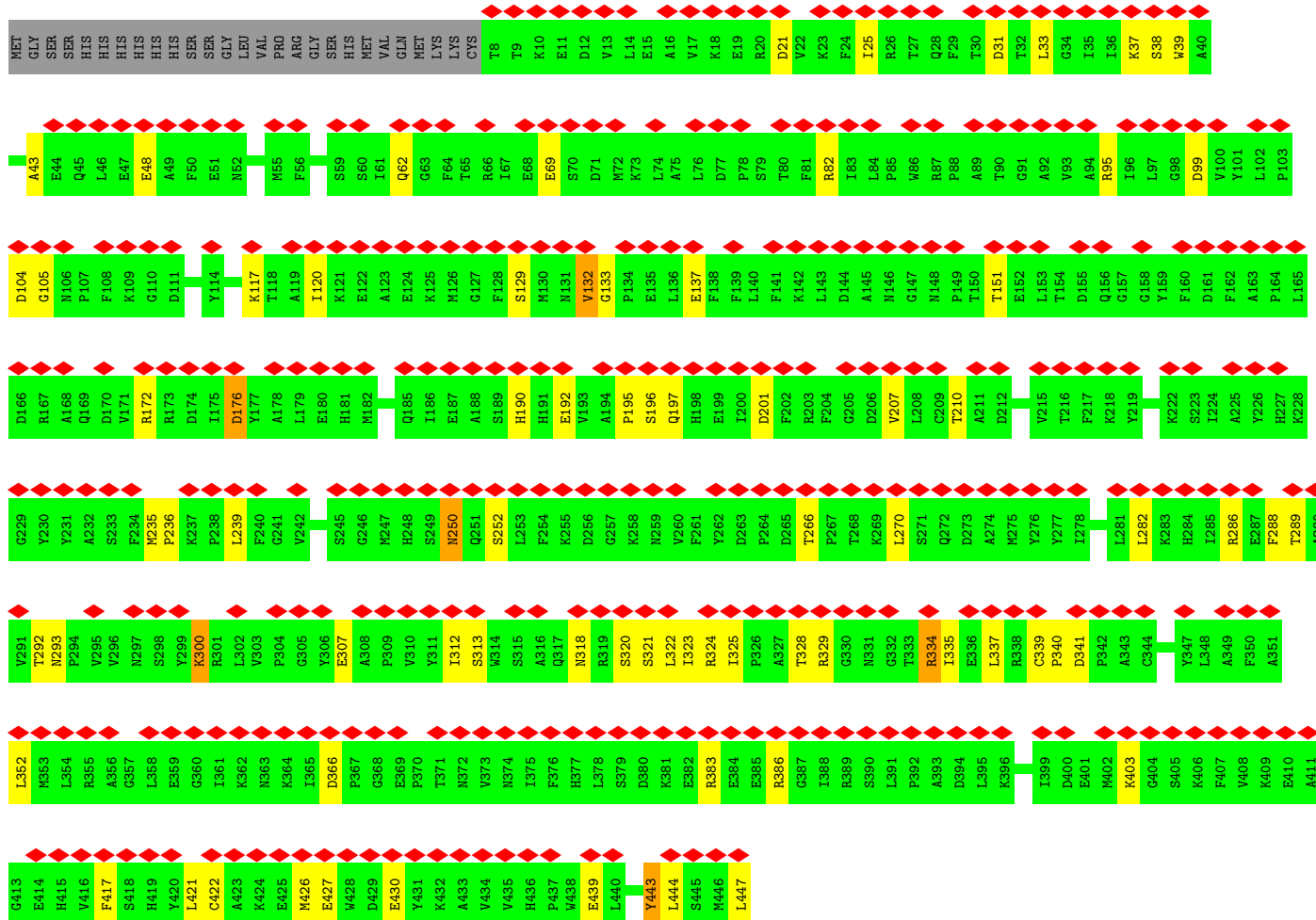
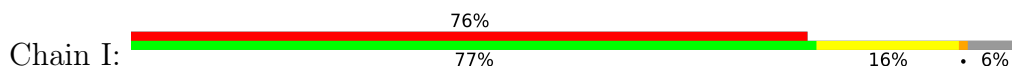


• Molecule 1: Glutamine synthetase

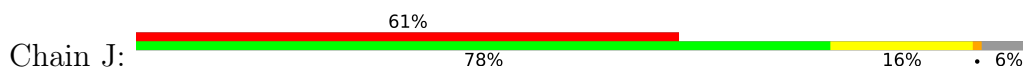


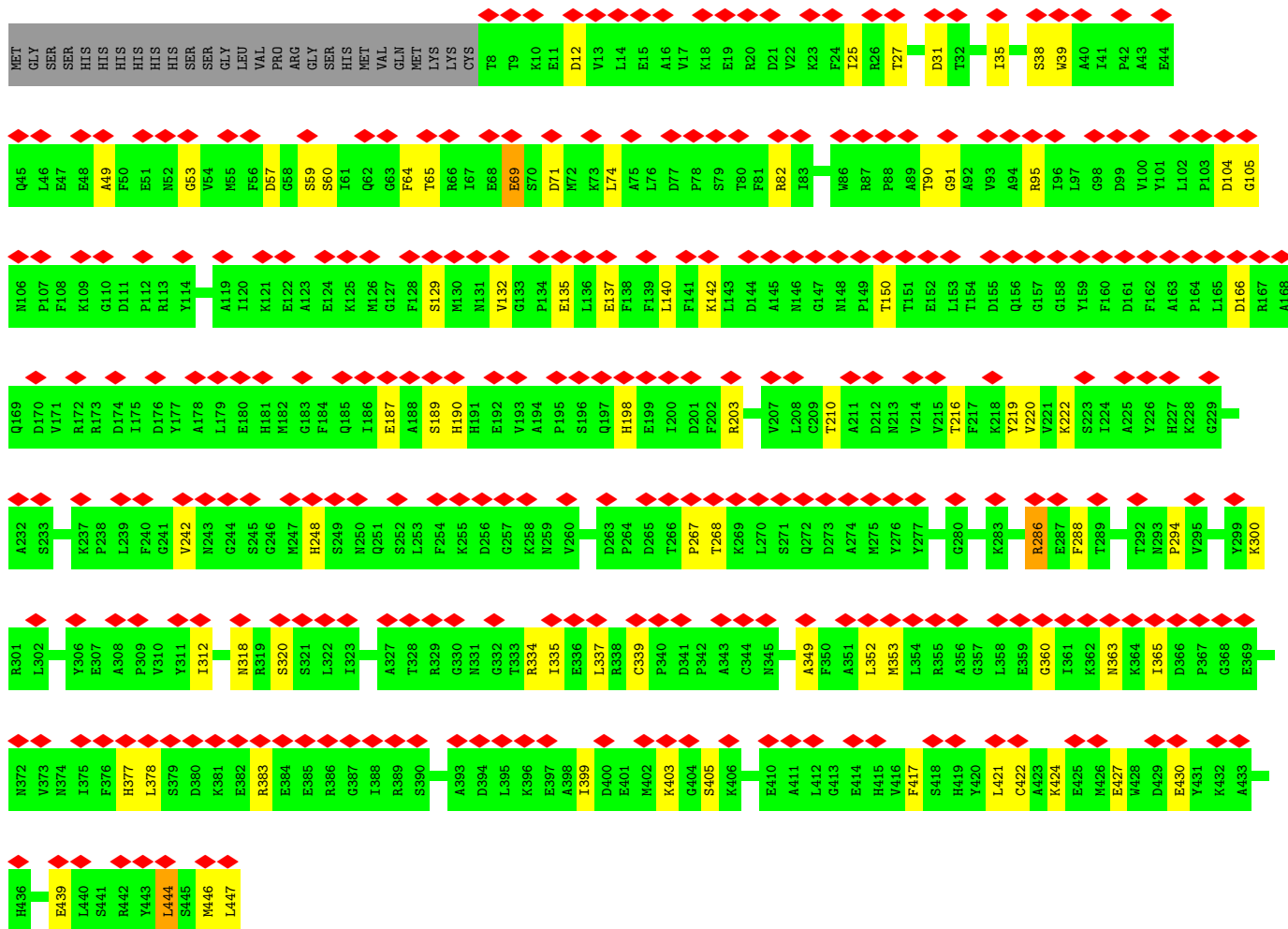


• Molecule 1: Glutamine synthetase

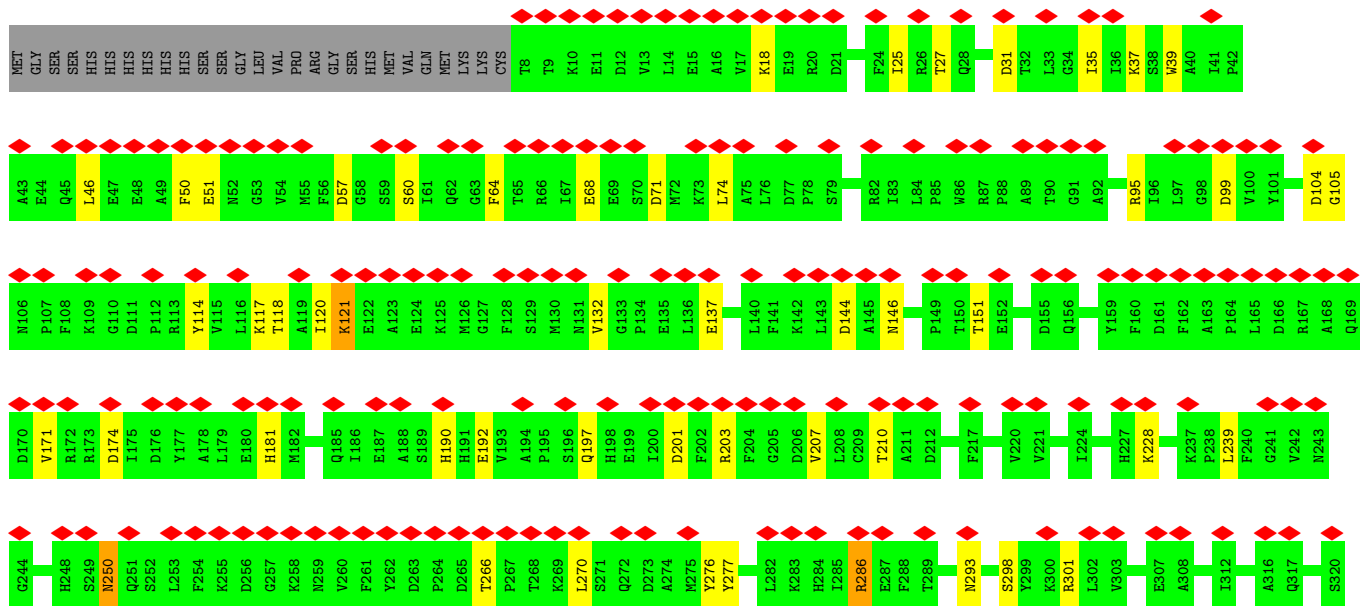
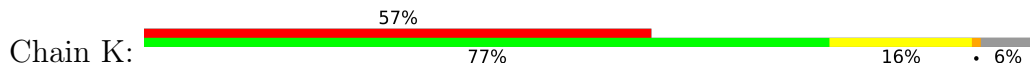


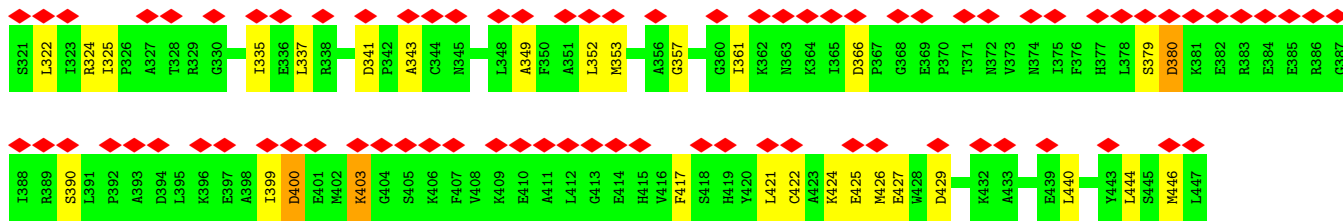
• Molecule 1: Glutamine synthetase



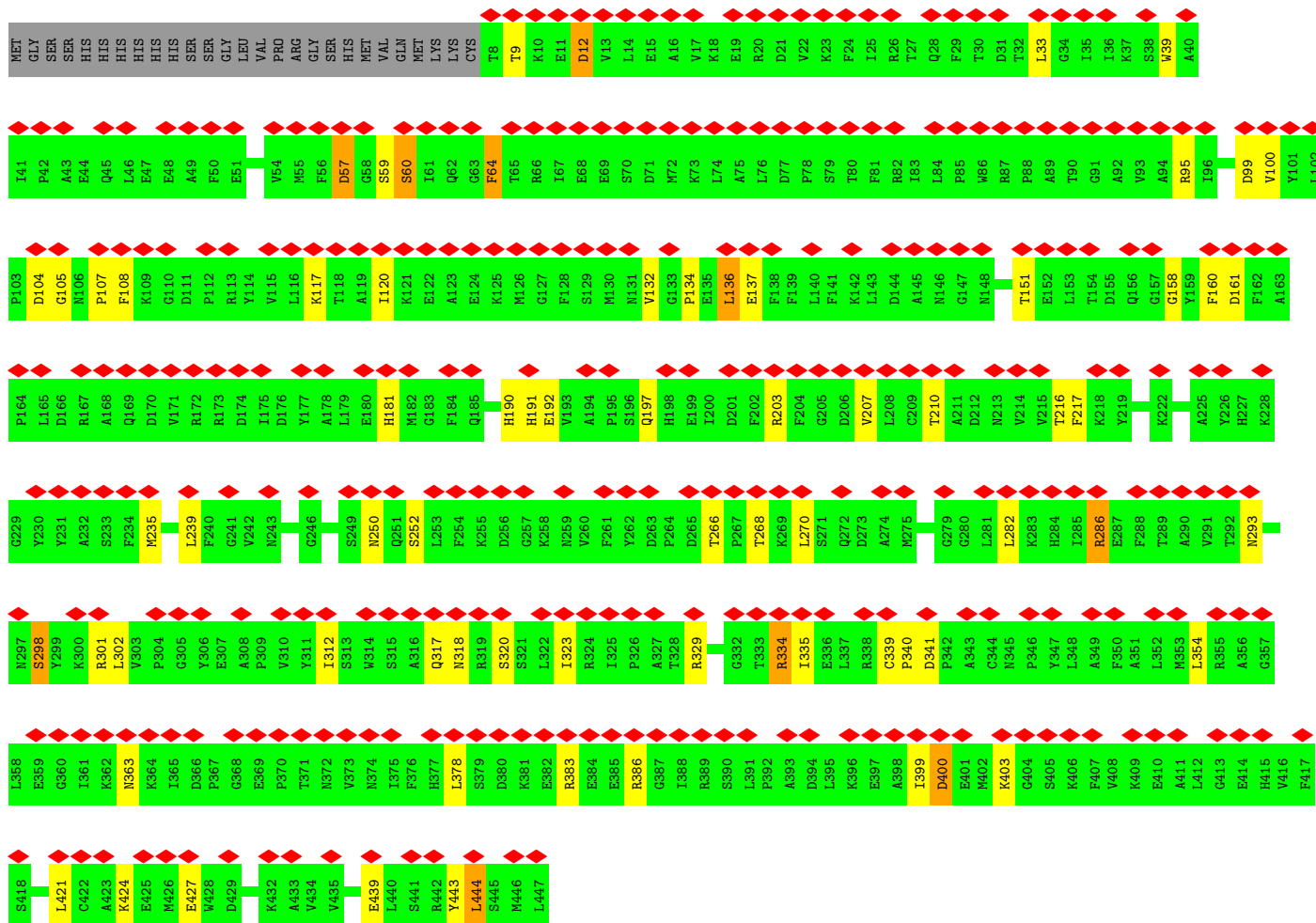
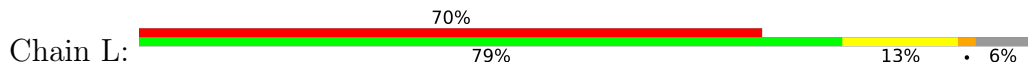


• Molecule 1: Glutamine synthetase





• Molecule 1: Glutamine synthetase



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	164400	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	30	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.648	Depositor
Minimum map value	-1.125	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.080	Depositor
Recommended contour level	0.332	Depositor
Map size (Å)	246.4, 246.4, 246.4	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.88, 0.88, 0.88	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, ADP, P3S

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	0.34	0/3542	0.53	0/4805
1	B	0.34	0/3541	0.57	4/4805 (0.1%)
1	C	0.35	0/3545	0.58	7/4808 (0.1%)
1	D	0.35	1/3539 (0.0%)	0.56	3/4801 (0.1%)
1	E	0.33	0/3533	0.54	2/4795 (0.0%)
1	F	0.34	0/3541	0.54	2/4804 (0.0%)
1	G	0.33	0/3541	0.54	2/4805 (0.0%)
1	H	0.33	0/3538	0.54	2/4800 (0.0%)
1	I	0.34	0/3549	0.54	2/4814 (0.0%)
1	J	0.34	0/3541	0.54	2/4804 (0.0%)
1	K	0.33	0/3541	0.54	2/4804 (0.0%)
1	L	0.34	0/3531	0.54	2/4791 (0.0%)
All	All	0.34	1/42482 (0.0%)	0.55	30/57636 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	339	CYS	CB-SG	-5.37	1.73	1.81

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	295	VAL	CG1-CB-CG2	7.64	123.13	110.90
1	C	295	VAL	CG1-CB-CG2	7.35	122.66	110.90
1	D	171	VAL	CG1-CB-CG2	7.17	122.38	110.90
1	B	132	VAL	CG1-CB-CG2	6.68	121.60	110.90
1	C	242	VAL	CG1-CB-CG2	6.46	121.23	110.90

There are no chirality outliers.

There are no planarity outliers.

## 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	A	3452	3282	3343	68	0
1	B	3451	3299	3334	41	0
1	C	3455	3324	3352	56	0
1	D	3449	3303	3334	56	0
1	E	3443	3282	3324	41	0
1	F	3451	3304	3341	49	0
1	G	3451	3305	3334	46	0
1	H	3448	3302	3339	42	0
1	I	3459	3305	3351	51	0
1	J	3451	3304	3341	41	0
1	K	3451	3304	3341	47	0
1	L	3441	3287	3333	51	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
2	C	3	0	0	0	0
2	D	3	0	0	0	0
2	E	3	0	0	0	0
2	F	3	0	0	0	0
2	G	3	0	0	0	0
2	H	3	0	0	0	0
2	I	3	0	0	0	0
2	J	3	0	0	0	0
2	K	3	0	0	0	0
2	L	3	0	0	0	0
3	A	15	10	10	1	0
3	B	15	10	10	0	0
3	C	15	10	10	1	0
3	D	15	10	10	1	0
3	E	15	10	10	1	0
3	F	15	10	10	1	0
3	G	15	10	10	1	0
3	H	15	10	10	0	0
3	I	15	10	10	1	0
3	J	15	10	10	1	0
3	K	15	10	10	1	0
3	L	15	10	10	1	0
4	A	27	11	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	27	11	12	1	0
4	C	27	11	12	0	0
4	D	27	11	12	0	0
4	E	27	11	12	0	0
4	F	27	11	12	1	0
4	G	27	11	12	0	0
4	H	27	11	12	1	0
4	I	27	11	12	1	0
4	J	27	11	12	0	0
4	K	27	11	12	1	0
4	L	27	11	12	1	0
All	All	41942	39853	40331	520	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 6.

The worst 5 of 520 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:D:287:GLU:OE1	1:D:405:SER:OG	1.84	0.95
1:L:57:ASP:OD1	1:L:60:SER:OG	1.87	0.92
1:E:244:GLY:O	3:E:501:P3S:N	2.03	0.92
1:A:403:LYS:NZ	1:A:425:GLU:OE2	2.05	0.89
1:E:298:SER:OG	1:E:341:ASP:OD2	1.90	0.89

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	438/467 (94%)	426 (97%)	12 (3%)	0	<b>100</b> <b>100</b>

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	438/467 (94%)	419 (96%)	19 (4%)	0	100	100
1	C	438/467 (94%)	420 (96%)	18 (4%)	0	100	100
1	D	438/467 (94%)	425 (97%)	13 (3%)	0	100	100
1	E	438/467 (94%)	422 (96%)	16 (4%)	0	100	100
1	F	438/467 (94%)	425 (97%)	13 (3%)	0	100	100
1	G	438/467 (94%)	420 (96%)	18 (4%)	0	100	100
1	H	438/467 (94%)	426 (97%)	12 (3%)	0	100	100
1	I	438/467 (94%)	422 (96%)	16 (4%)	0	100	100
1	J	438/467 (94%)	421 (96%)	17 (4%)	0	100	100
1	K	438/467 (94%)	423 (97%)	15 (3%)	0	100	100
1	L	438/467 (94%)	425 (97%)	13 (3%)	0	100	100
All	All	5256/5604 (94%)	5074 (96%)	182 (4%)	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	361/400 (90%)	344 (95%)	17 (5%)	26	40
1	B	361/400 (90%)	338 (94%)	23 (6%)	17	27
1	C	362/400 (90%)	339 (94%)	23 (6%)	17	27
1	D	360/400 (90%)	340 (94%)	20 (6%)	21	33
1	E	359/400 (90%)	344 (96%)	15 (4%)	30	45
1	F	361/400 (90%)	338 (94%)	23 (6%)	17	27
1	G	361/400 (90%)	350 (97%)	11 (3%)	41	59
1	H	360/400 (90%)	337 (94%)	23 (6%)	17	27
1	I	363/400 (91%)	341 (94%)	22 (6%)	18	29
1	J	361/400 (90%)	338 (94%)	23 (6%)	17	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	K	361/400 (90%)	338 (94%)	23 (6%)	17	27
1	L	358/400 (90%)	341 (95%)	17 (5%)	26	40
All	All	4328/4800 (90%)	4088 (94%)	240 (6%)	25	33

5 of 240 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	334	ARG
1	K	429	ASP
1	H	181	HIS
1	K	400	ASP
1	L	334	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	L	227	HIS
1	K	250	ASN
1	I	297	ASN
1	I	227	HIS
1	J	181	HIS

### 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 60 ligands modelled in this entry, 36 are monoatomic - leaving 24 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	ADP	B	505	2	24,29,29	0.90	1 (4%)	29,45,45	1.39	4 (13%)
3	P3S	J	501	2	11,14,14	1.79	2 (18%)	12,21,21	12.82	5 (41%)
3	P3S	G	601	2	11,14,14	1.80	2 (18%)	12,21,21	12.98	4 (33%)
3	P3S	D	504	2	11,14,14	1.78	3 (27%)	12,21,21	12.92	4 (33%)
3	P3S	H	601	2	11,14,14	1.78	3 (27%)	12,21,21	12.80	5 (41%)
4	ADP	G	602	2	24,29,29	0.89	1 (4%)	29,45,45	1.39	4 (13%)
4	ADP	H	602	2	24,29,29	0.89	1 (4%)	29,45,45	1.39	4 (13%)
3	P3S	B	504	2	11,14,14	1.85	4 (36%)	12,21,21	12.59	5 (41%)
3	P3S	C	504	2	11,14,14	1.71	2 (18%)	12,21,21	12.44	5 (41%)
3	P3S	I	501	2	11,14,14	1.78	2 (18%)	12,21,21	12.76	4 (33%)
4	ADP	F	602	2	24,29,29	0.90	1 (4%)	29,45,45	1.42	5 (17%)
4	ADP	J	502	2	24,29,29	0.90	1 (4%)	29,45,45	1.48	5 (17%)
3	P3S	F	601	2	11,14,14	1.76	2 (18%)	12,21,21	12.78	5 (41%)
3	P3S	L	501	2	11,14,14	1.79	2 (18%)	12,21,21	12.78	4 (33%)
4	ADP	I	502	2	24,29,29	0.89	1 (4%)	29,45,45	1.41	3 (10%)
4	ADP	D	505	2	24,29,29	0.90	1 (4%)	29,45,45	1.44	5 (17%)
4	ADP	K	502	2	24,29,29	0.90	1 (4%)	29,45,45	1.45	5 (17%)
4	ADP	A	505	2	24,29,29	0.90	1 (4%)	29,45,45	1.40	4 (13%)
3	P3S	K	501	2	11,14,14	1.81	3 (27%)	12,21,21	12.92	3 (25%)
4	ADP	E	502	2	24,29,29	0.88	1 (4%)	29,45,45	1.39	4 (13%)
3	P3S	A	504	2	11,14,14	1.77	2 (18%)	12,21,21	12.72	4 (33%)
4	ADP	C	505	2	24,29,29	0.89	1 (4%)	29,45,45	1.47	5 (17%)
3	P3S	E	501	2	11,14,14	1.78	2 (18%)	12,21,21	12.42	5 (41%)
4	ADP	L	502	2	24,29,29	0.91	1 (4%)	29,45,45	1.43	4 (13%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	ADP	B	505	2	-	2/12/32/32	0/3/3/3
3	P3S	J	501	2	-	8/9/16/16	-
3	P3S	G	601	2	-	3/9/16/16	-
3	P3S	D	504	2	-	5/9/16/16	-
3	P3S	H	601	2	-	5/9/16/16	-
4	ADP	G	602	2	-	4/12/32/32	0/3/3/3
4	ADP	H	602	2	-	1/12/32/32	0/3/3/3
3	P3S	B	504	2	-	5/9/16/16	-
3	P3S	C	504	2	-	8/9/16/16	-
3	P3S	I	501	2	-	5/9/16/16	-
4	ADP	F	602	2	-	1/12/32/32	0/3/3/3
4	ADP	J	502	2	-	2/12/32/32	0/3/3/3
3	P3S	F	601	2	-	5/9/16/16	-
3	P3S	L	501	2	-	5/9/16/16	-
4	ADP	I	502	2	-	4/12/32/32	0/3/3/3
4	ADP	D	505	2	-	1/12/32/32	0/3/3/3
4	ADP	K	502	2	-	4/12/32/32	0/3/3/3
4	ADP	A	505	2	-	1/12/32/32	0/3/3/3
3	P3S	K	501	2	-	6/9/16/16	-
4	ADP	E	502	2	-	4/12/32/32	0/3/3/3
3	P3S	A	504	2	-	5/9/16/16	-
4	ADP	C	505	2	-	1/12/32/32	0/3/3/3
3	P3S	E	501	2	-	6/9/16/16	-
4	ADP	L	502	2	-	3/12/32/32	0/3/3/3

The worst 5 of 41 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	504	P3S	PA-NE	3.34	1.71	1.59
3	G	601	P3S	PA-NE	3.31	1.71	1.59
3	F	601	P3S	PA-NE	3.30	1.71	1.59
3	E	501	P3S	PA-NE	3.29	1.71	1.59
3	I	501	P3S	PA-NE	3.26	1.71	1.59

The worst 5 of 105 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	K	501	P3S	OE-SD-CG	39.11	138.98	108.37
3	D	504	P3S	OE-SD-CG	39.05	138.93	108.37

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	601	P3S	OE-SD-CG	38.86	138.78	108.37
3	J	501	P3S	OE-SD-CG	38.85	138.78	108.37
3	G	601	P3S	OE-SD-CG	38.53	138.53	108.37

There are no chirality outliers.

5 of 94 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	504	P3S	CB-CG-SD-CE
3	A	504	P3S	O-C-CA-N
3	B	504	P3S	CB-CG-SD-CE
3	B	504	P3S	O-C-CA-N
3	C	504	P3S	CB-CG-SD-OE

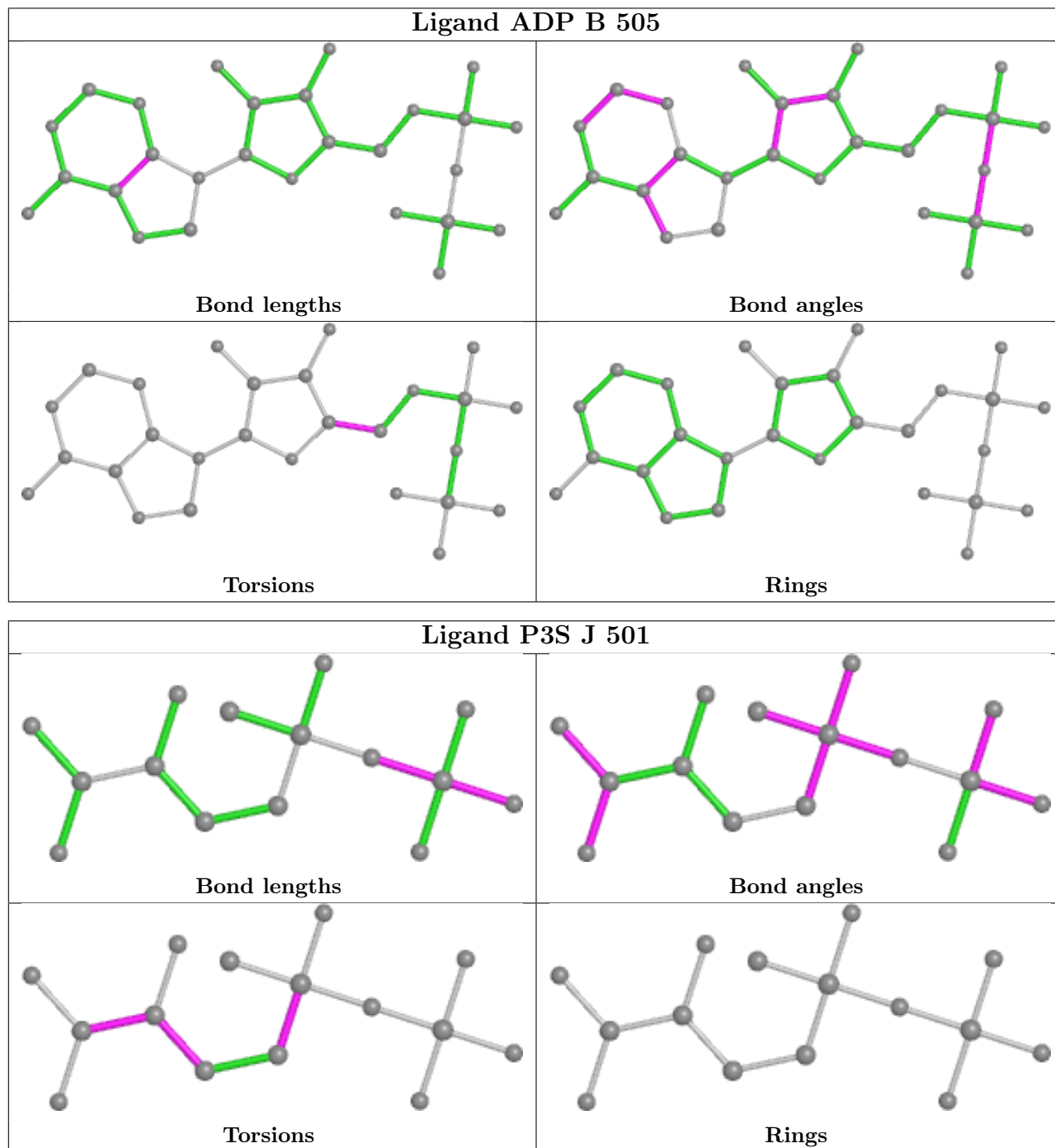
There are no ring outliers.

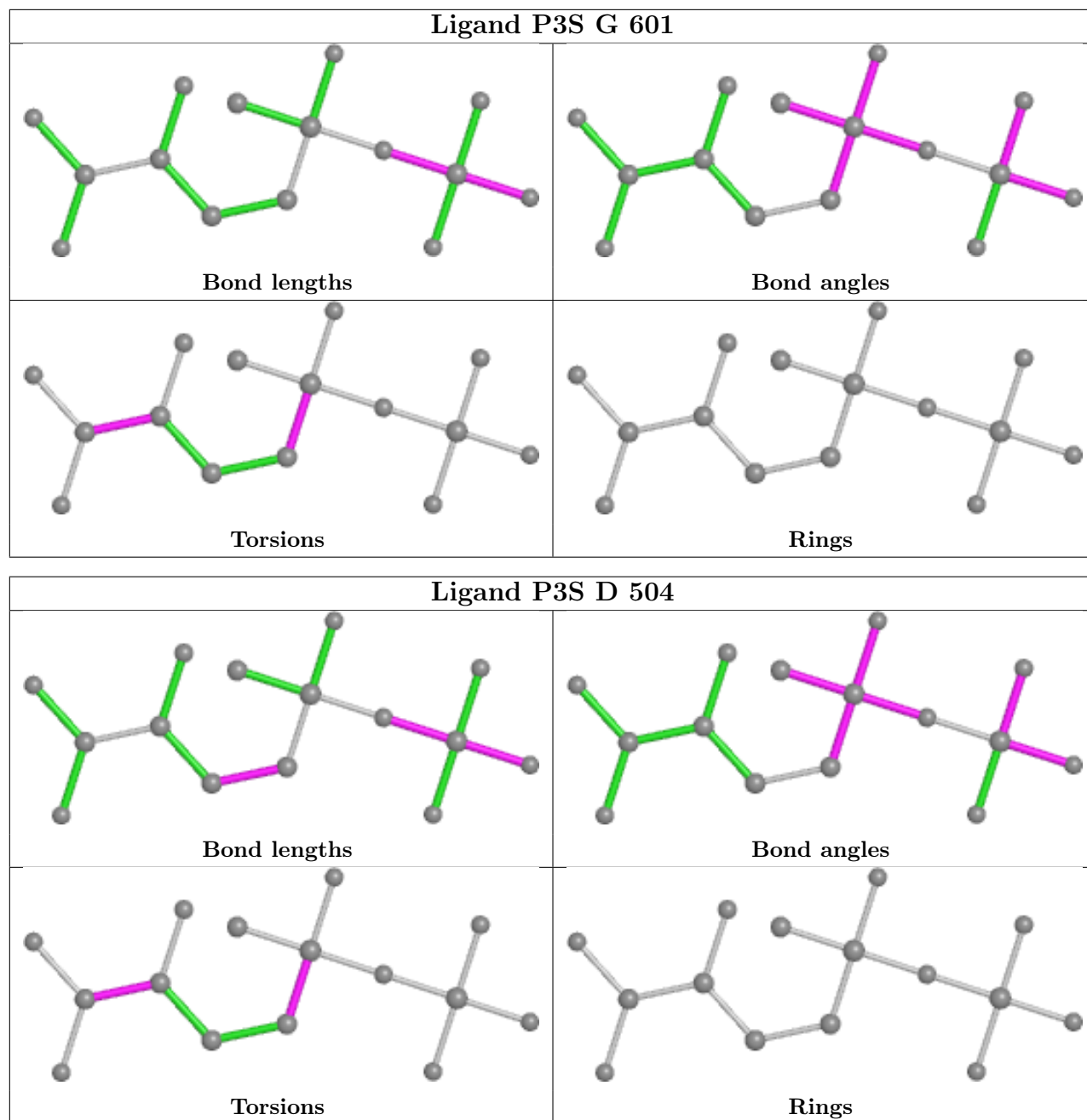
17 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	505	ADP	1	0
3	J	501	P3S	1	0
3	G	601	P3S	1	0
3	D	504	P3S	1	0
4	H	602	ADP	1	0
3	C	504	P3S	1	0
3	I	501	P3S	1	0
4	F	602	ADP	1	0
3	F	601	P3S	1	0
3	L	501	P3S	1	0
4	I	502	ADP	1	0
4	K	502	ADP	1	0
4	A	505	ADP	1	0
3	K	501	P3S	1	0
3	A	504	P3S	1	0
3	E	501	P3S	1	0
4	L	502	ADP	1	0

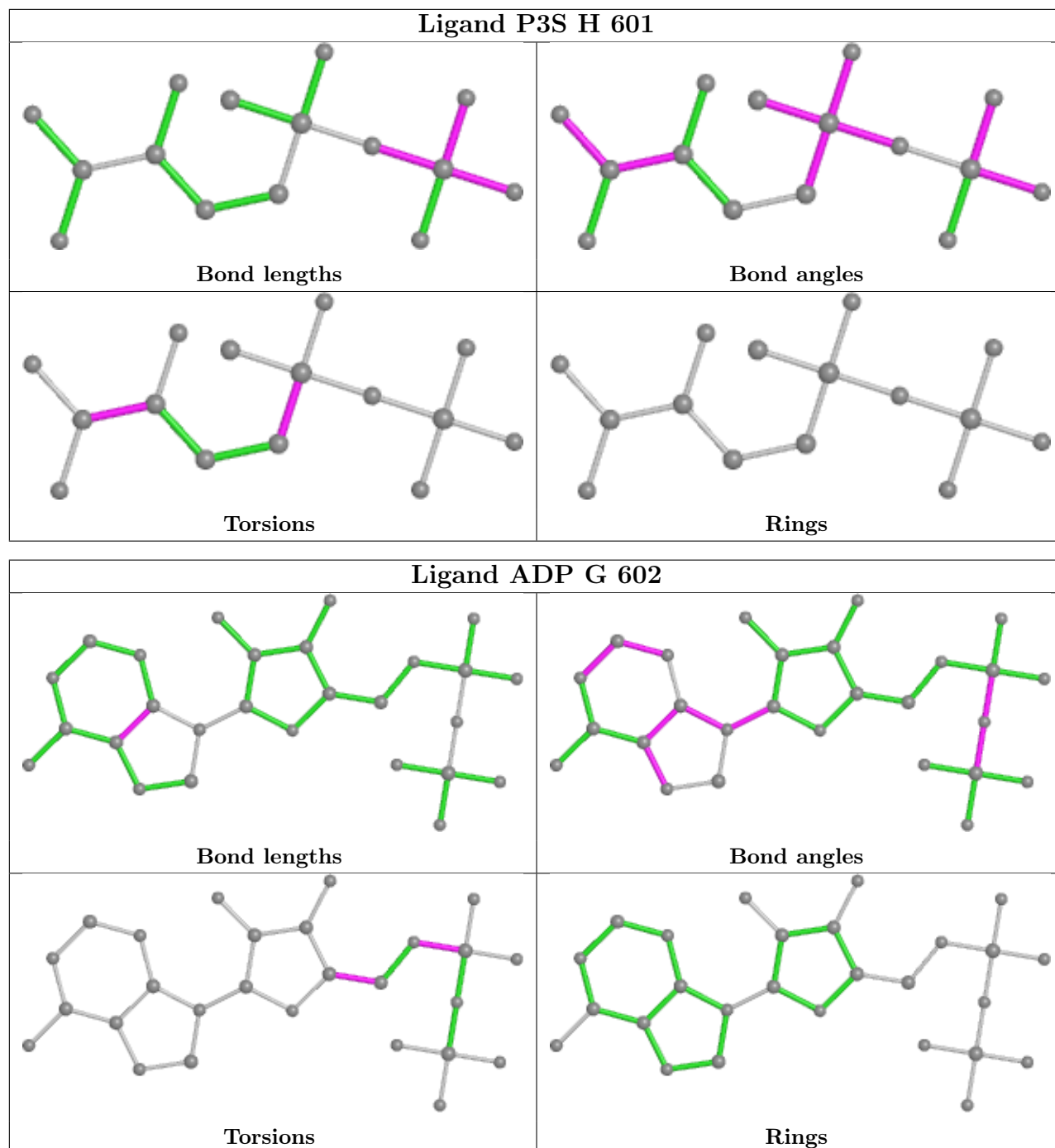
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

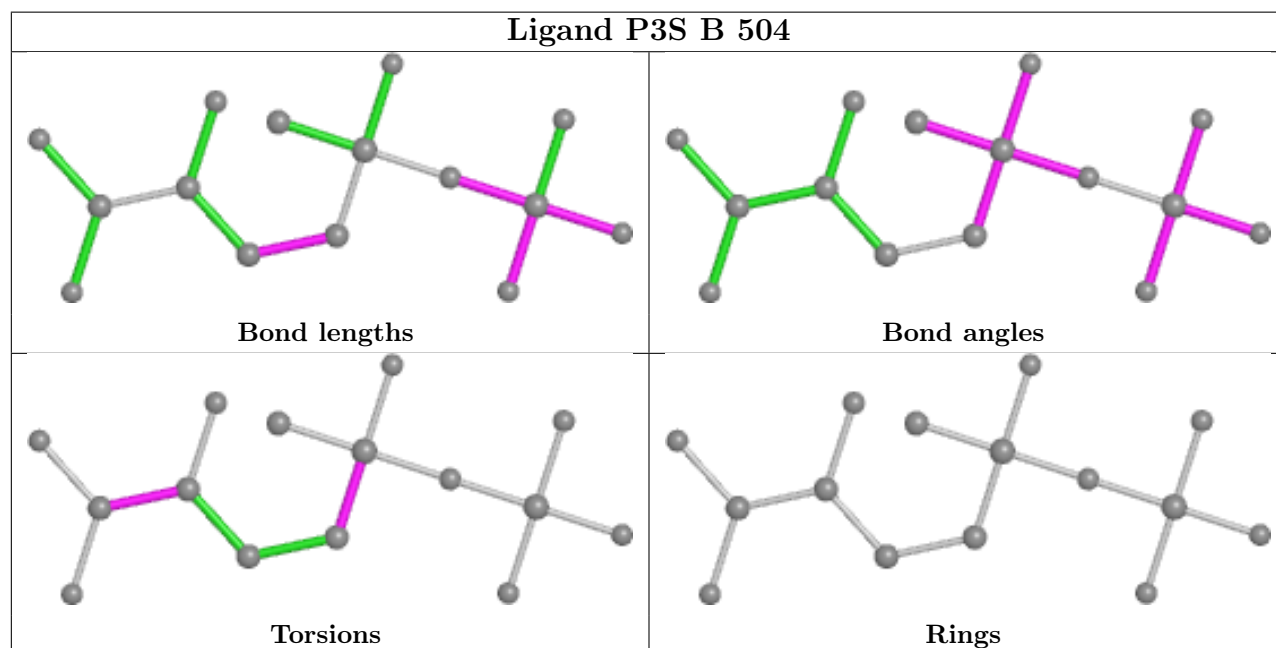
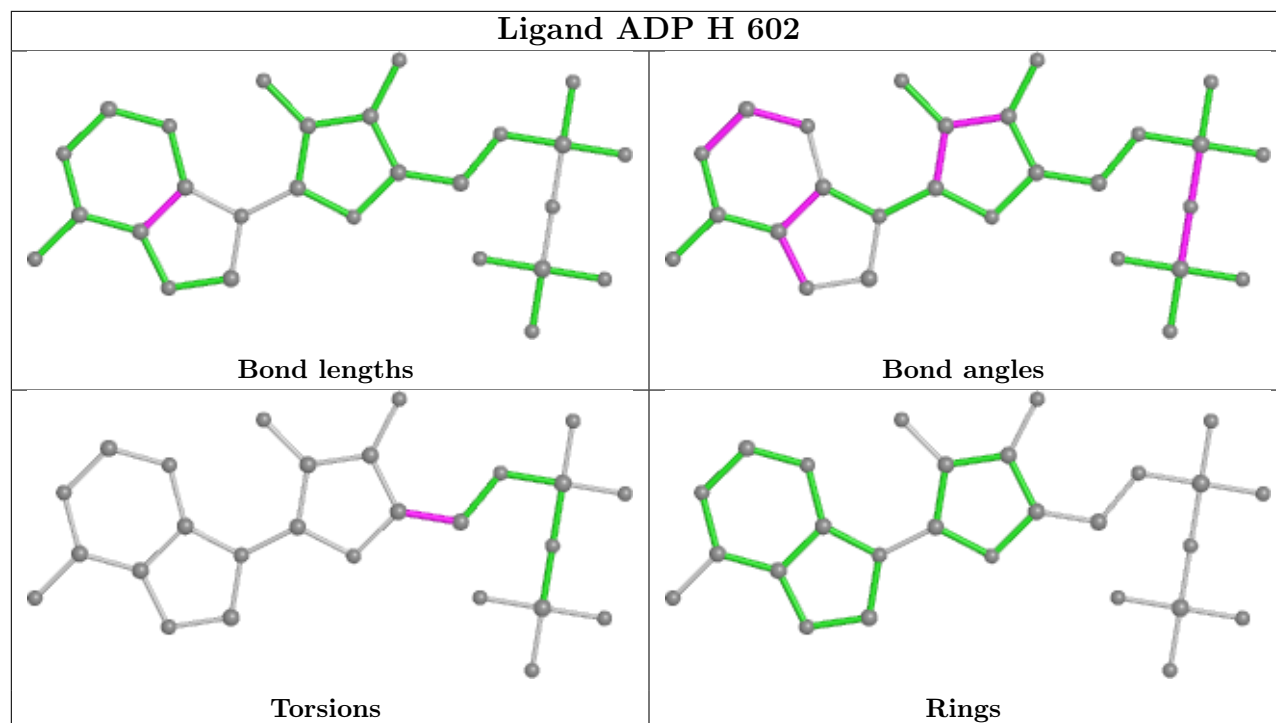
highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified 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.

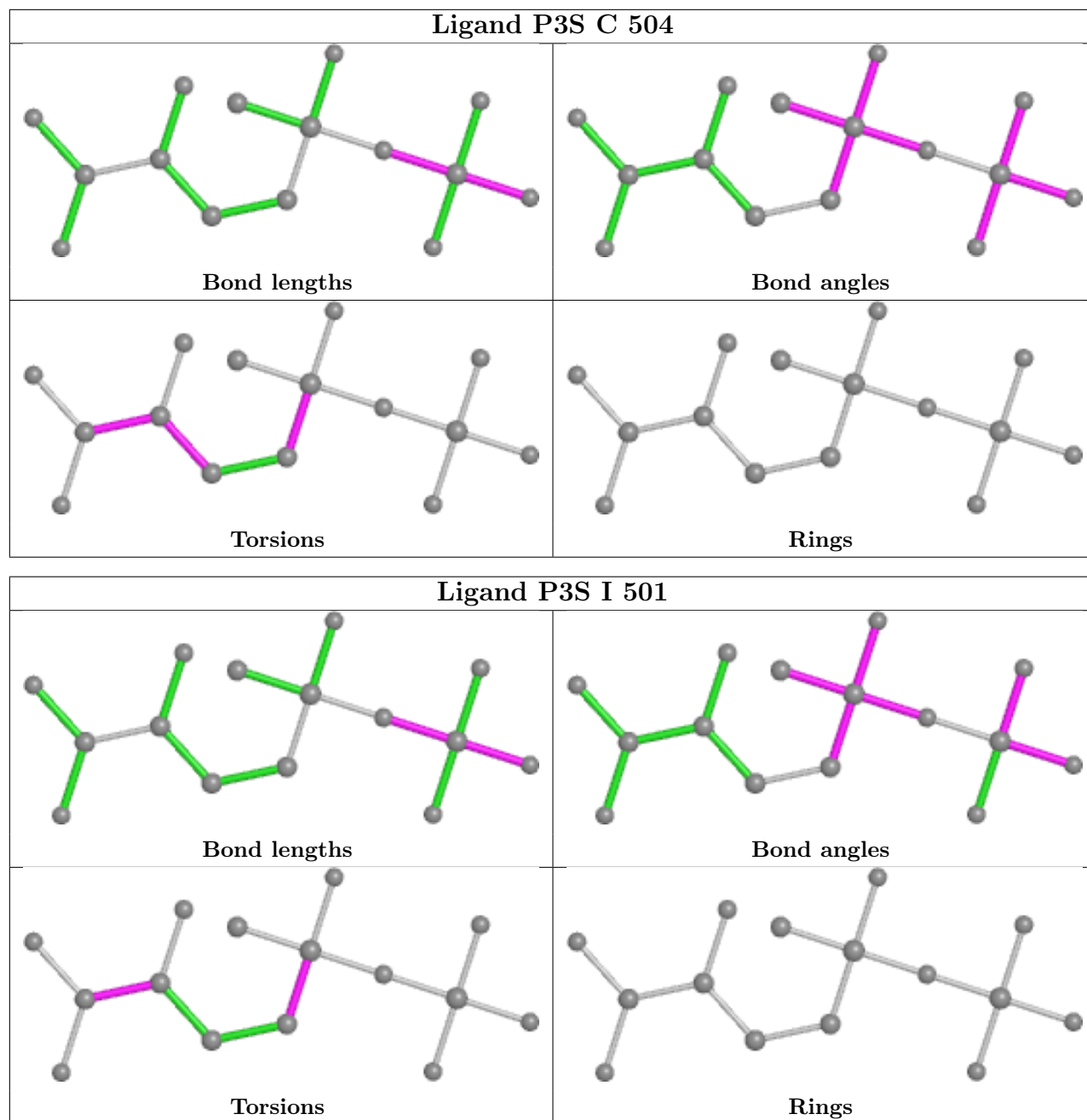


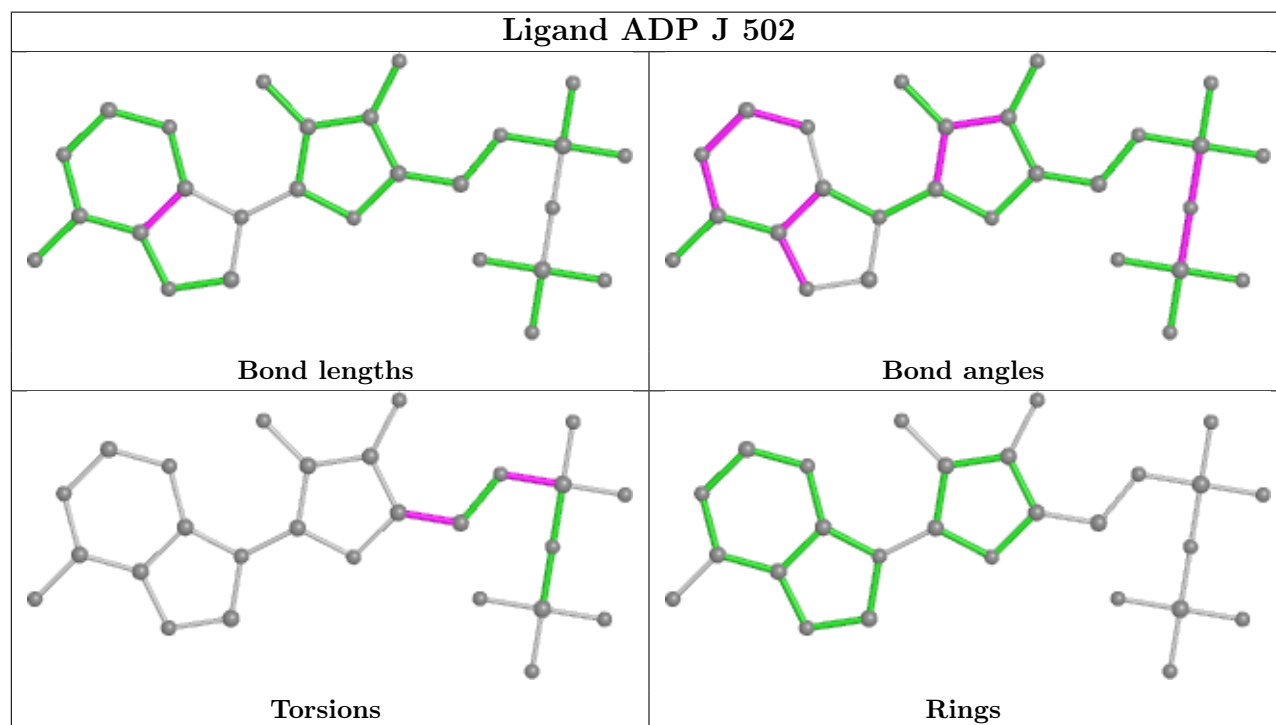
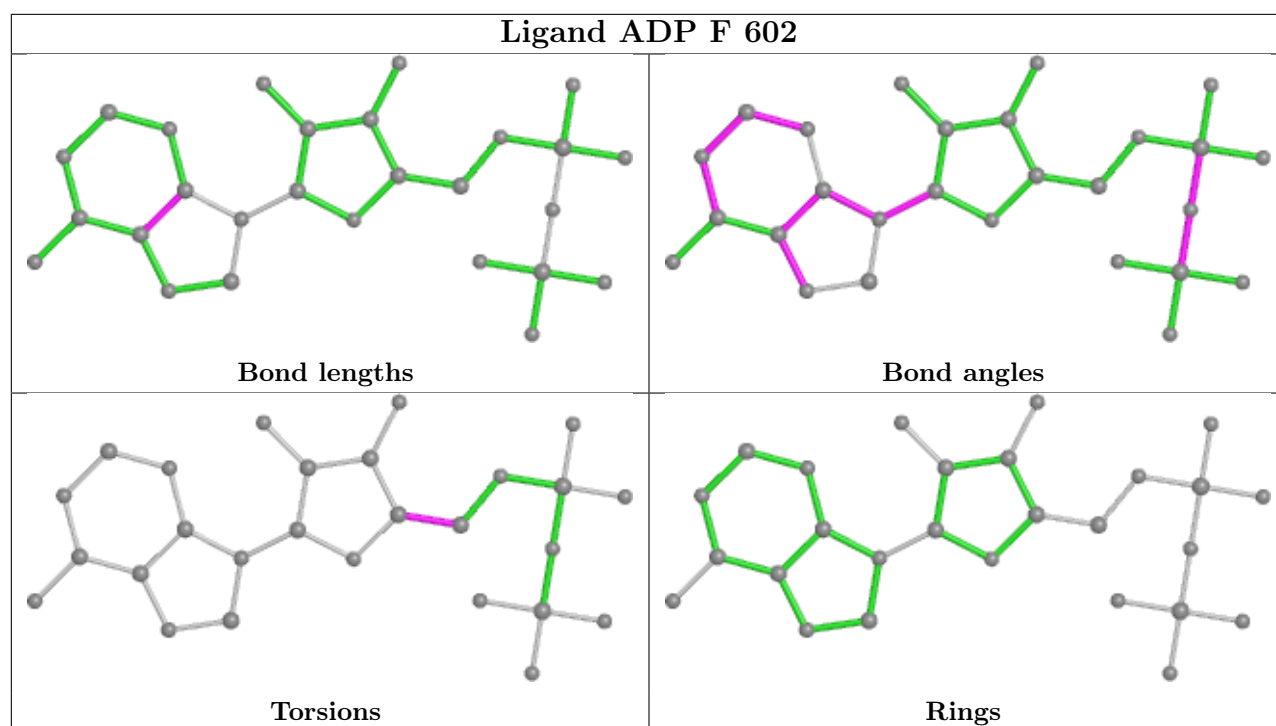


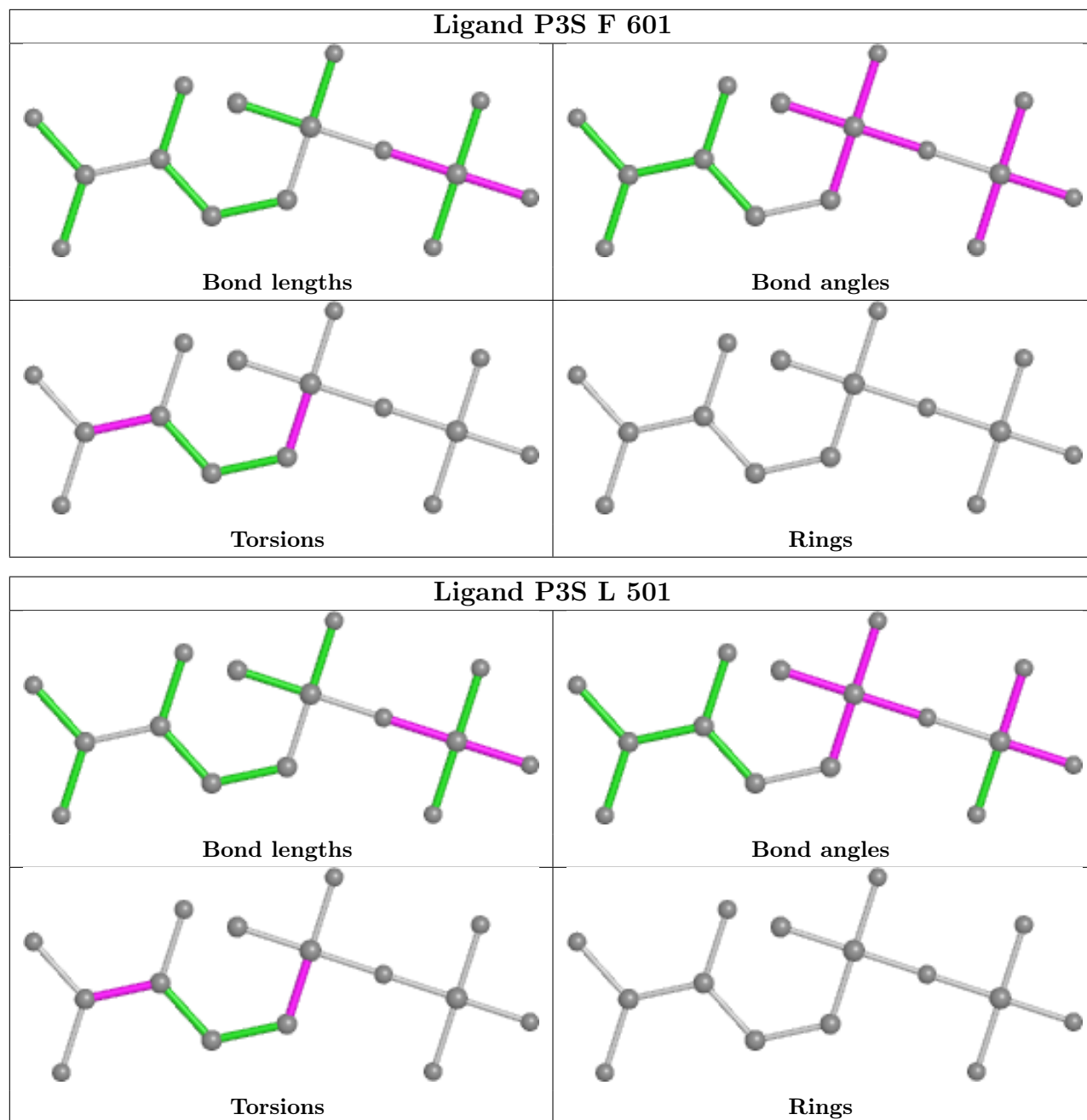


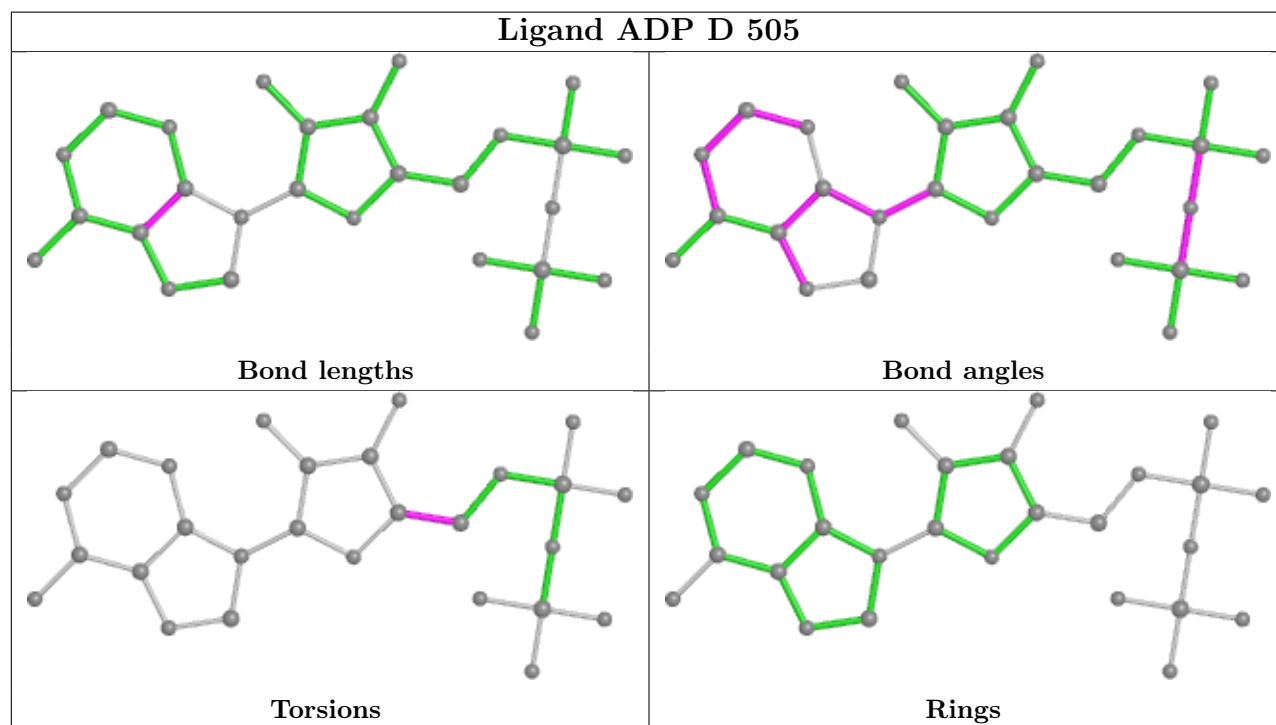
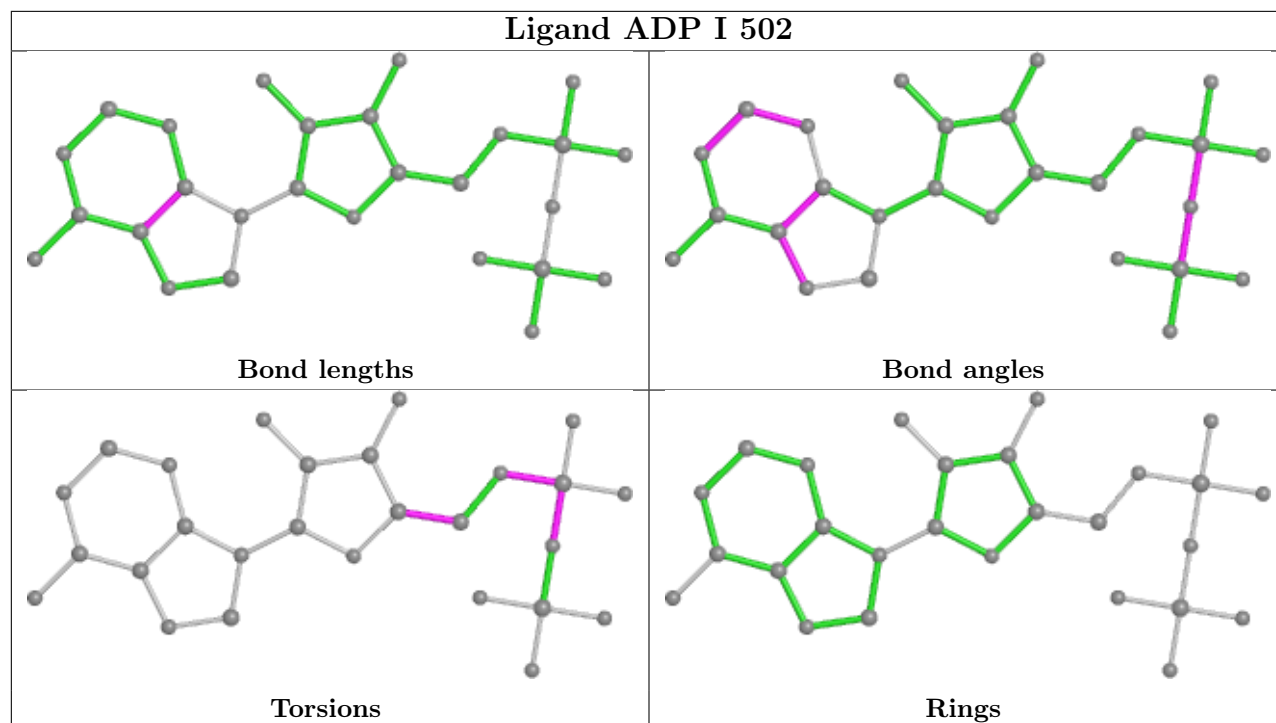


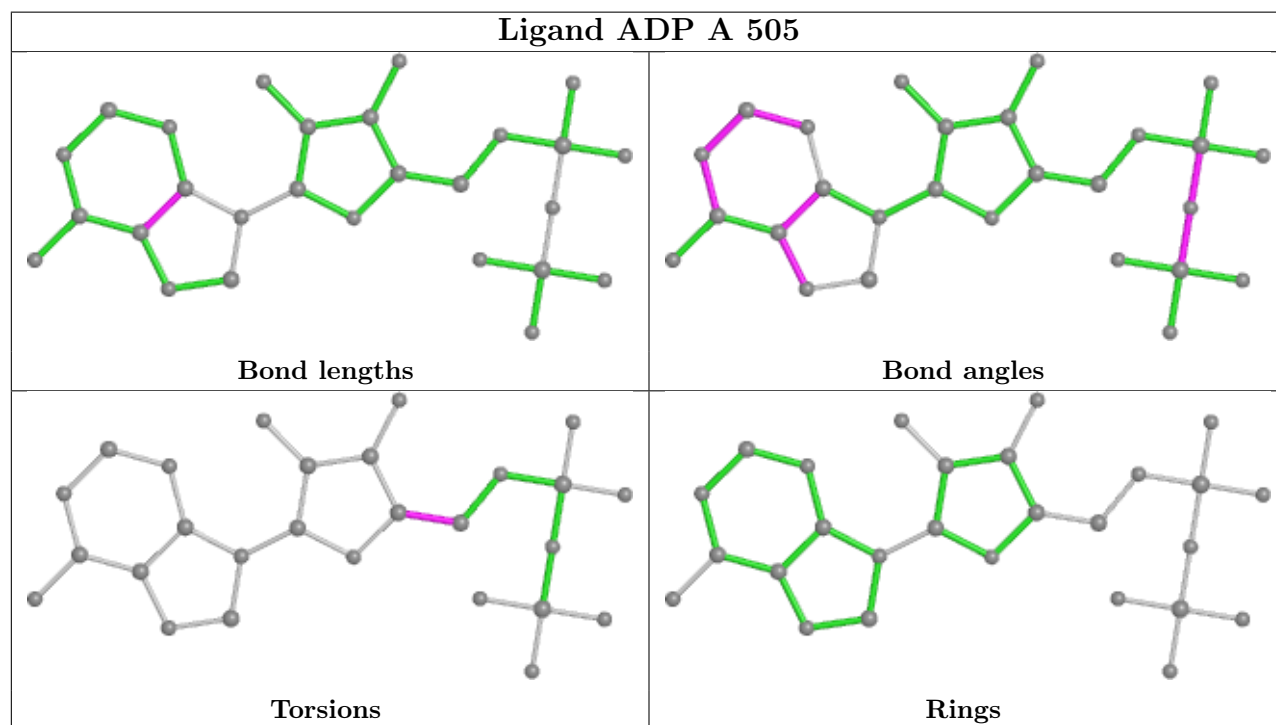
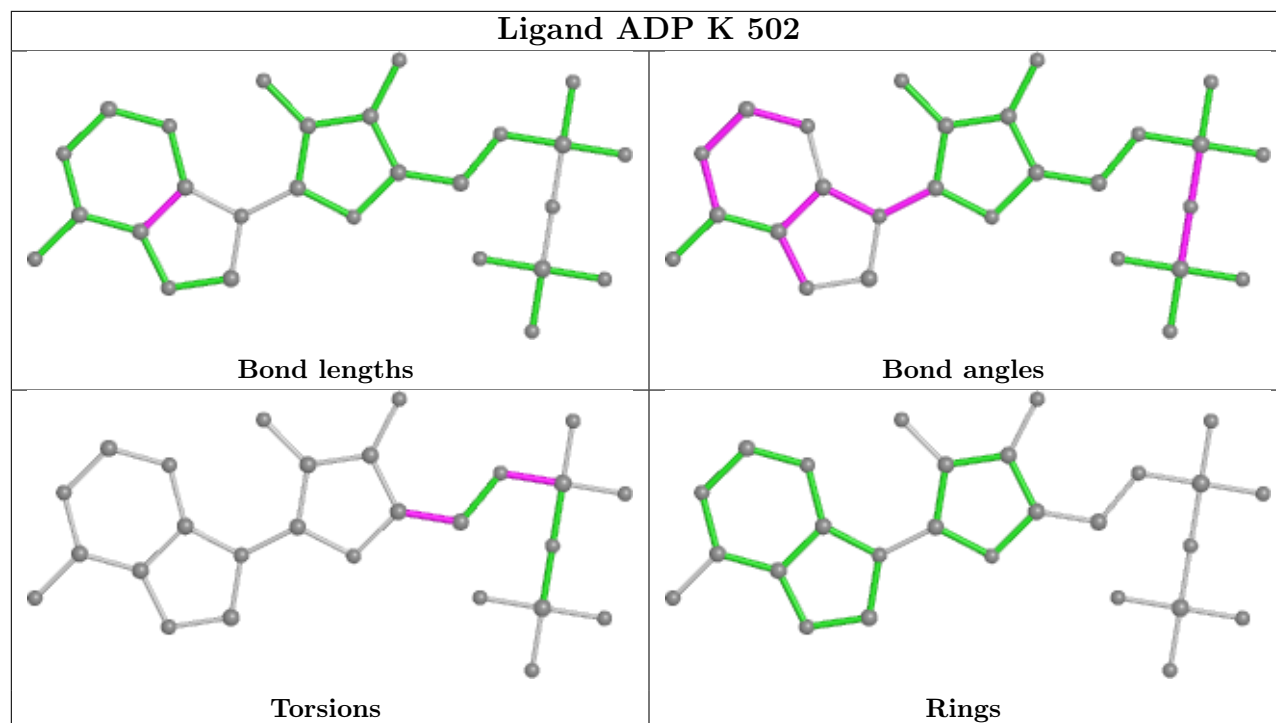


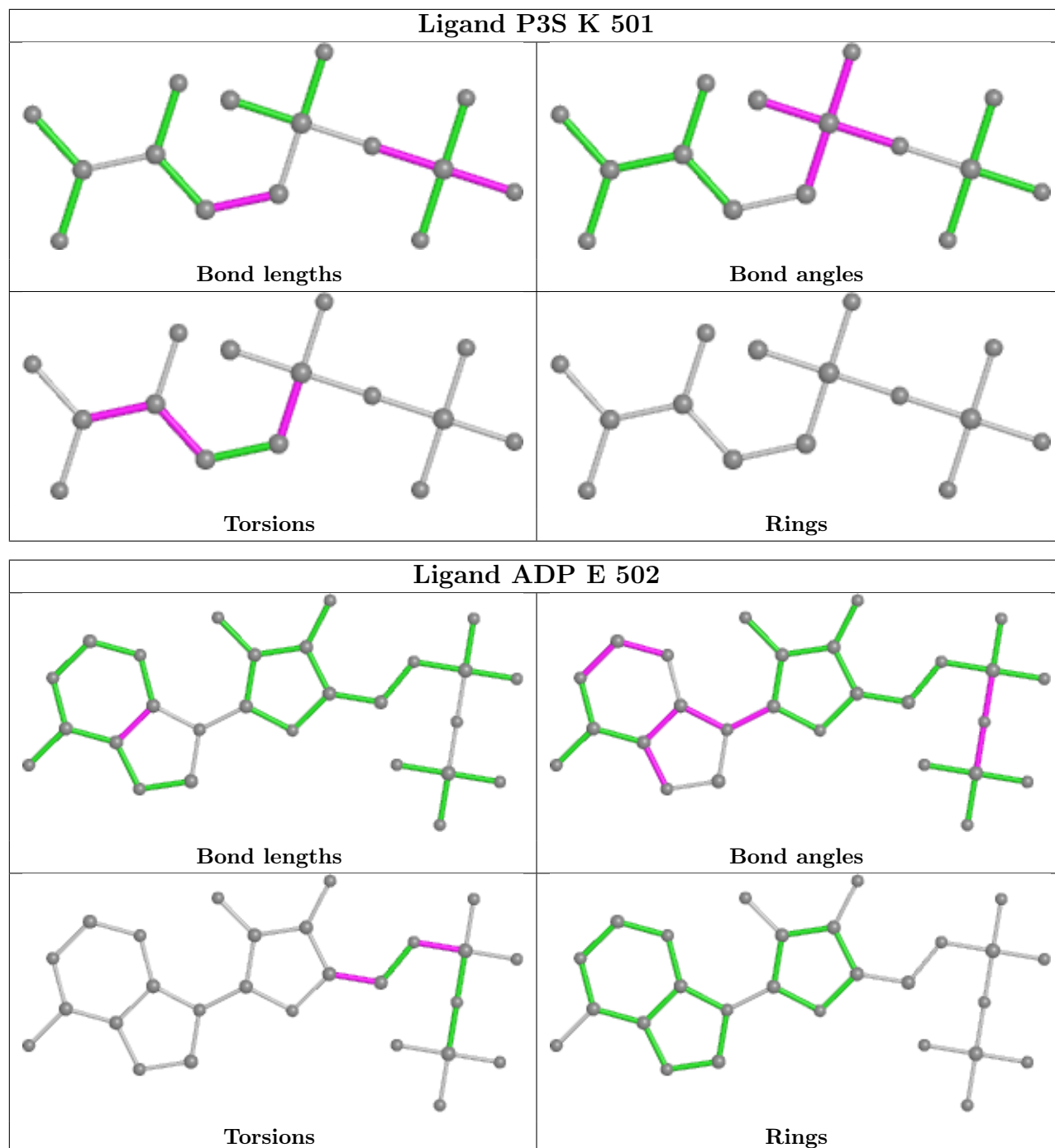




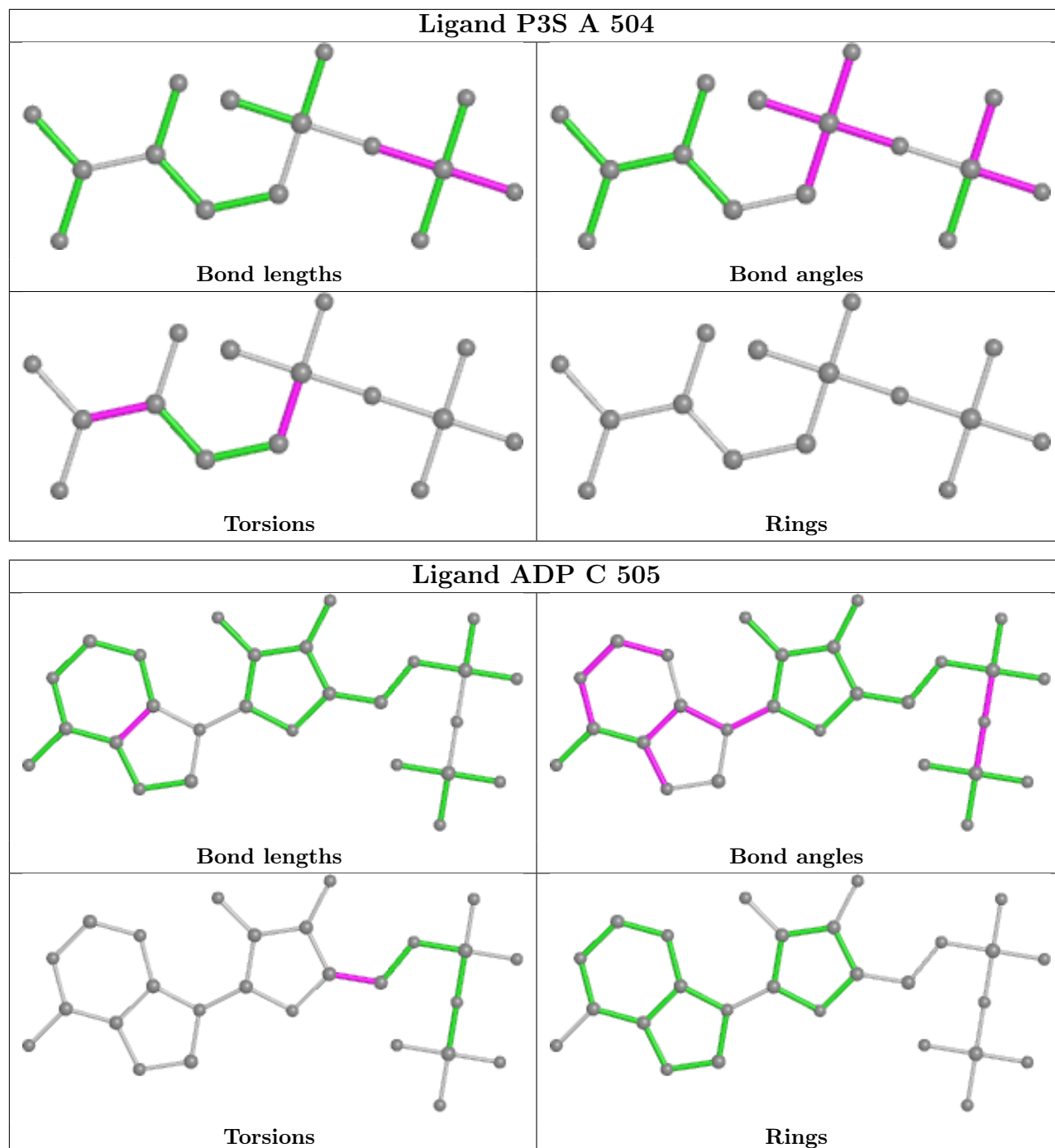


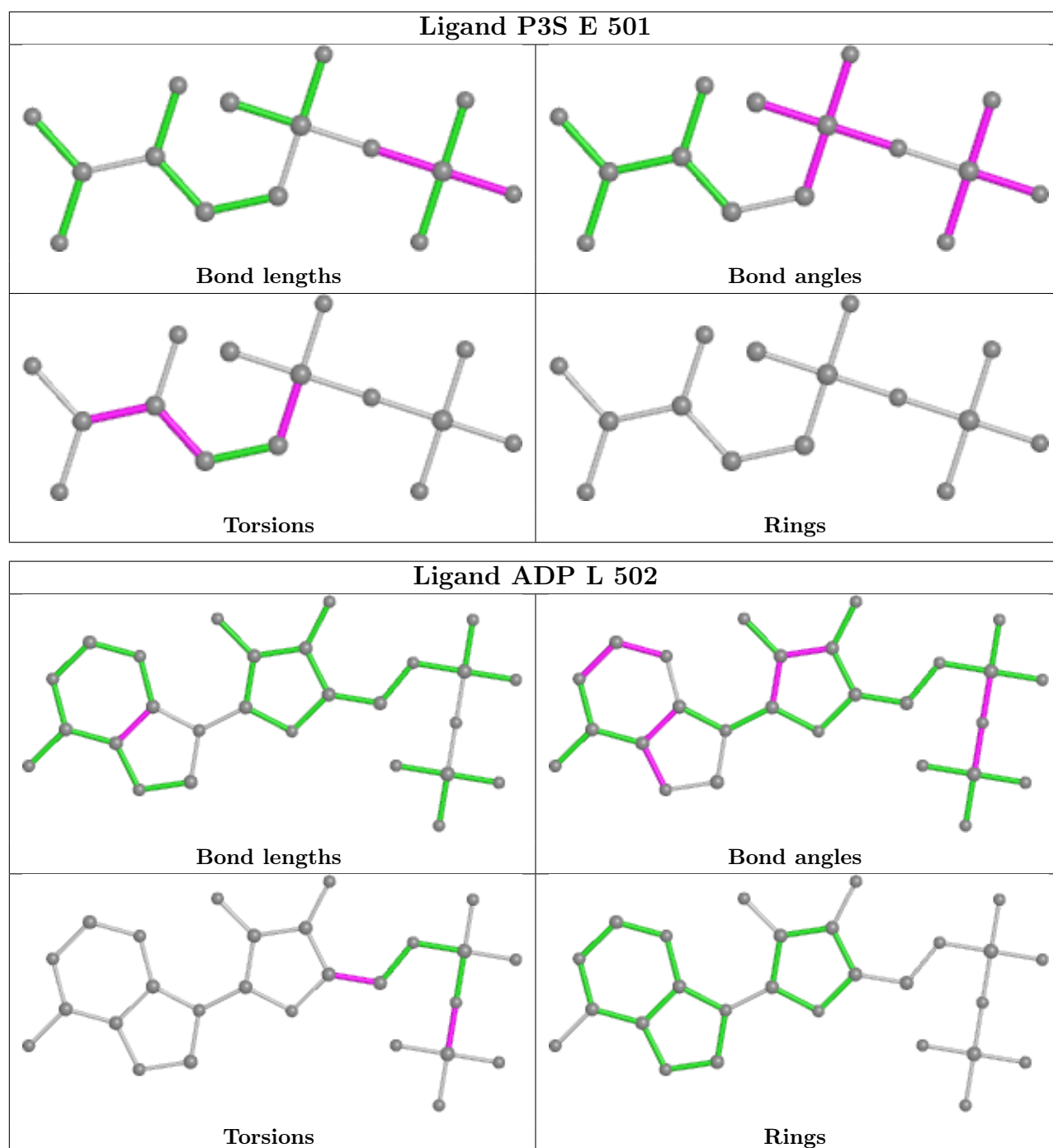












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

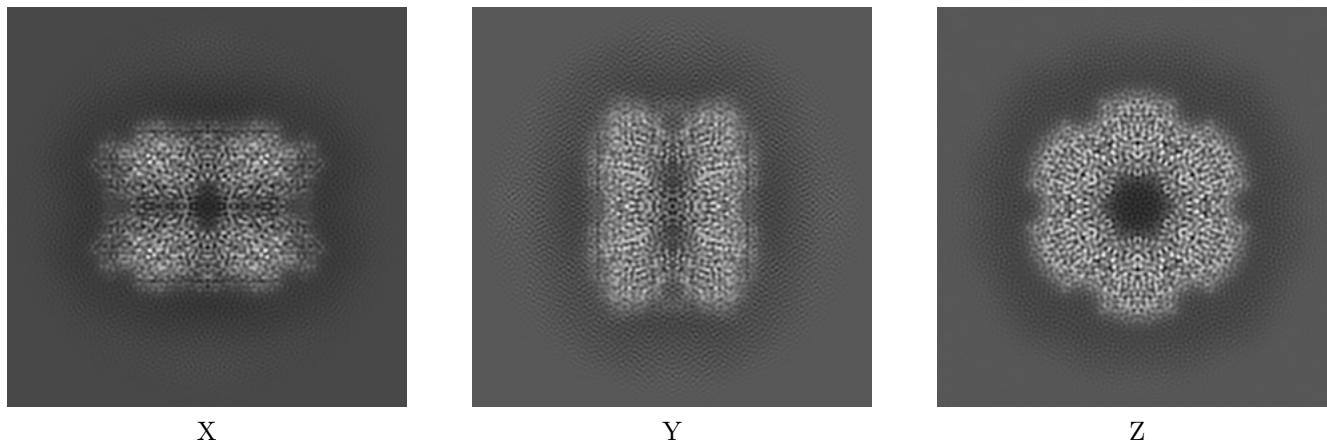
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-41232. These allow visual inspection of the internal detail of the map and identification of artifacts.

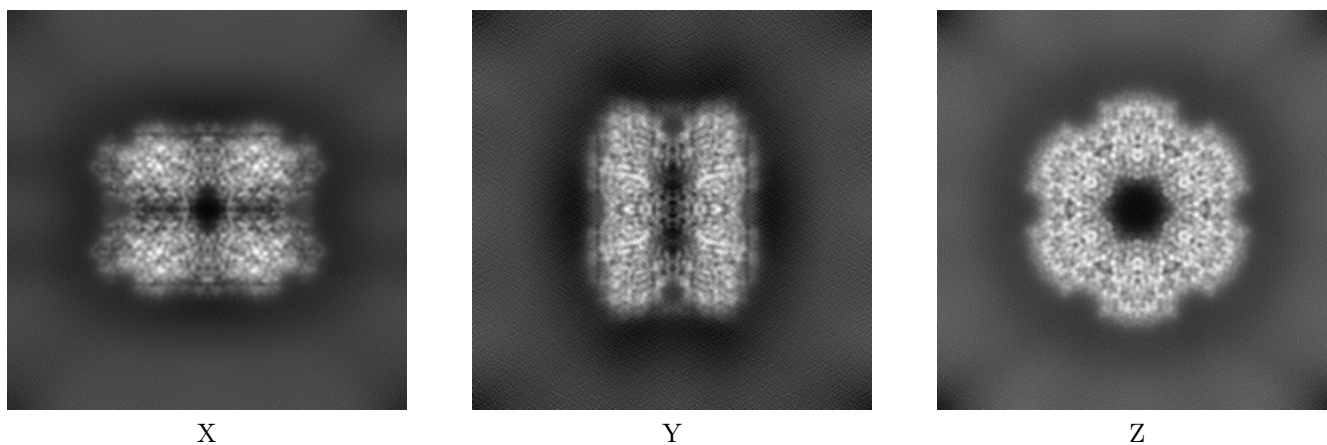
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

#### 6.1.1 Primary map



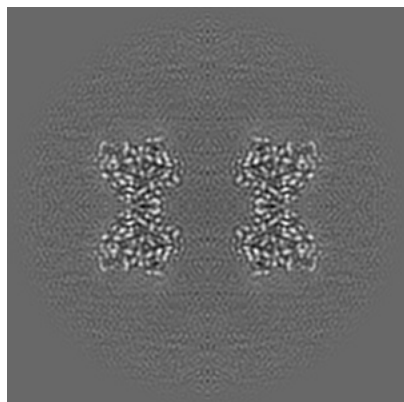
#### 6.1.2 Raw map



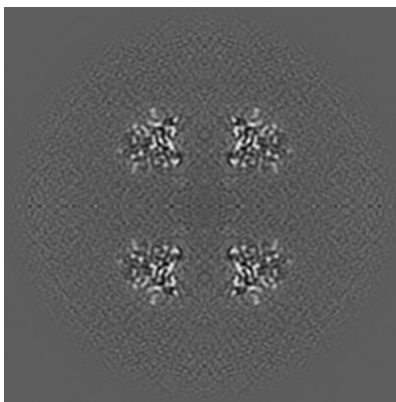
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

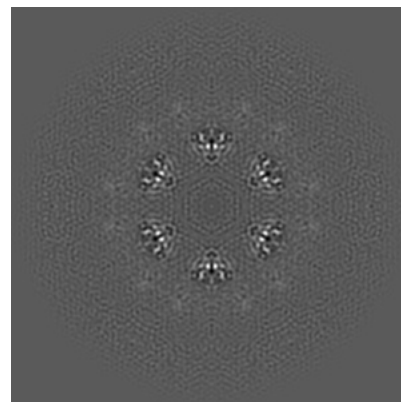
### 6.2.1 Primary map



X Index: 140

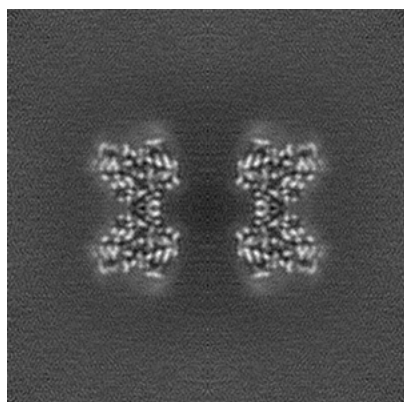


Y Index: 140

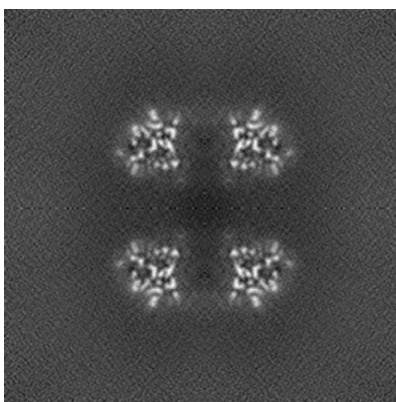


Z Index: 140

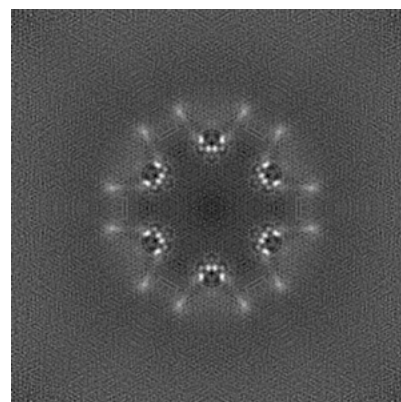
### 6.2.2 Raw map



X Index: 140



Y Index: 140

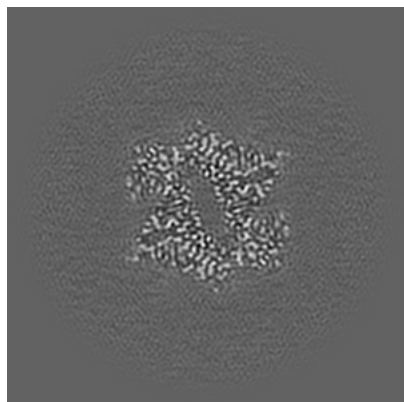


Z Index: 140

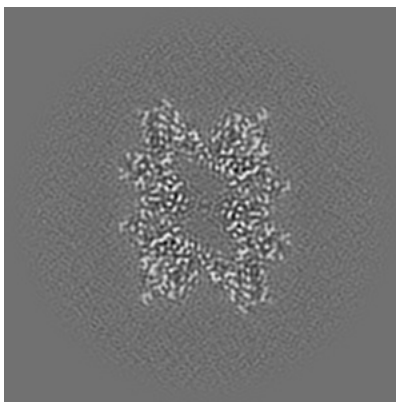
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

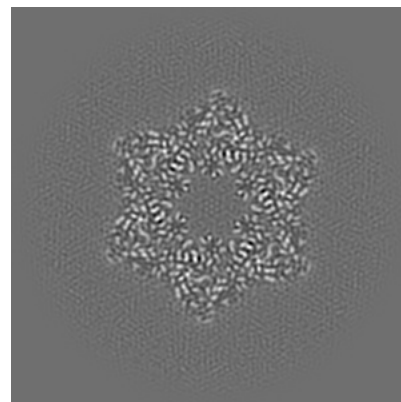
### 6.3.1 Primary map



X Index: 99

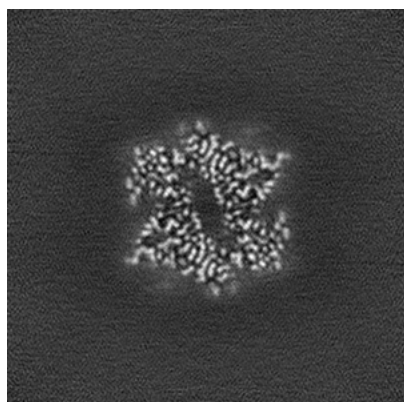


Y Index: 172

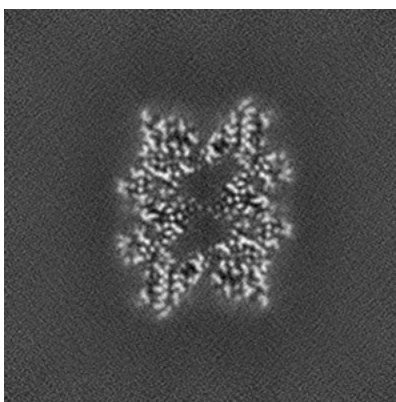


Z Index: 113

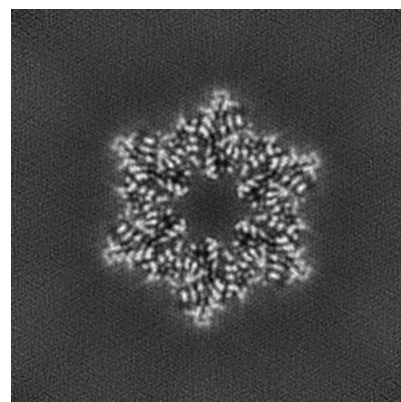
### 6.3.2 Raw map



X Index: 99



Y Index: 107

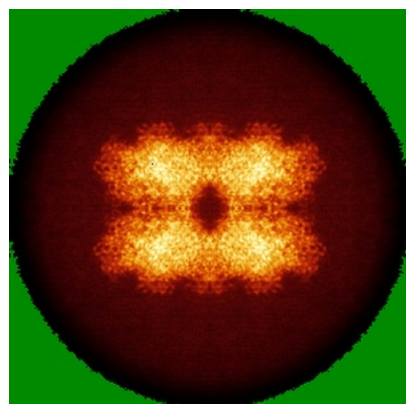


Z Index: 110

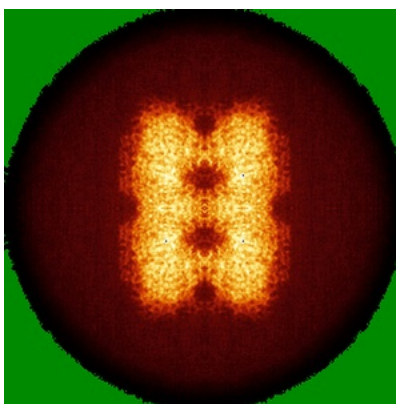
The images above show the largest variance slices of the map in three orthogonal directions.

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

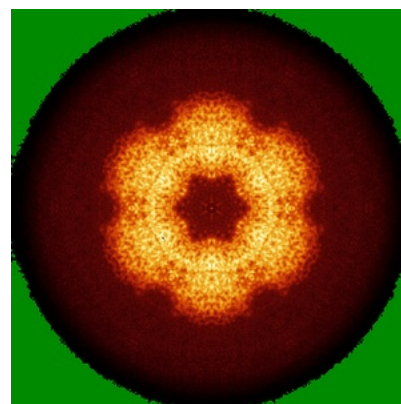
### 6.4.1 Primary map



X

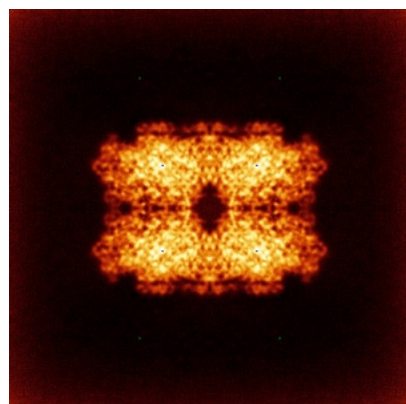


Y

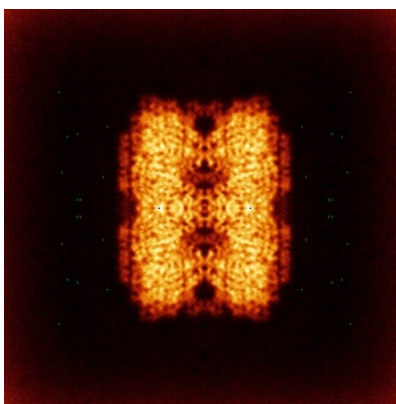


Z

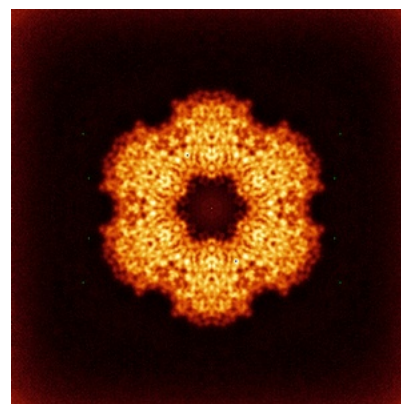
### 6.4.2 Raw map



X



Y

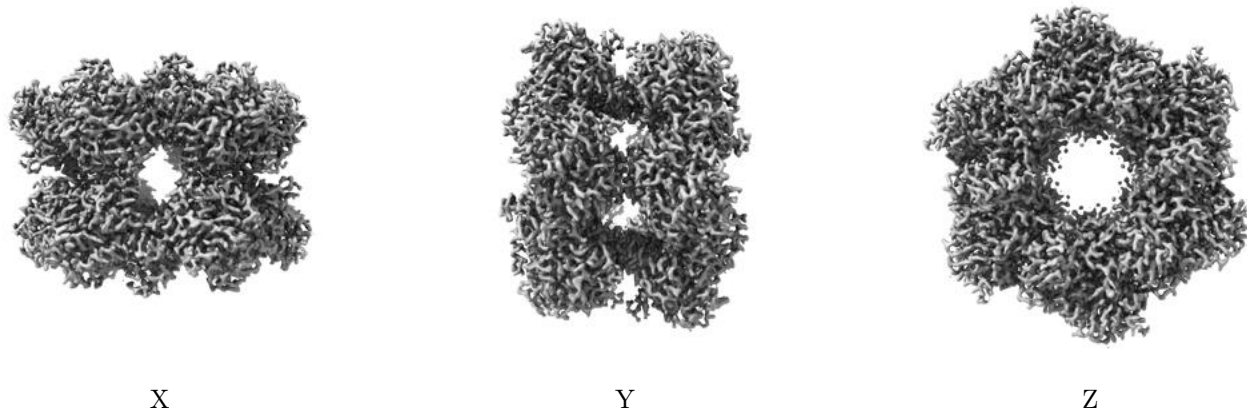


Z

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.

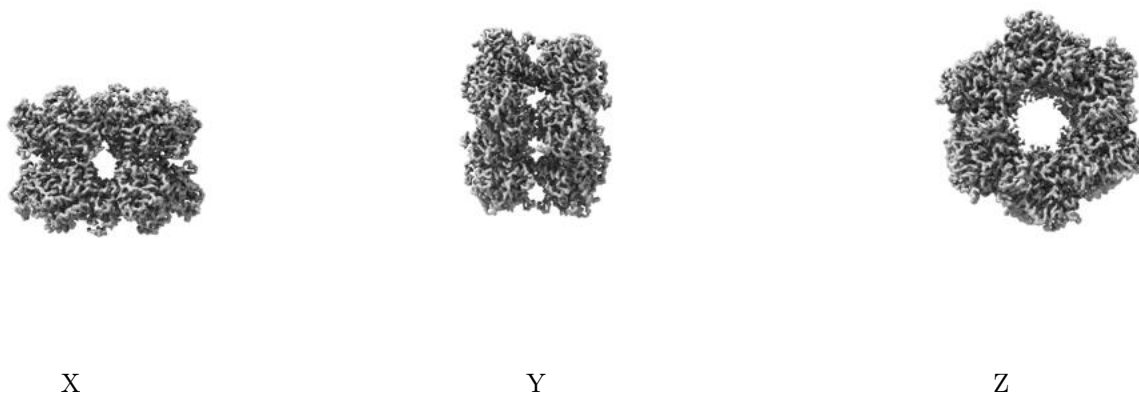
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.332. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

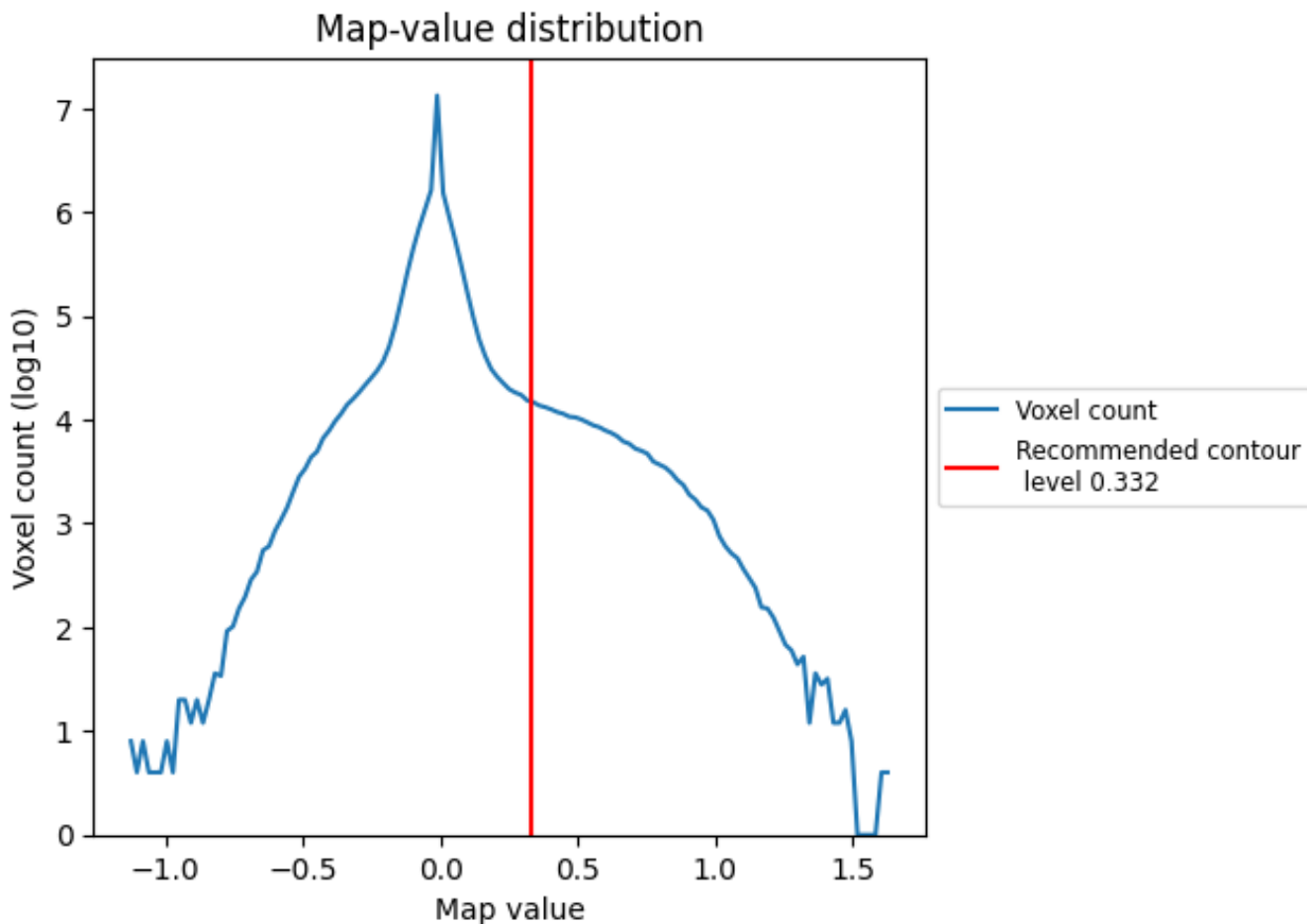
## 6.6 Mask visualisation [i](#)

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.

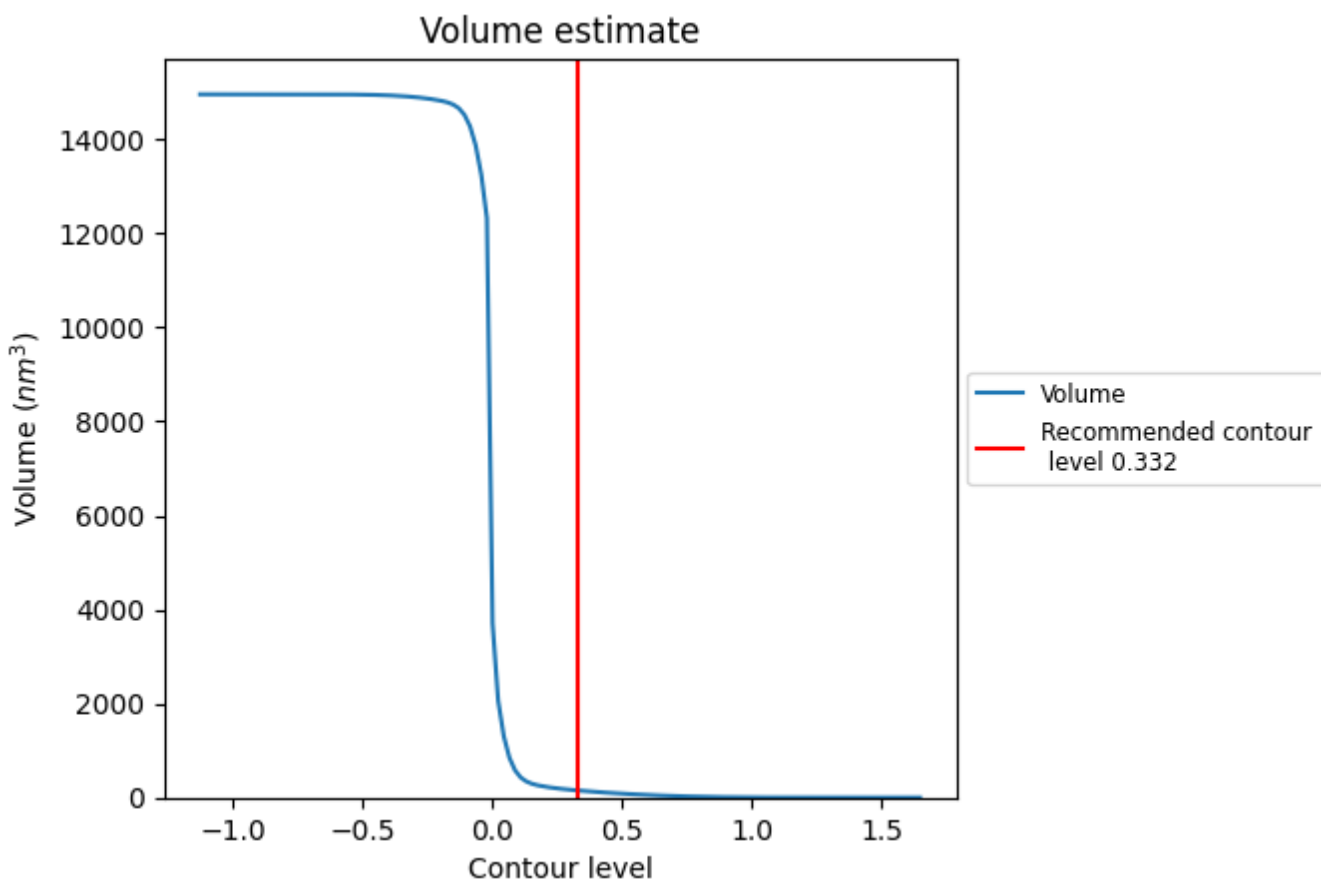
### 7.1 Map-value distribution [i](#)



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.



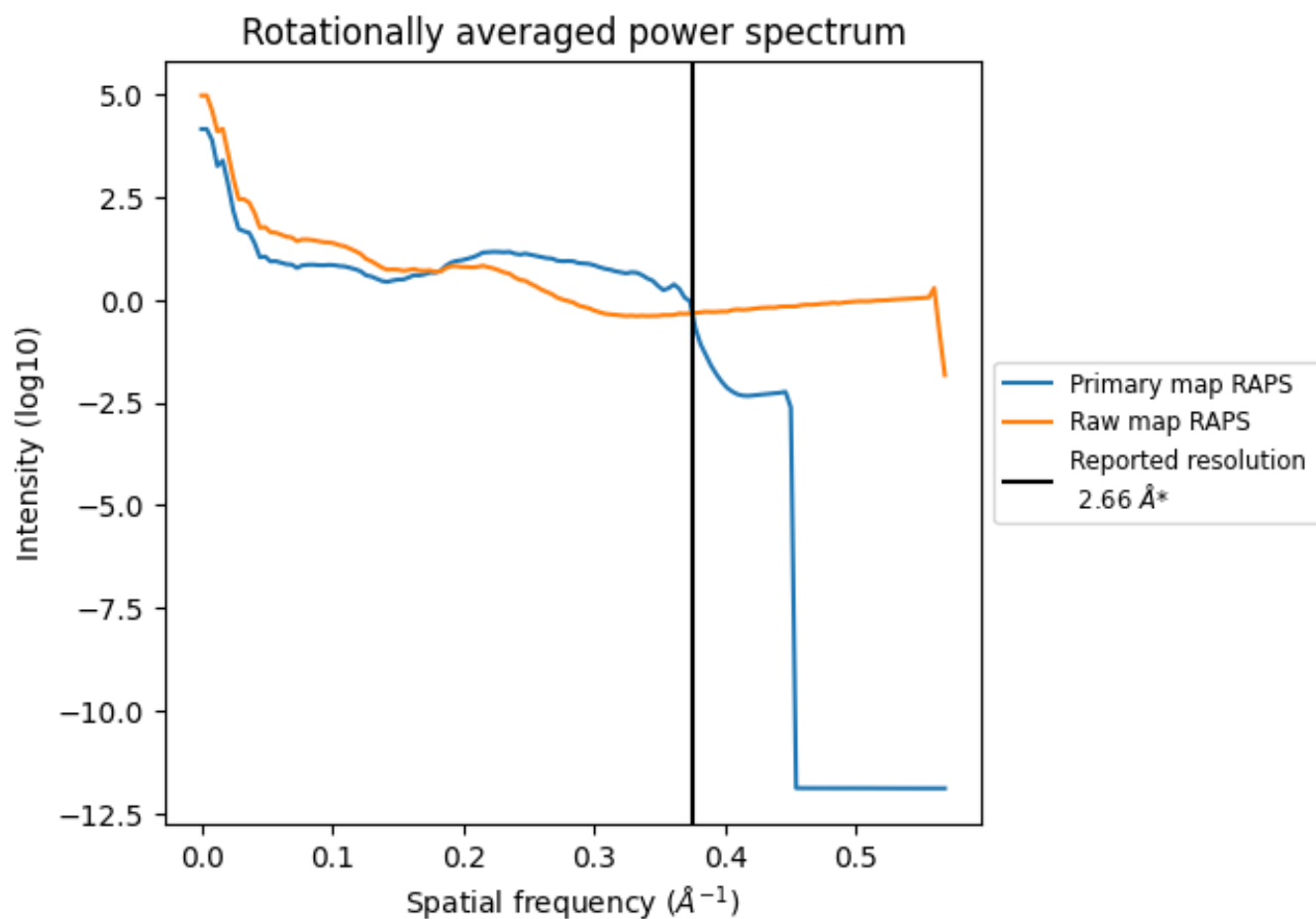
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 150 nm<sup>3</sup>; this corresponds to an approximate mass of 135 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](#)

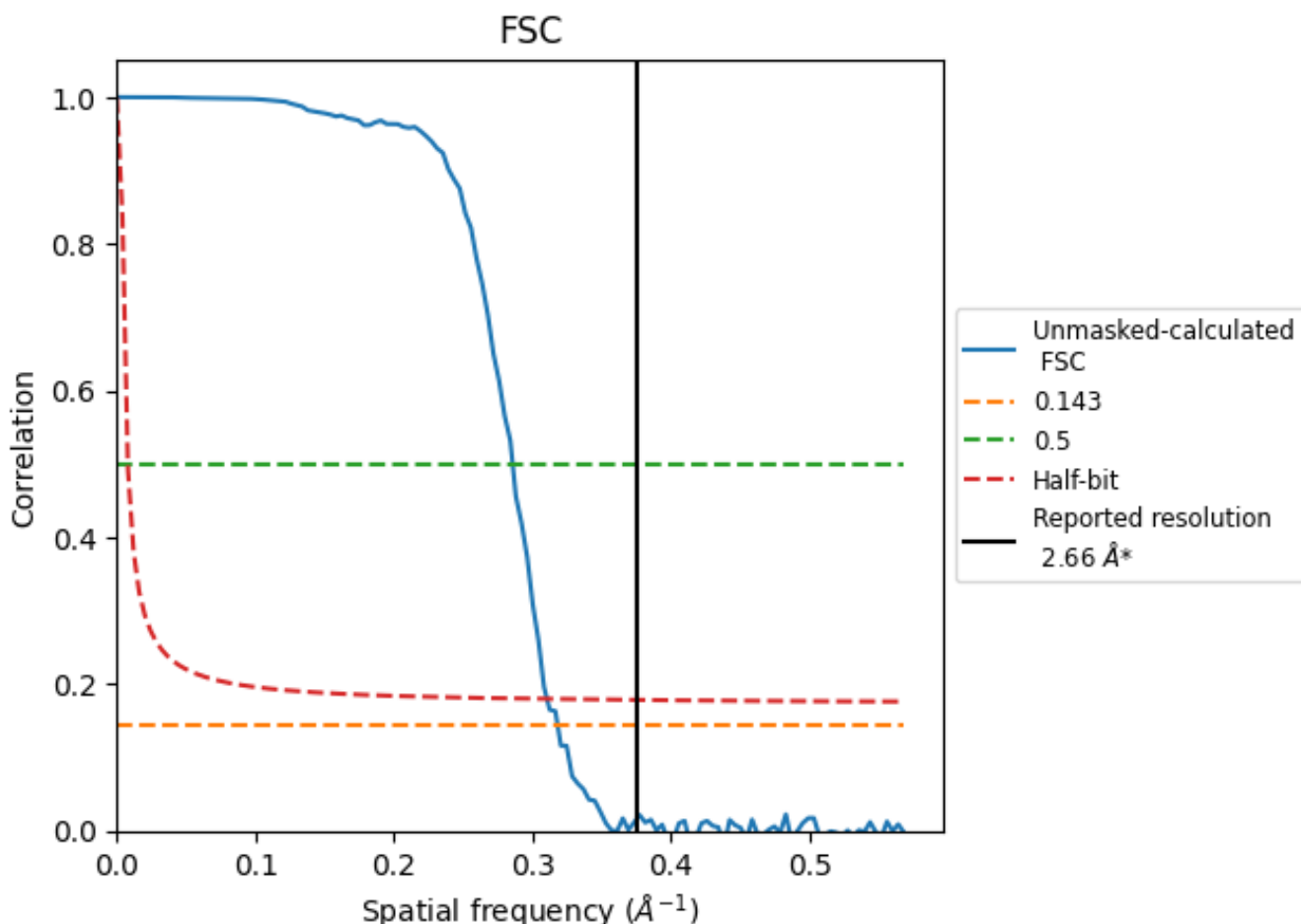


\*Reported resolution corresponds to spatial frequency of 0.376 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.376 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

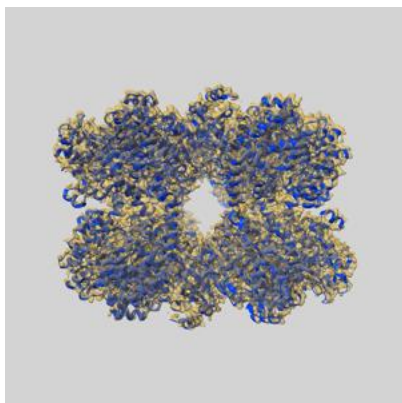
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.66	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.14	3.50	3.22

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.14 differs from the reported value 2.66 by more than 10 %

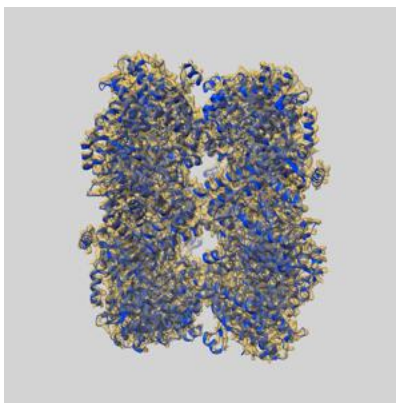
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-41232 and PDB model 8TFK. Per-residue inclusion information can be found in section 3 on page 14.

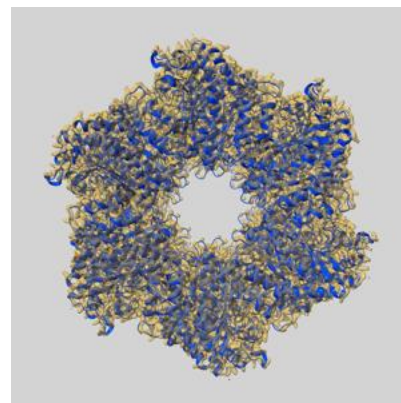
### 9.1 Map-model overlay [i](#)



X



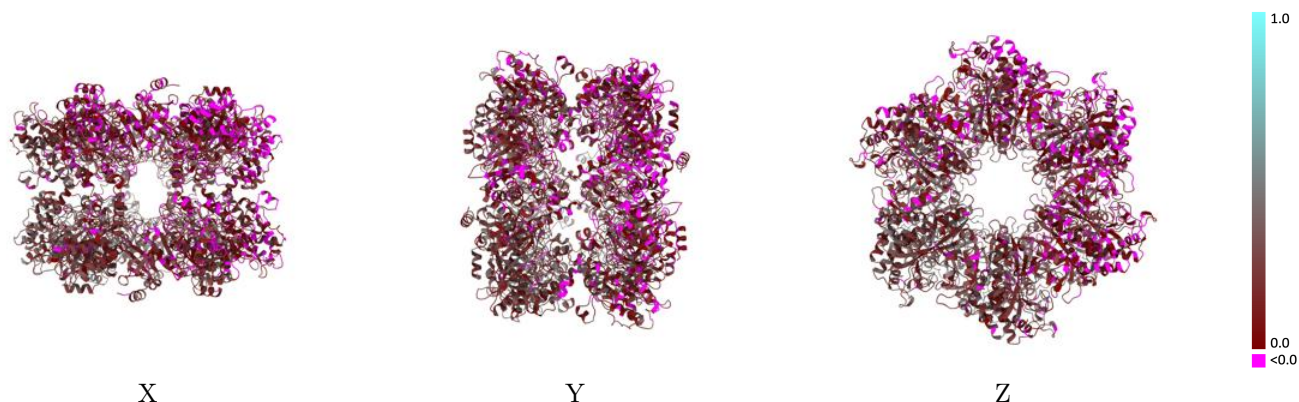
Y



Z

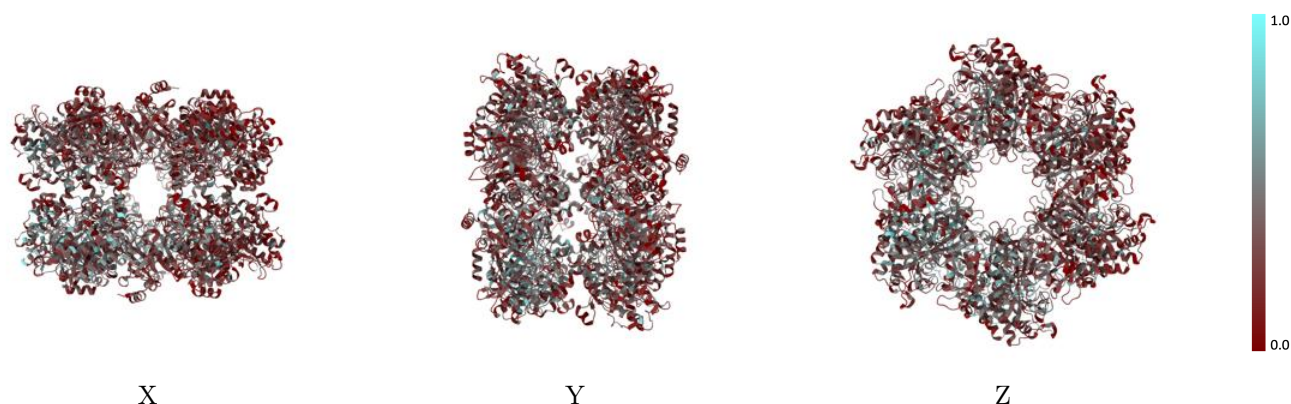
The images above show the 3D surface view of the map at the recommended contour level 0.332 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



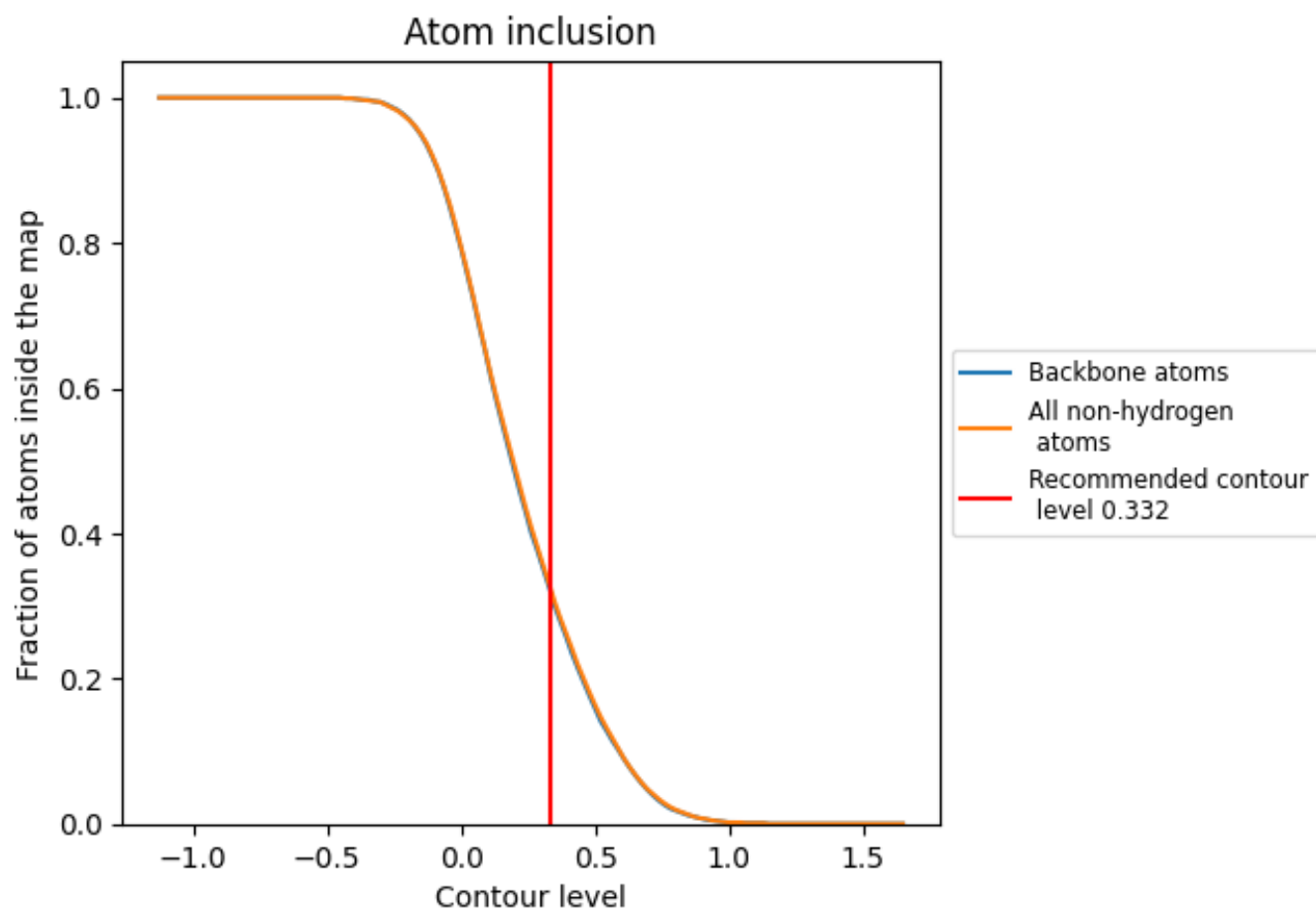
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.332).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 32% of all backbone atoms, 33% 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 (0.332) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.3270	0.1940
A	0.2740	0.1450
B	0.2830	0.1480
C	0.3220	0.1990
D	0.4350	0.3100
E	0.4920	0.3660
F	0.3680	0.2390
G	0.2600	0.1020
H	0.2580	0.0970
I	0.2590	0.1050
J	0.3500	0.2190
K	0.3620	0.2430
L	0.2950	0.1490

