Full wwPDB EM Validation Report ⓘ

Feb 5, 2024 – 03:12 PM EST

PDB ID	:	8FBP
EMDB ID	:	EMD-28965
Title	:	Glutamine synthetase from Pseudomonas aeruginosa, filament double-unit in compressed conformation
Authors	:	Phan, I.Q.; Staker, B.; Shek, R.; Moser, T.H.; Evans, J.E.; van Voorhis, W.C.; Myler, P.J.; Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on	:	2022-11-29
Resolution	:	2.80 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ 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:

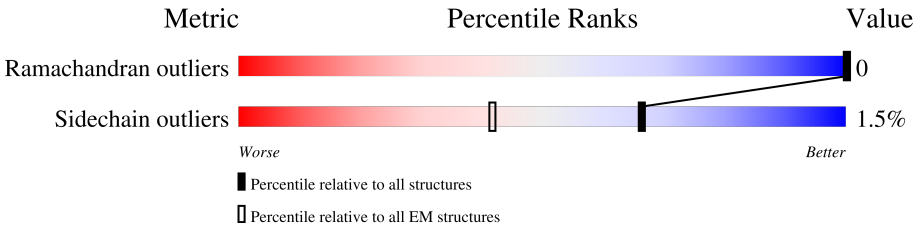
EMDB validation analysis	:	0.0.1.dev70
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.80 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	477	26% 87% • 12%
1	B	477	20% 87% 13%
1	C	477	19% 86% • 12%
1	D	477	22% 87% • 13%
1	E	477	22% 86% • 13%
1	F	477	28% 87% • 13%
1	G	477	26% 86% • 13%
1	H	477	26% 86% • 13%
1	I	477	16% 86% • 13%

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Mol	Chain	Length	Quality of chain
1	J	477	7% 85% 13%
1	K	477	26% 86% 12%
1	L	477	13% 87% 13%
1	M	477	21% 86% 14%
1	N	477	26% 87% 13%
1	O	477	12% 86% 13%
1	P	477	87% 12%
1	Q	477	5% 86% 13%
1	R	477	7% 86% 13%
1	S	477	11% 86% 13%
1	T	477	15% 86% 13%
1	U	477	17% 87% 12%
1	V	477	13% 86% 13%
1	W	477	6% 86% 13%
1	X	477	86% 13%
1	Y	477	8% 86% 13%
1	Z	477	87% 13%
1	a	477	5% 87% 13%
1	b	477	12% 86% 13%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 91071 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Glutamine synthetase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	418	Total 3265	C 2078	N 541	O 630	S 16	0	0
1	B	417	Total 3256	C 2074	N 540	O 626	S 16	0	0
1	C	419	Total 3274	C 2084	N 543	O 631	S 16	0	0
1	D	416	Total 3247	C 2068	N 538	O 625	S 16	0	0
1	E	415	Total 3241	C 2065	N 537	O 623	S 16	0	0
1	F	417	Total 3256	C 2074	N 540	O 626	S 16	0	0
1	G	417	Total 3256	C 2074	N 540	O 626	S 16	0	0
1	H	415	Total 3241	C 2065	N 537	O 623	S 16	0	0
1	I	416	Total 3250	C 2070	N 538	O 626	S 16	0	0
1	J	414	Total 3235	C 2062	N 536	O 621	S 16	0	0
1	K	419	Total 3274	C 2083	N 543	O 632	S 16	0	0
1	L	416	Total 3250	C 2071	N 539	O 624	S 16	0	0
1	M	412	Total 3223	C 2054	N 534	O 619	S 16	0	0
1	N	415	Total 3239	C 2064	N 537	O 622	S 16	0	0
1	O	415	Total 3244	C 2068	N 538	O 622	S 16	0	0
1	P	421	Total 3296	C 2100	N 546	O 634	S 16	0	0
1	Q	415	Total 3244	C 2068	N 538	O 622	S 16	0	0

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Mol	Chain	Residues	Atoms					AltConf	Trace
1	R	415	Total	C	N	O	S	0	0
			3244	2068	538	622	16		
1	S	415	Total	C	N	O	S	0	0
			3244	2068	538	622	16		
1	T	416	Total	C	N	O	S	0	0
			3250	2071	539	624	16		
1	U	418	Total	C	N	O	S	0	0
			3272	2087	542	627	16		
1	V	415	Total	C	N	O	S	0	0
			3246	2069	538	623	16		
1	W	415	Total	C	N	O	S	0	0
			3244	2068	538	622	16		
1	X	417	Total	C	N	O	S	0	0
			3256	2074	540	626	16		
1	Y	417	Total	C	N	O	S	0	0
			3256	2074	540	626	16		
1	Z	417	Total	C	N	O	S	0	0
			3256	2074	540	626	16		
1	a	417	Total	C	N	O	S	0	0
			3256	2074	540	626	16		
1	b	417	Total	C	N	O	S	0	0
			3256	2074	540	626	16		

There are 224 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP Q9HU65
A	2	ALA	-	expression tag	UNP Q9HU65
A	3	HIS	-	expression tag	UNP Q9HU65
A	4	HIS	-	expression tag	UNP Q9HU65
A	5	HIS	-	expression tag	UNP Q9HU65
A	6	HIS	-	expression tag	UNP Q9HU65
A	7	HIS	-	expression tag	UNP Q9HU65
A	8	HIS	-	expression tag	UNP Q9HU65
B	1	MET	-	initiating methionine	UNP Q9HU65
B	2	ALA	-	expression tag	UNP Q9HU65
B	3	HIS	-	expression tag	UNP Q9HU65
B	4	HIS	-	expression tag	UNP Q9HU65
B	5	HIS	-	expression tag	UNP Q9HU65
B	6	HIS	-	expression tag	UNP Q9HU65
B	7	HIS	-	expression tag	UNP Q9HU65
B	8	HIS	-	expression tag	UNP Q9HU65
C	1	MET	-	initiating methionine	UNP Q9HU65

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Chain	Residue	Modelled	Actual	Comment	Reference
C	2	ALA	-	expression tag	UNP Q9HU65
C	3	HIS	-	expression tag	UNP Q9HU65
C	4	HIS	-	expression tag	UNP Q9HU65
C	5	HIS	-	expression tag	UNP Q9HU65
C	6	HIS	-	expression tag	UNP Q9HU65
C	7	HIS	-	expression tag	UNP Q9HU65
C	8	HIS	-	expression tag	UNP Q9HU65
D	1	MET	-	initiating methionine	UNP Q9HU65
D	2	ALA	-	expression tag	UNP Q9HU65
D	3	HIS	-	expression tag	UNP Q9HU65
D	4	HIS	-	expression tag	UNP Q9HU65
D	5	HIS	-	expression tag	UNP Q9HU65
D	6	HIS	-	expression tag	UNP Q9HU65
D	7	HIS	-	expression tag	UNP Q9HU65
D	8	HIS	-	expression tag	UNP Q9HU65
E	1	MET	-	initiating methionine	UNP Q9HU65
E	2	ALA	-	expression tag	UNP Q9HU65
E	3	HIS	-	expression tag	UNP Q9HU65
E	4	HIS	-	expression tag	UNP Q9HU65
E	5	HIS	-	expression tag	UNP Q9HU65
E	6	HIS	-	expression tag	UNP Q9HU65
E	7	HIS	-	expression tag	UNP Q9HU65
E	8	HIS	-	expression tag	UNP Q9HU65
F	1	MET	-	initiating methionine	UNP Q9HU65
F	2	ALA	-	expression tag	UNP Q9HU65
F	3	HIS	-	expression tag	UNP Q9HU65
F	4	HIS	-	expression tag	UNP Q9HU65
F	5	HIS	-	expression tag	UNP Q9HU65
F	6	HIS	-	expression tag	UNP Q9HU65
F	7	HIS	-	expression tag	UNP Q9HU65
F	8	HIS	-	expression tag	UNP Q9HU65
G	1	MET	-	initiating methionine	UNP Q9HU65
G	2	ALA	-	expression tag	UNP Q9HU65
G	3	HIS	-	expression tag	UNP Q9HU65
G	4	HIS	-	expression tag	UNP Q9HU65
G	5	HIS	-	expression tag	UNP Q9HU65
G	6	HIS	-	expression tag	UNP Q9HU65
G	7	HIS	-	expression tag	UNP Q9HU65
G	8	HIS	-	expression tag	UNP Q9HU65
H	1	MET	-	initiating methionine	UNP Q9HU65
H	2	ALA	-	expression tag	UNP Q9HU65
H	3	HIS	-	expression tag	UNP Q9HU65

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Chain	Residue	Modelled	Actual	Comment	Reference
H	4	HIS	-	expression tag	UNP Q9HU65
H	5	HIS	-	expression tag	UNP Q9HU65
H	6	HIS	-	expression tag	UNP Q9HU65
H	7	HIS	-	expression tag	UNP Q9HU65
H	8	HIS	-	expression tag	UNP Q9HU65
I	1	MET	-	initiating methionine	UNP Q9HU65
I	2	ALA	-	expression tag	UNP Q9HU65
I	3	HIS	-	expression tag	UNP Q9HU65
I	4	HIS	-	expression tag	UNP Q9HU65
I	5	HIS	-	expression tag	UNP Q9HU65
I	6	HIS	-	expression tag	UNP Q9HU65
I	7	HIS	-	expression tag	UNP Q9HU65
I	8	HIS	-	expression tag	UNP Q9HU65
J	1	MET	-	initiating methionine	UNP Q9HU65
J	2	ALA	-	expression tag	UNP Q9HU65
J	3	HIS	-	expression tag	UNP Q9HU65
J	4	HIS	-	expression tag	UNP Q9HU65
J	5	HIS	-	expression tag	UNP Q9HU65
J	6	HIS	-	expression tag	UNP Q9HU65
J	7	HIS	-	expression tag	UNP Q9HU65
J	8	HIS	-	expression tag	UNP Q9HU65
K	1	MET	-	initiating methionine	UNP Q9HU65
K	2	ALA	-	expression tag	UNP Q9HU65
K	3	HIS	-	expression tag	UNP Q9HU65
K	4	HIS	-	expression tag	UNP Q9HU65
K	5	HIS	-	expression tag	UNP Q9HU65
K	6	HIS	-	expression tag	UNP Q9HU65
K	7	HIS	-	expression tag	UNP Q9HU65
K	8	HIS	-	expression tag	UNP Q9HU65
L	1	MET	-	initiating methionine	UNP Q9HU65
L	2	ALA	-	expression tag	UNP Q9HU65
L	3	HIS	-	expression tag	UNP Q9HU65
L	4	HIS	-	expression tag	UNP Q9HU65
L	5	HIS	-	expression tag	UNP Q9HU65
L	6	HIS	-	expression tag	UNP Q9HU65
L	7	HIS	-	expression tag	UNP Q9HU65
L	8	HIS	-	expression tag	UNP Q9HU65
M	1	MET	-	initiating methionine	UNP Q9HU65
M	2	ALA	-	expression tag	UNP Q9HU65
M	3	HIS	-	expression tag	UNP Q9HU65
M	4	HIS	-	expression tag	UNP Q9HU65
M	5	HIS	-	expression tag	UNP Q9HU65

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Chain	Residue	Modelled	Actual	Comment	Reference
M	6	HIS	-	expression tag	UNP Q9HU65
M	7	HIS	-	expression tag	UNP Q9HU65
M	8	HIS	-	expression tag	UNP Q9HU65
N	1	MET	-	initiating methionine	UNP Q9HU65
N	2	ALA	-	expression tag	UNP Q9HU65
N	3	HIS	-	expression tag	UNP Q9HU65
N	4	HIS	-	expression tag	UNP Q9HU65
N	5	HIS	-	expression tag	UNP Q9HU65
N	6	HIS	-	expression tag	UNP Q9HU65
N	7	HIS	-	expression tag	UNP Q9HU65
N	8	HIS	-	expression tag	UNP Q9HU65
O	1	MET	-	initiating methionine	UNP Q9HU65
O	2	ALA	-	expression tag	UNP Q9HU65
O	3	HIS	-	expression tag	UNP Q9HU65
O	4	HIS	-	expression tag	UNP Q9HU65
O	5	HIS	-	expression tag	UNP Q9HU65
O	6	HIS	-	expression tag	UNP Q9HU65
O	7	HIS	-	expression tag	UNP Q9HU65
O	8	HIS	-	expression tag	UNP Q9HU65
P	1	MET	-	initiating methionine	UNP Q9HU65
P	2	ALA	-	expression tag	UNP Q9HU65
P	3	HIS	-	expression tag	UNP Q9HU65
P	4	HIS	-	expression tag	UNP Q9HU65
P	5	HIS	-	expression tag	UNP Q9HU65
P	6	HIS	-	expression tag	UNP Q9HU65
P	7	HIS	-	expression tag	UNP Q9HU65
P	8	HIS	-	expression tag	UNP Q9HU65
Q	1	MET	-	initiating methionine	UNP Q9HU65
Q	2	ALA	-	expression tag	UNP Q9HU65
Q	3	HIS	-	expression tag	UNP Q9HU65
Q	4	HIS	-	expression tag	UNP Q9HU65
Q	5	HIS	-	expression tag	UNP Q9HU65
Q	6	HIS	-	expression tag	UNP Q9HU65
Q	7	HIS	-	expression tag	UNP Q9HU65
Q	8	HIS	-	expression tag	UNP Q9HU65
R	1	MET	-	initiating methionine	UNP Q9HU65
R	2	ALA	-	expression tag	UNP Q9HU65
R	3	HIS	-	expression tag	UNP Q9HU65
R	4	HIS	-	expression tag	UNP Q9HU65
R	5	HIS	-	expression tag	UNP Q9HU65
R	6	HIS	-	expression tag	UNP Q9HU65
R	7	HIS	-	expression tag	UNP Q9HU65

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Chain	Residue	Modelled	Actual	Comment	Reference
R	8	HIS	-	expression tag	UNP Q9HU65
S	1	MET	-	initiating methionine	UNP Q9HU65
S	2	ALA	-	expression tag	UNP Q9HU65
S	3	HIS	-	expression tag	UNP Q9HU65
S	4	HIS	-	expression tag	UNP Q9HU65
S	5	HIS	-	expression tag	UNP Q9HU65
S	6	HIS	-	expression tag	UNP Q9HU65
S	7	HIS	-	expression tag	UNP Q9HU65
S	8	HIS	-	expression tag	UNP Q9HU65
T	1	MET	-	initiating methionine	UNP Q9HU65
T	2	ALA	-	expression tag	UNP Q9HU65
T	3	HIS	-	expression tag	UNP Q9HU65
T	4	HIS	-	expression tag	UNP Q9HU65
T	5	HIS	-	expression tag	UNP Q9HU65
T	6	HIS	-	expression tag	UNP Q9HU65
T	7	HIS	-	expression tag	UNP Q9HU65
T	8	HIS	-	expression tag	UNP Q9HU65
U	1	MET	-	initiating methionine	UNP Q9HU65
U	2	ALA	-	expression tag	UNP Q9HU65
U	3	HIS	-	expression tag	UNP Q9HU65
U	4	HIS	-	expression tag	UNP Q9HU65
U	5	HIS	-	expression tag	UNP Q9HU65
U	6	HIS	-	expression tag	UNP Q9HU65
U	7	HIS	-	expression tag	UNP Q9HU65
U	8	HIS	-	expression tag	UNP Q9HU65
V	1	MET	-	initiating methionine	UNP Q9HU65
V	2	ALA	-	expression tag	UNP Q9HU65
V	3	HIS	-	expression tag	UNP Q9HU65
V	4	HIS	-	expression tag	UNP Q9HU65
V	5	HIS	-	expression tag	UNP Q9HU65
V	6	HIS	-	expression tag	UNP Q9HU65
V	7	HIS	-	expression tag	UNP Q9HU65
V	8	HIS	-	expression tag	UNP Q9HU65
W	1	MET	-	initiating methionine	UNP Q9HU65
W	2	ALA	-	expression tag	UNP Q9HU65
W	3	HIS	-	expression tag	UNP Q9HU65
W	4	HIS	-	expression tag	UNP Q9HU65
W	5	HIS	-	expression tag	UNP Q9HU65
W	6	HIS	-	expression tag	UNP Q9HU65
W	7	HIS	-	expression tag	UNP Q9HU65
W	8	HIS	-	expression tag	UNP Q9HU65
X	1	MET	-	initiating methionine	UNP Q9HU65

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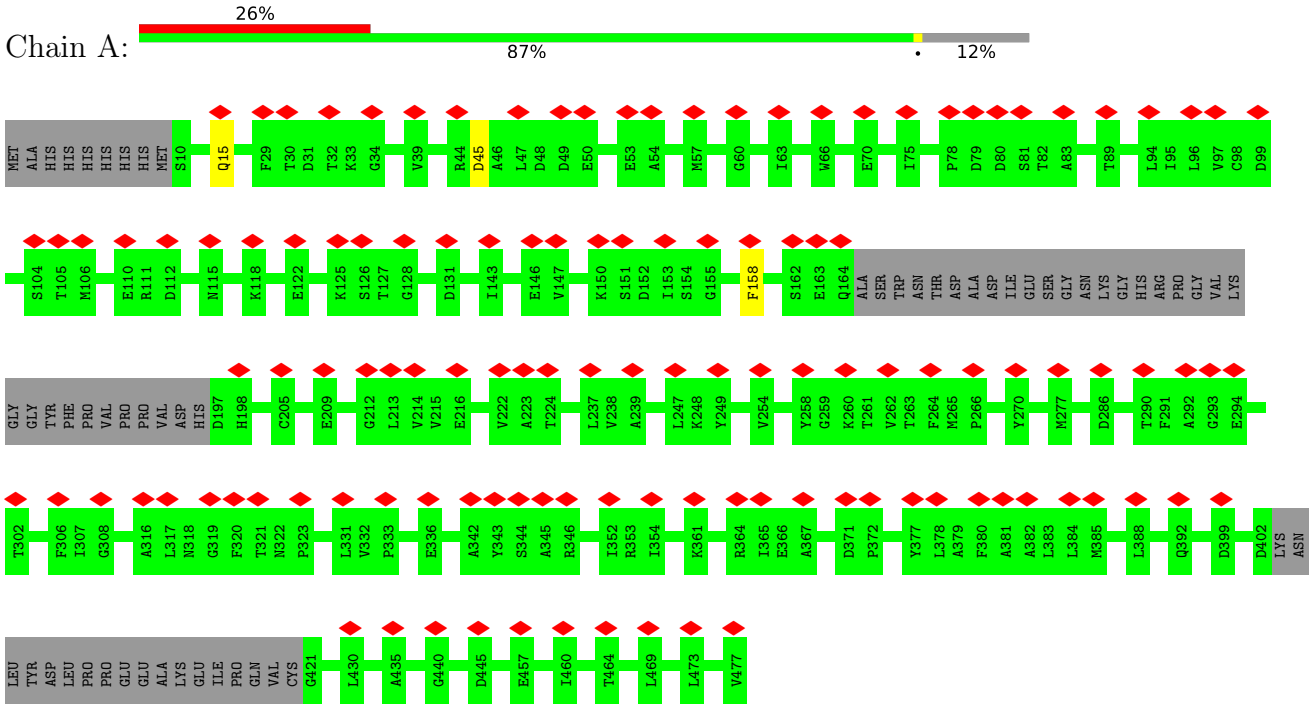
Chain	Residue	Modelled	Actual	Comment	Reference
X	2	ALA	-	expression tag	UNP Q9HU65
X	3	HIS	-	expression tag	UNP Q9HU65
X	4	HIS	-	expression tag	UNP Q9HU65
X	5	HIS	-	expression tag	UNP Q9HU65
X	6	HIS	-	expression tag	UNP Q9HU65
X	7	HIS	-	expression tag	UNP Q9HU65
X	8	HIS	-	expression tag	UNP Q9HU65
Y	1	MET	-	initiating methionine	UNP Q9HU65
Y	2	ALA	-	expression tag	UNP Q9HU65
Y	3	HIS	-	expression tag	UNP Q9HU65
Y	4	HIS	-	expression tag	UNP Q9HU65
Y	5	HIS	-	expression tag	UNP Q9HU65
Y	6	HIS	-	expression tag	UNP Q9HU65
Y	7	HIS	-	expression tag	UNP Q9HU65
Y	8	HIS	-	expression tag	UNP Q9HU65
Z	1	MET	-	initiating methionine	UNP Q9HU65
Z	2	ALA	-	expression tag	UNP Q9HU65
Z	3	HIS	-	expression tag	UNP Q9HU65
Z	4	HIS	-	expression tag	UNP Q9HU65
Z	5	HIS	-	expression tag	UNP Q9HU65
Z	6	HIS	-	expression tag	UNP Q9HU65
Z	7	HIS	-	expression tag	UNP Q9HU65
Z	8	HIS	-	expression tag	UNP Q9HU65
a	1	MET	-	initiating methionine	UNP Q9HU65
a	2	ALA	-	expression tag	UNP Q9HU65
a	3	HIS	-	expression tag	UNP Q9HU65
a	4	HIS	-	expression tag	UNP Q9HU65
a	5	HIS	-	expression tag	UNP Q9HU65
a	6	HIS	-	expression tag	UNP Q9HU65
a	7	HIS	-	expression tag	UNP Q9HU65
a	8	HIS	-	expression tag	UNP Q9HU65
b	1	MET	-	initiating methionine	UNP Q9HU65
b	2	ALA	-	expression tag	UNP Q9HU65
b	3	HIS	-	expression tag	UNP Q9HU65
b	4	HIS	-	expression tag	UNP Q9HU65
b	5	HIS	-	expression tag	UNP Q9HU65
b	6	HIS	-	expression tag	UNP Q9HU65
b	7	HIS	-	expression tag	UNP Q9HU65
b	8	HIS	-	expression tag	UNP Q9HU65

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.

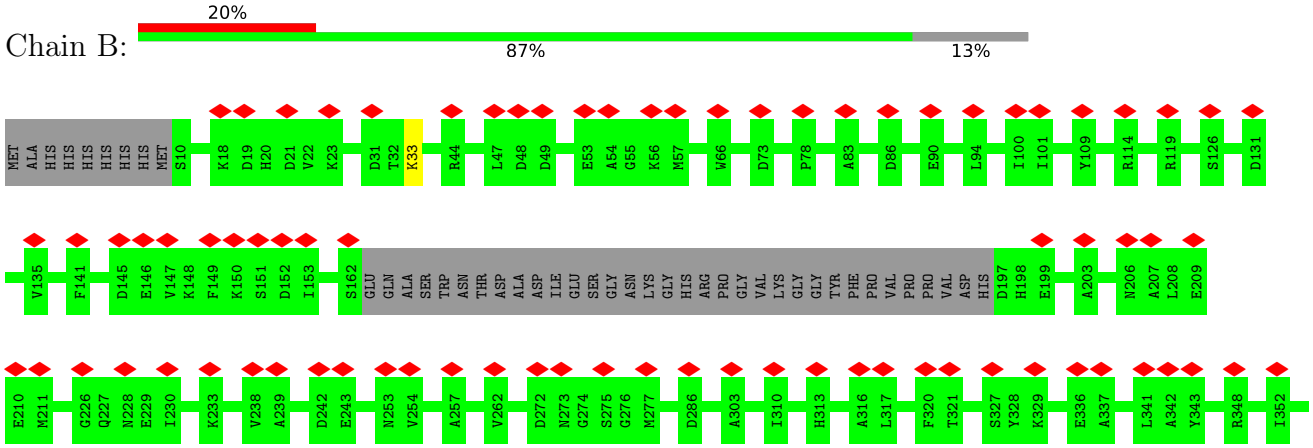
• Molecule 1: Glutamine synthetase

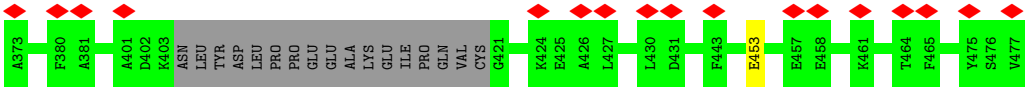
Chain A:



• Molecule 1: Glutamine synthetase

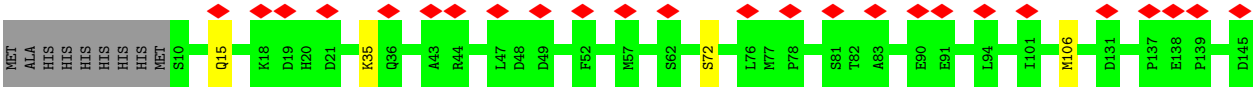
Chain B:

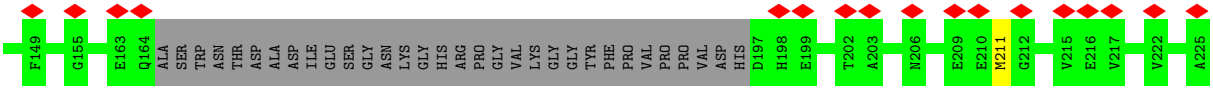


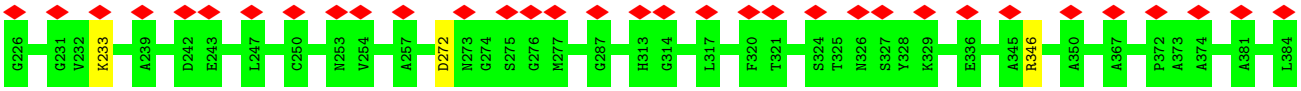


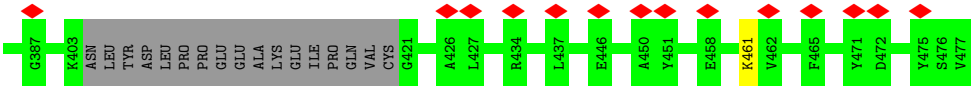
• Molecule 1: Glutamine synthetase

Chain C:



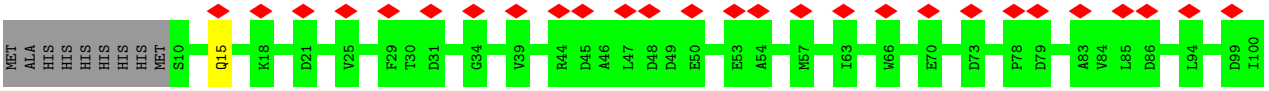


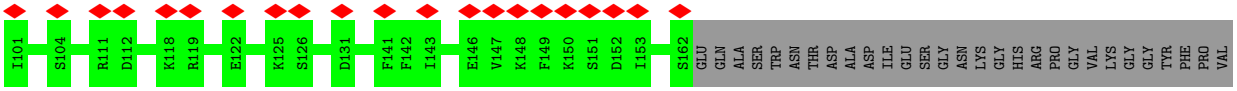


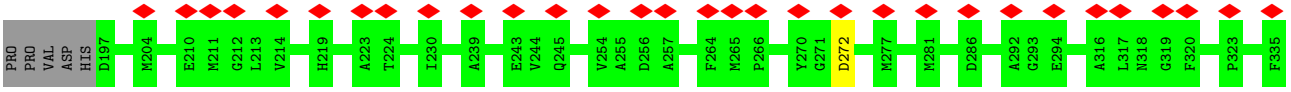


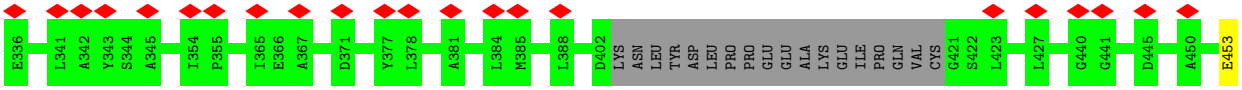
• Molecule 1: Glutamine synthetase

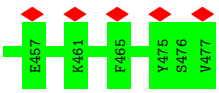
Chain D:





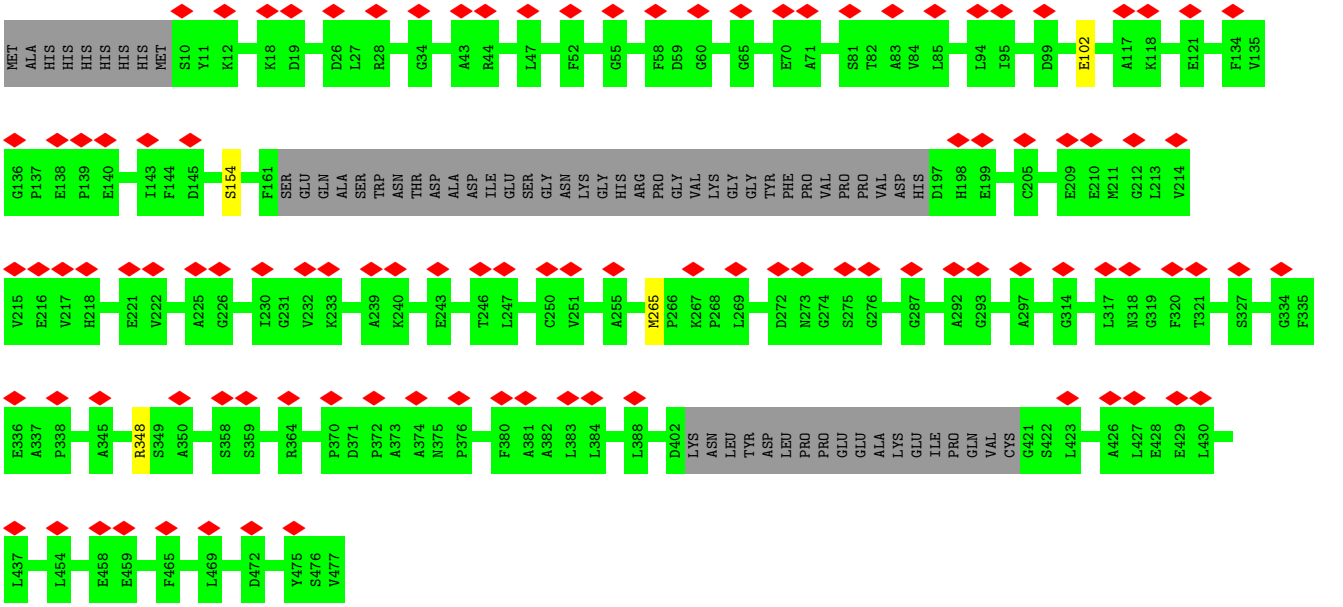




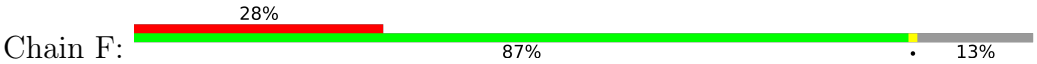


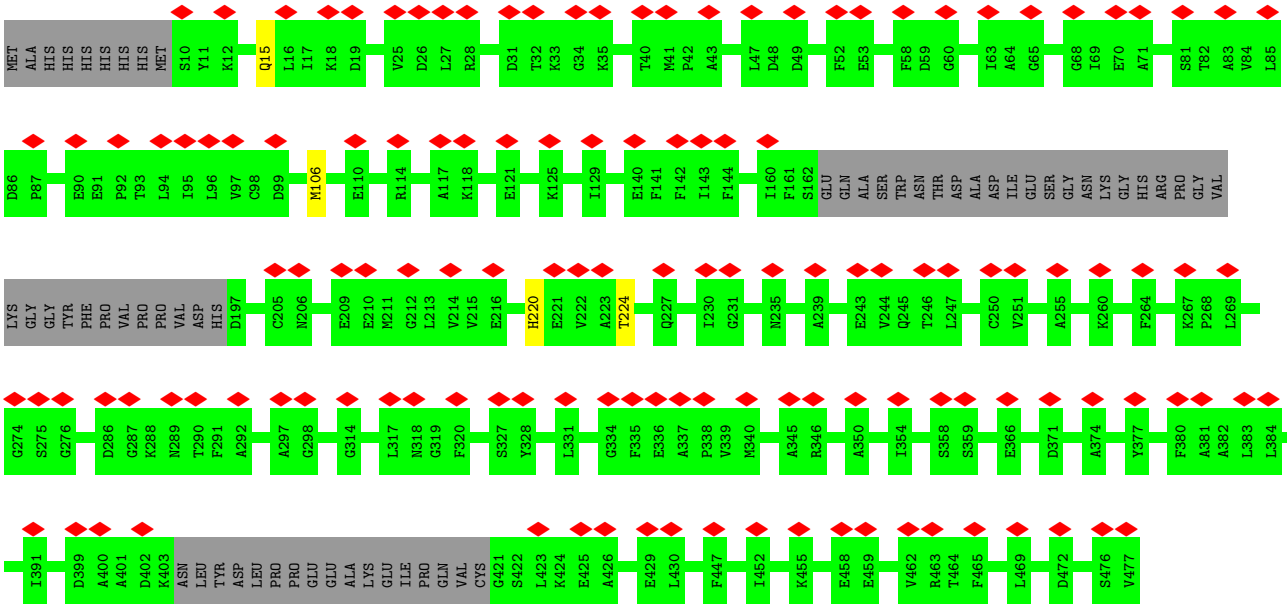
• Molecule 1: Glutamine synthetase

Chain E:

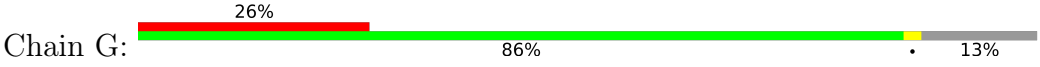


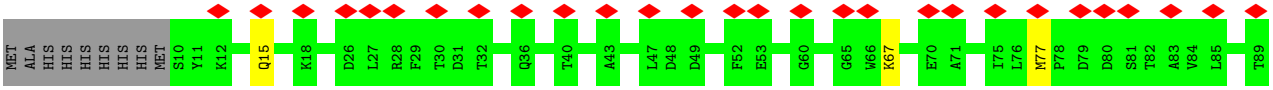
• Molecule 1: Glutamine synthetase

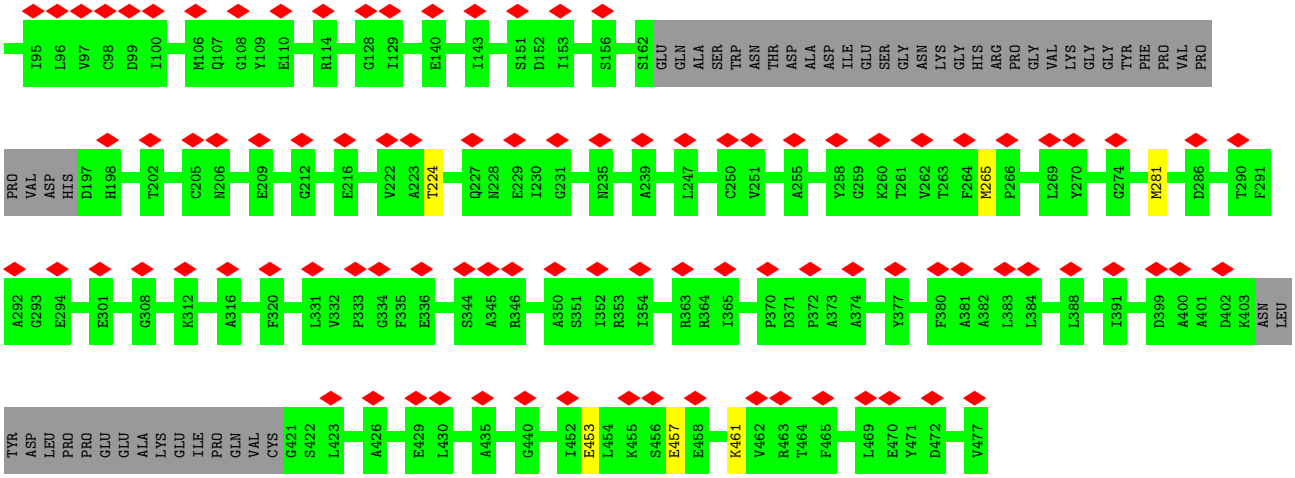




• Molecule 1: Glutamine synthetase

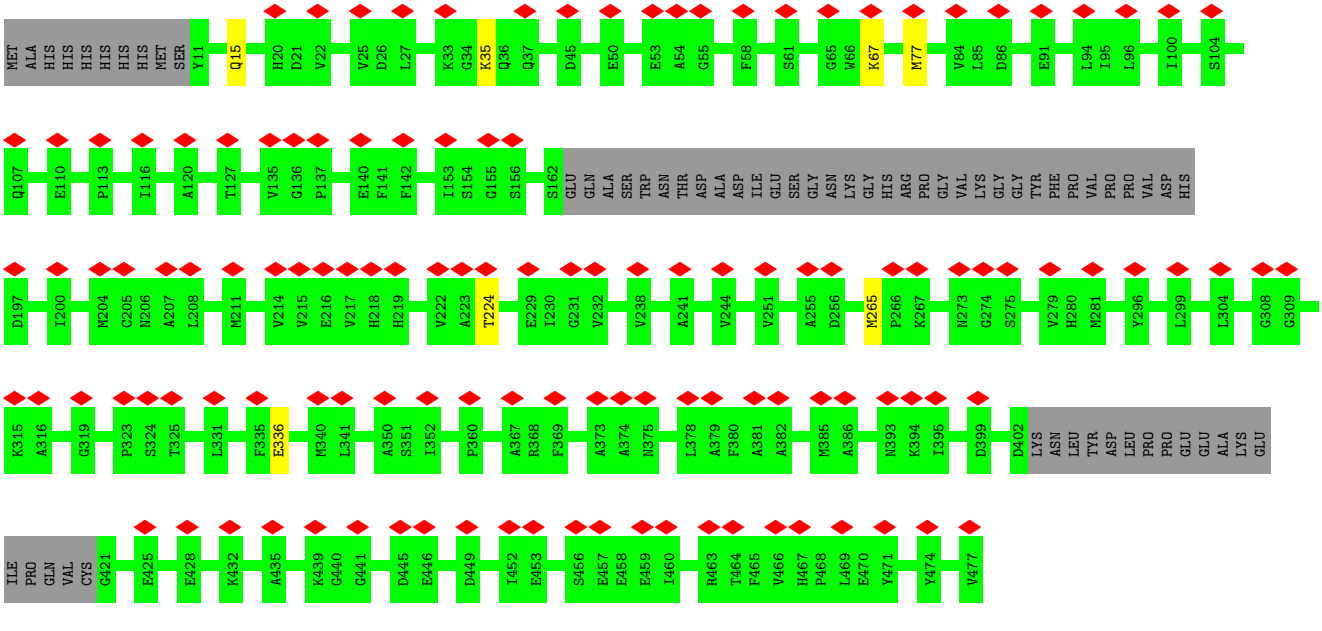






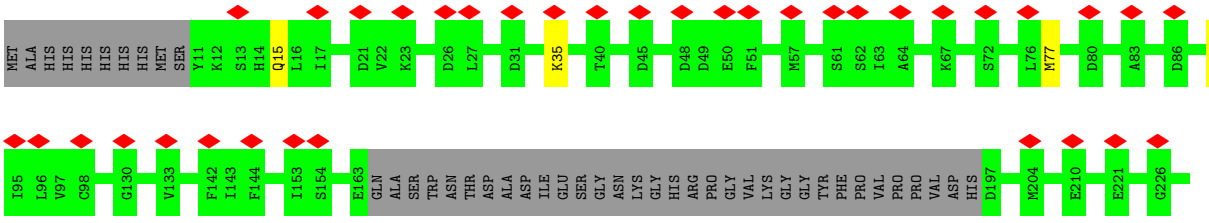
• Molecule 1: Glutamine synthetase

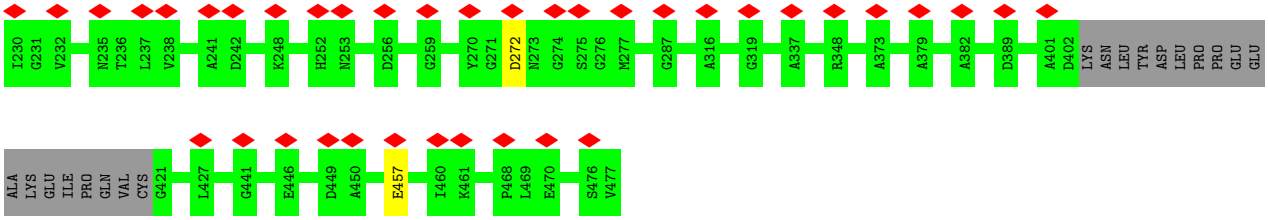
Chain H:



• Molecule 1: Glutamine synthetase

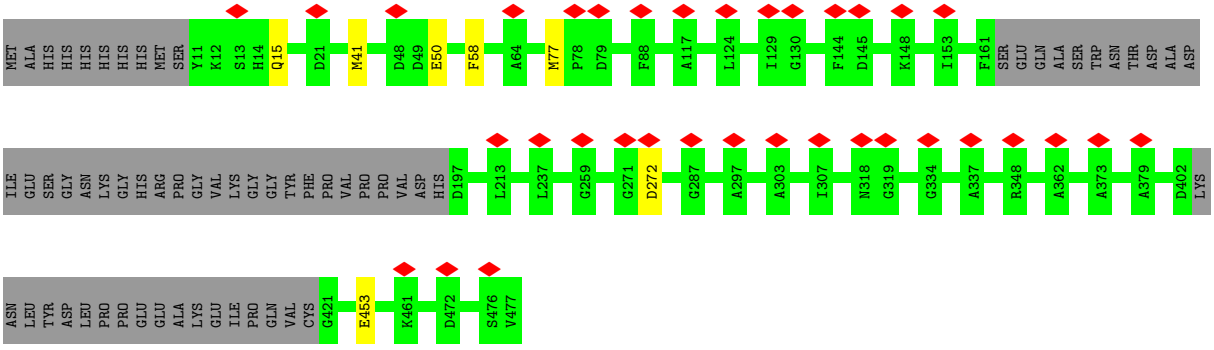
Chain I:





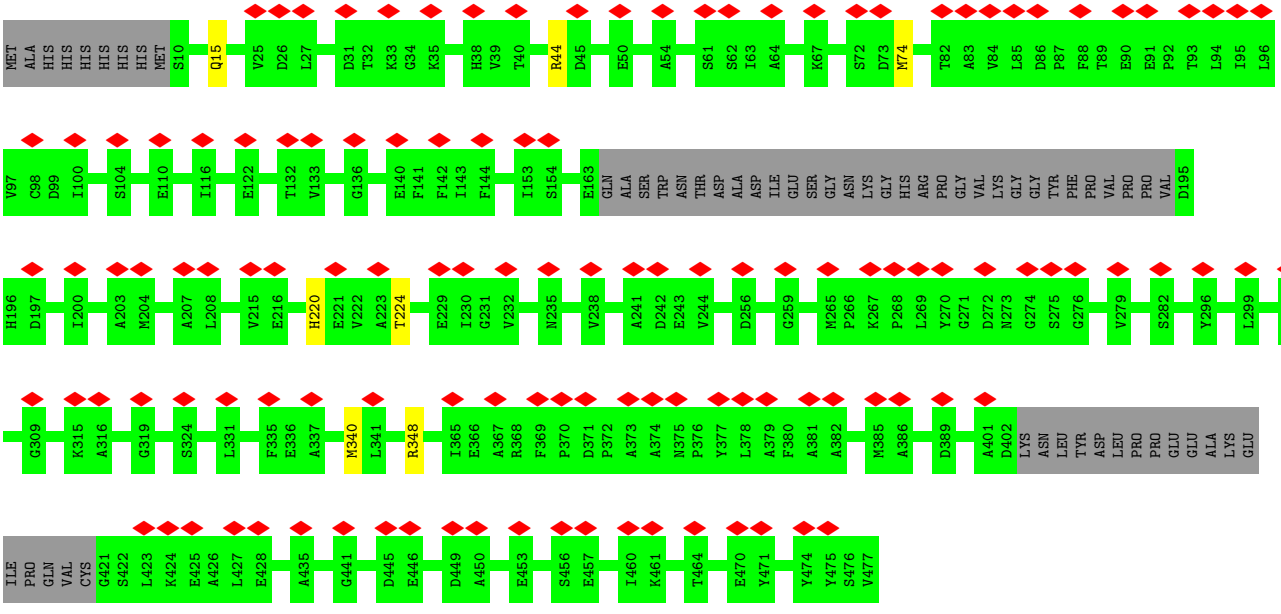
• Molecule 1: Glutamine synthetase

Chain J:



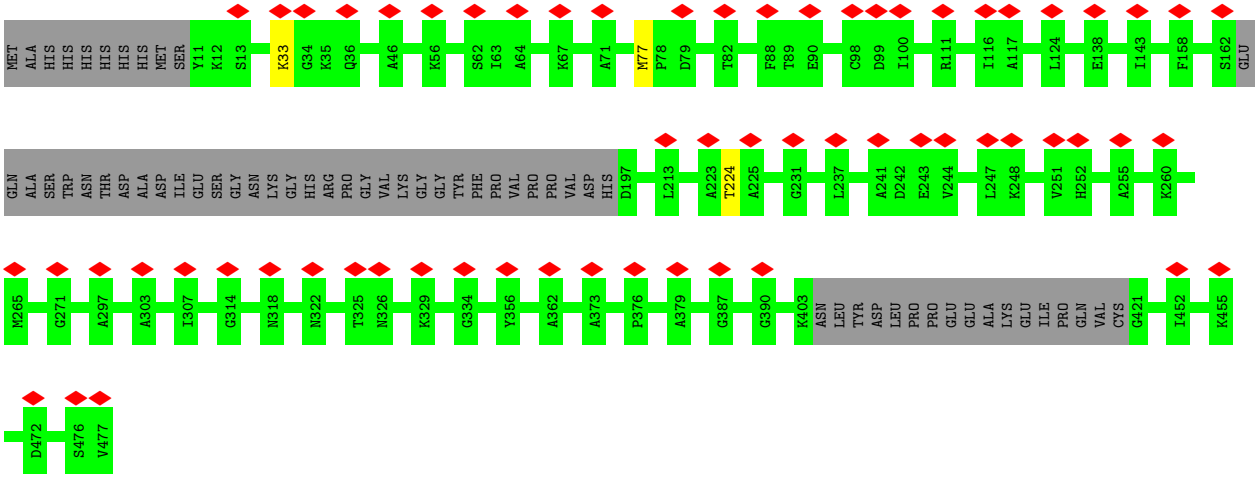
• Molecule 1: Glutamine synthetase

Chain K:



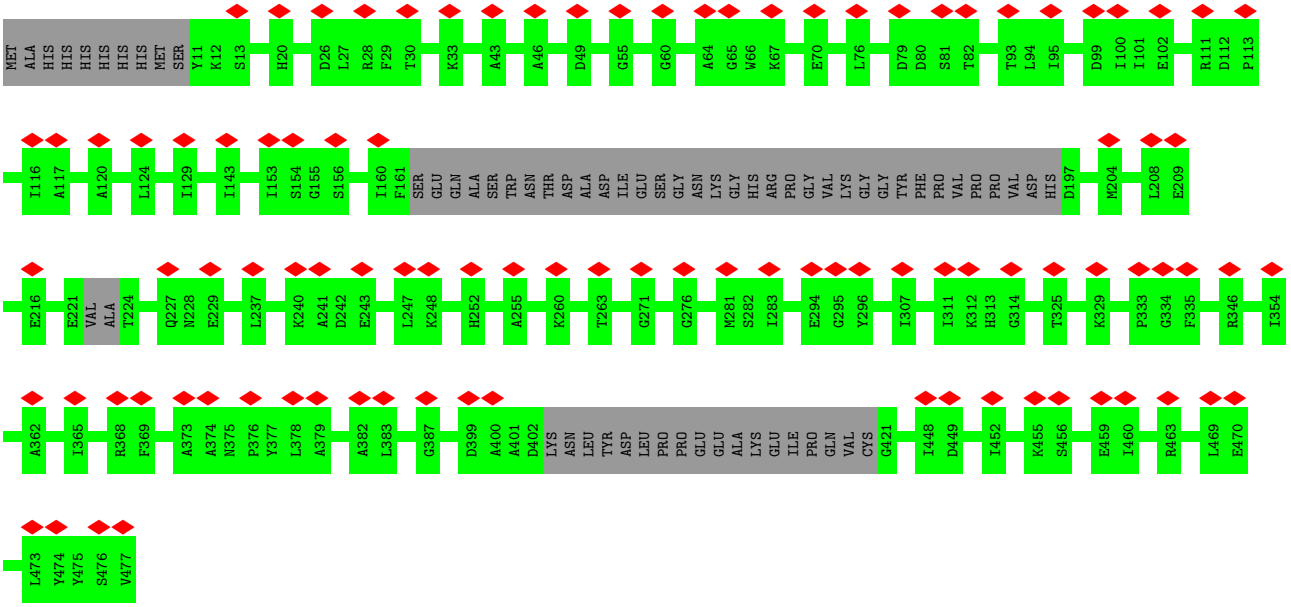
• Molecule 1: Glutamine synthetase

Chain L:



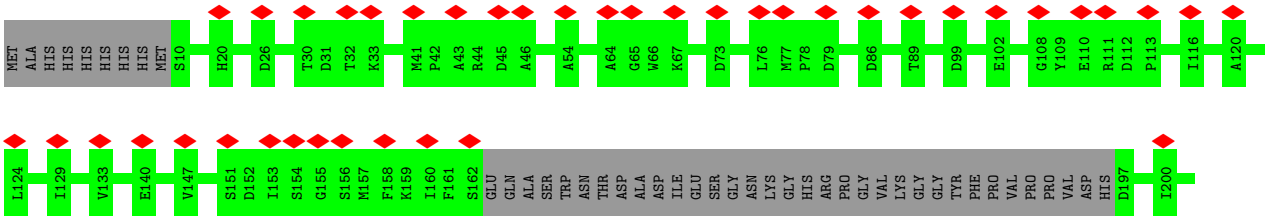
• Molecule 1: Glutamine synthetase

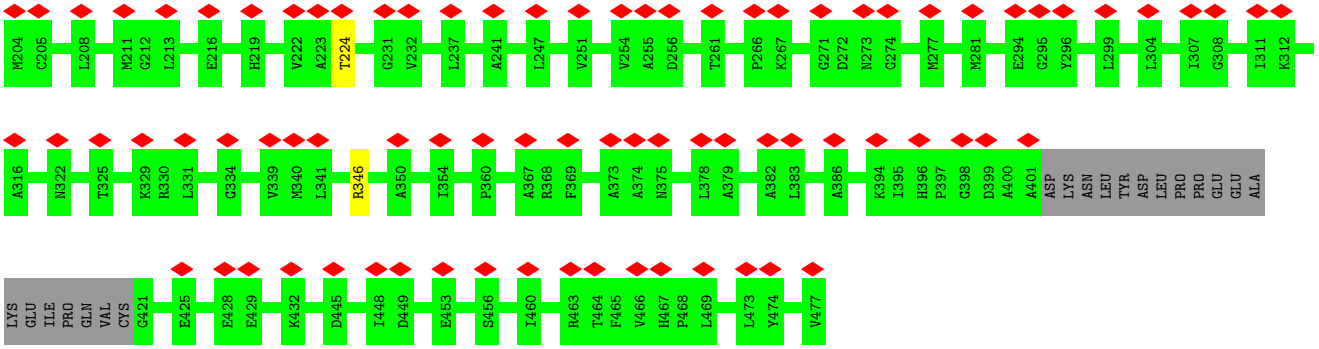
Chain M:



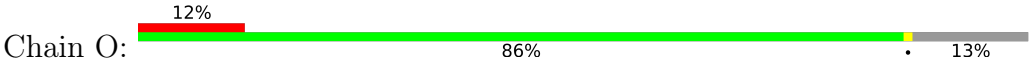
• Molecule 1: Glutamine synthetase

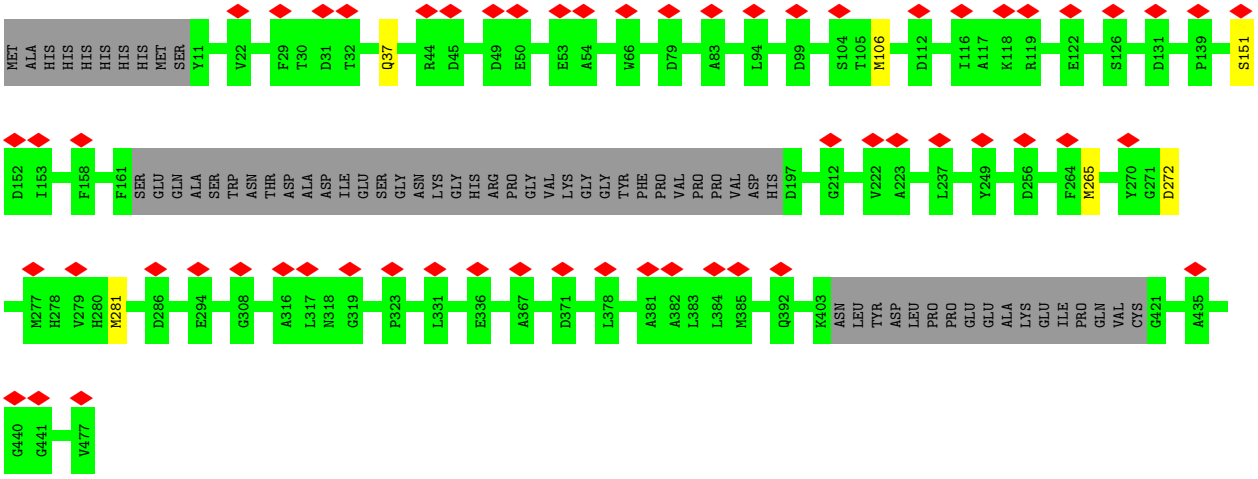
Chain N:



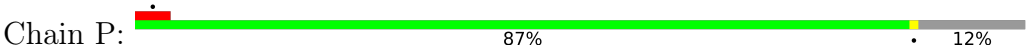


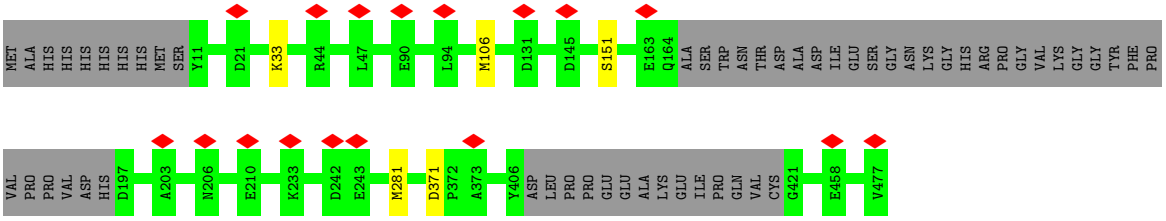
• Molecule 1: Glutamine synthetase



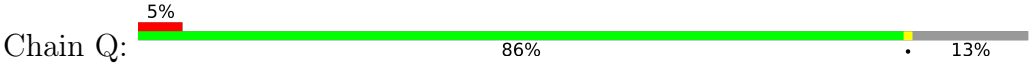


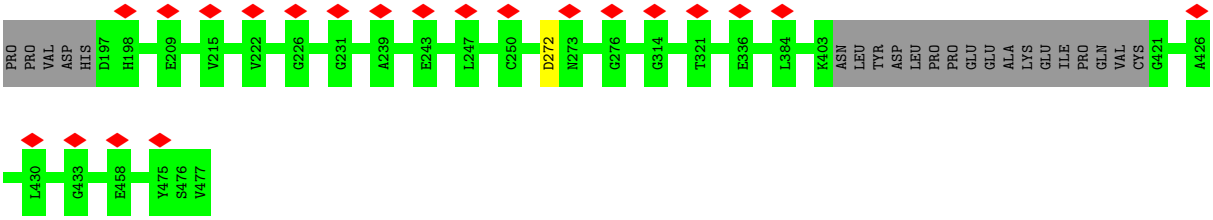
• Molecule 1: Glutamine synthetase





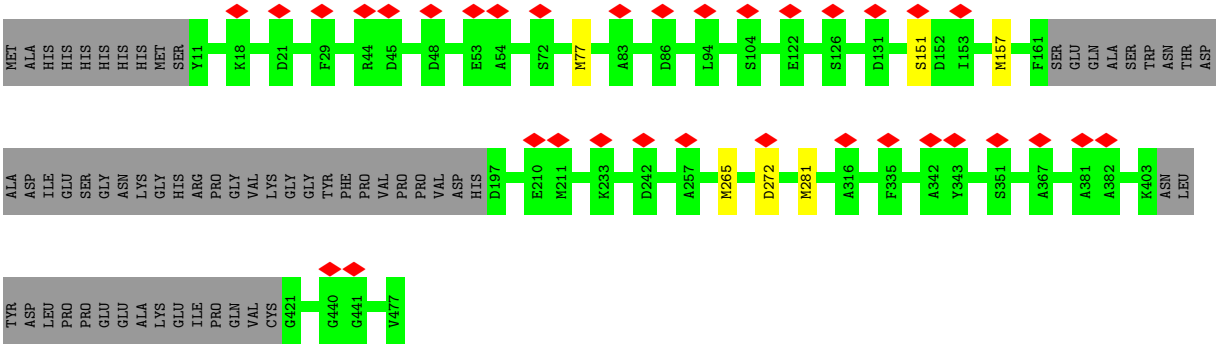
• Molecule 1: Glutamine synthetase





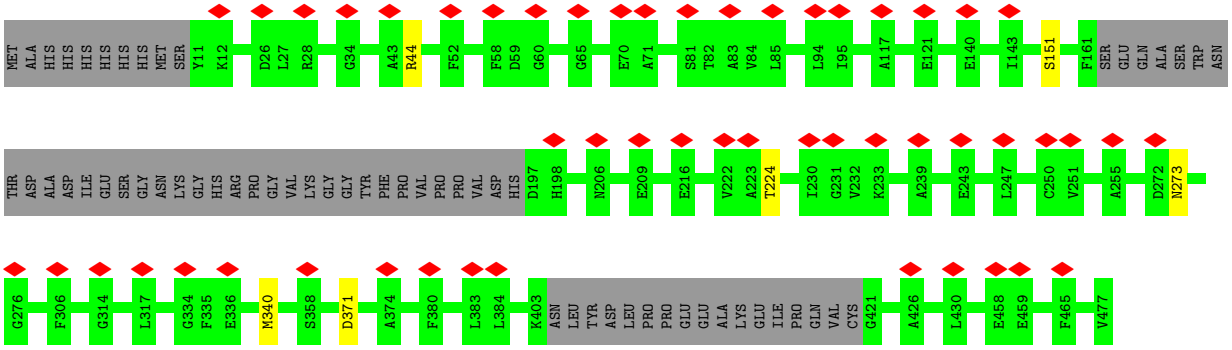
• Molecule 1: Glutamine synthetase

Chain R:



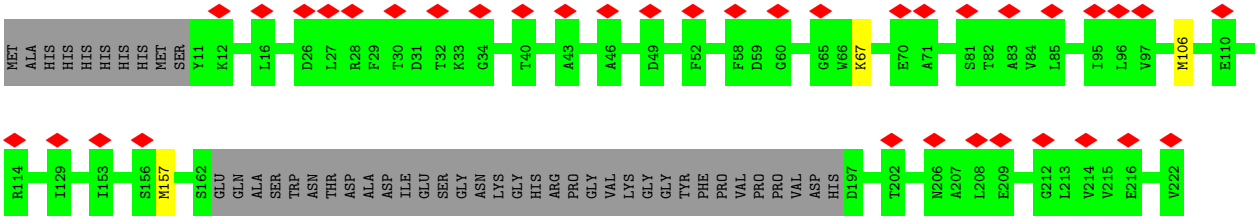
• Molecule 1: Glutamine synthetase

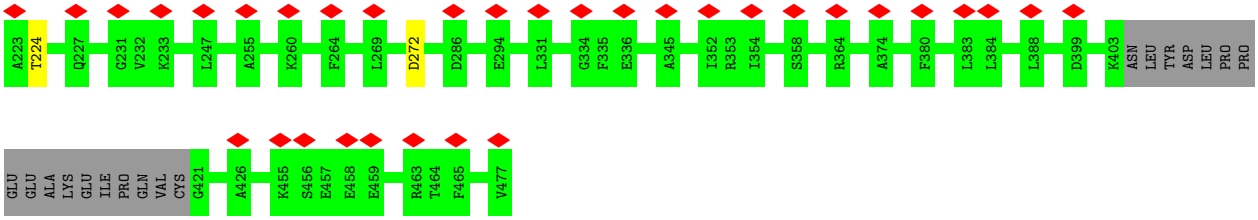
Chain S:



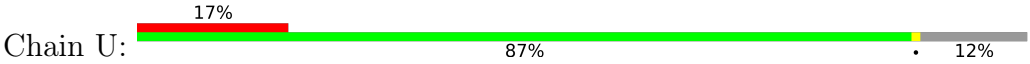
• Molecule 1: Glutamine synthetase

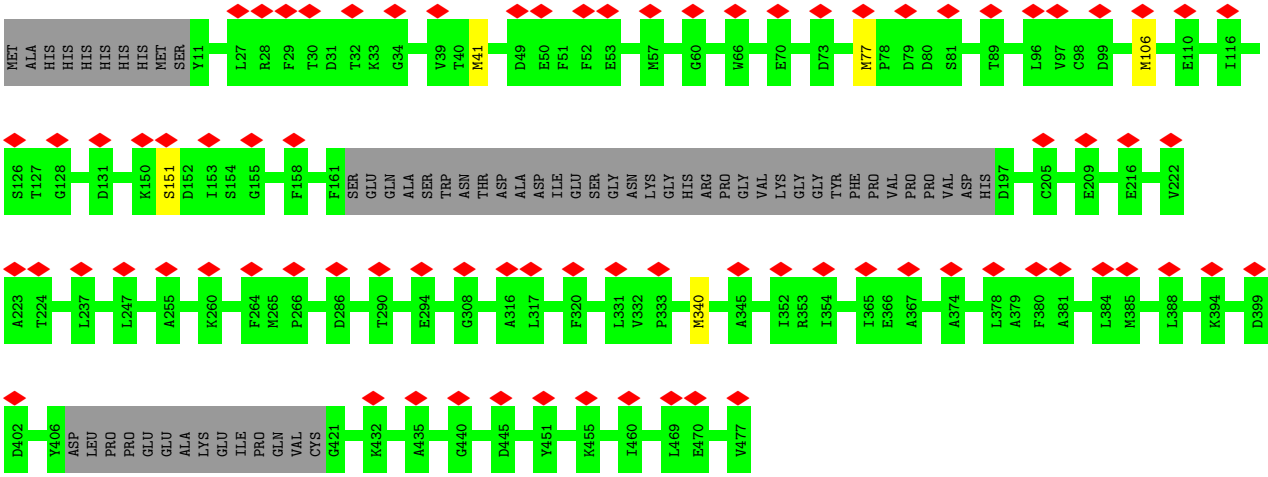
Chain T:



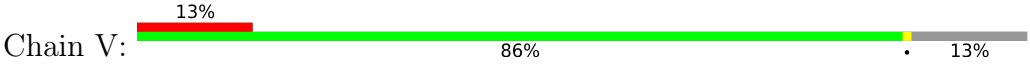


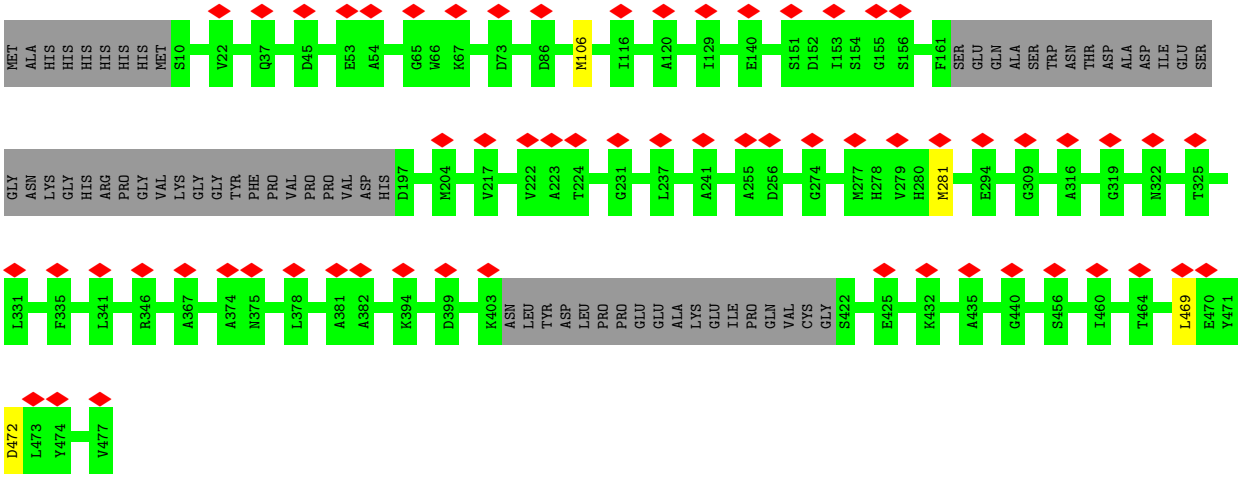
• Molecule 1: Glutamine synthetase



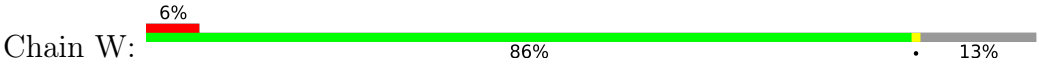


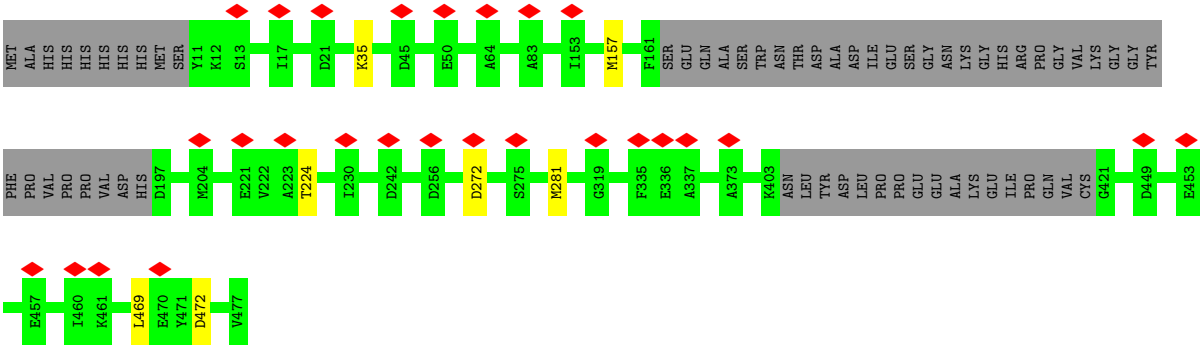
• Molecule 1: Glutamine synthetase





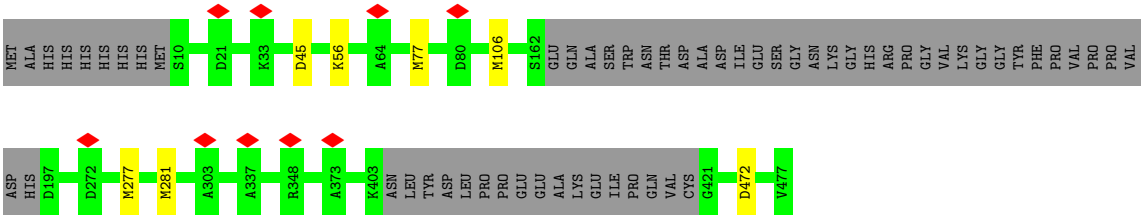
• Molecule 1: Glutamine synthetase





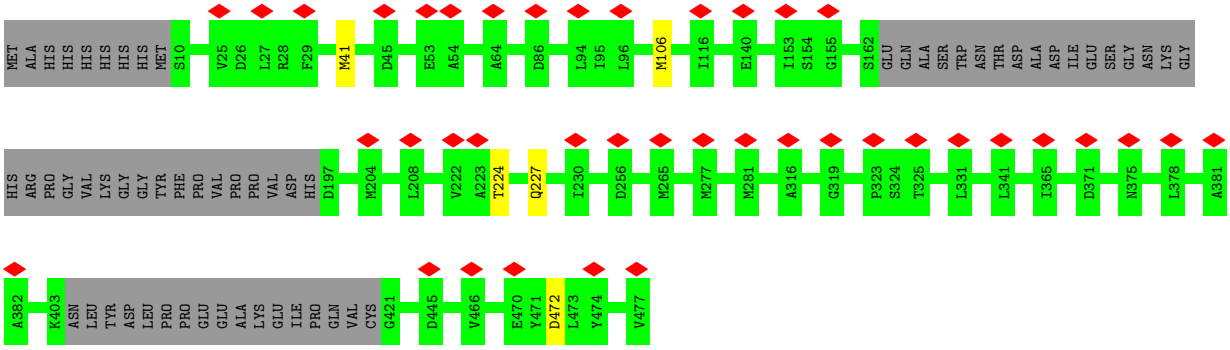
• Molecule 1: Glutamine synthetase

Chain X:



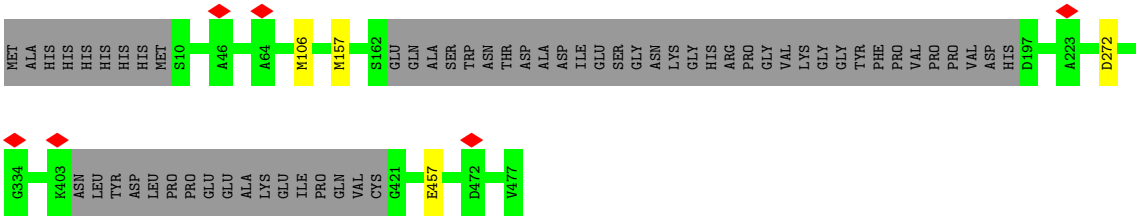
• Molecule 1: Glutamine synthetase

Chain Y:



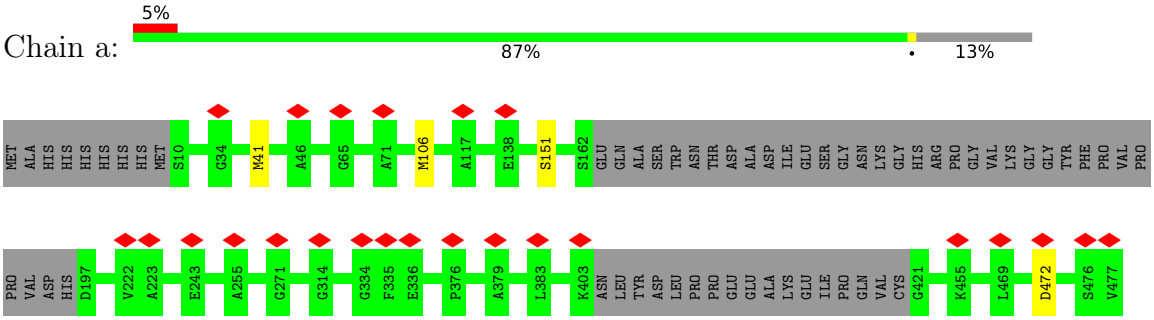
• Molecule 1: Glutamine synthetase

Chain Z:



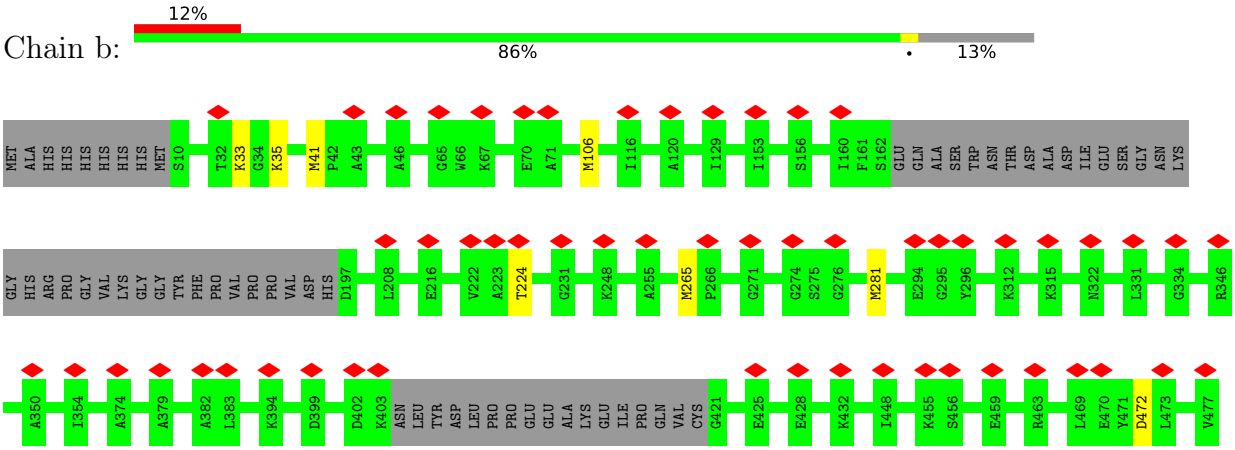
• Molecule 1: Glutamine synthetase

Chain a:



• Molecule 1: Glutamine synthetase

Chain b:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C7	Depositor
Number of particles used	346920	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION; Patch-based motion correction	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	40	Depositor
Minimum defocus (nm)	300	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.975	Depositor
Minimum map value	-0.349	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.051	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	345.6, 345.6, 345.6	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.35, 1.35, 1.35	Depositor

5 Model quality

5.1 Standard geometry

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	0.27	0/3339	0.48	0/4509
1	B	0.28	0/3330	0.48	0/4496
1	C	0.27	0/3348	0.48	0/4520
1	D	0.27	0/3321	0.47	0/4485
1	E	0.27	0/3315	0.48	0/4477
1	F	0.27	0/3330	0.48	0/4496
1	G	0.28	0/3330	0.48	0/4496
1	H	0.27	0/3315	0.48	0/4477
1	I	0.28	0/3324	0.48	0/4489
1	J	0.27	0/3309	0.48	0/4469
1	K	0.27	0/3349	0.48	0/4523
1	L	0.28	0/3324	0.49	0/4488
1	M	0.28	0/3296	0.48	0/4449
1	N	0.27	0/3313	0.47	0/4474
1	O	0.26	0/3318	0.49	0/4480
1	P	0.26	0/3371	0.49	0/4552
1	Q	0.26	0/3318	0.49	0/4480
1	R	0.26	0/3318	0.49	0/4480
1	S	0.26	0/3318	0.49	0/4480
1	T	0.26	0/3324	0.48	0/4488
1	U	0.26	0/3347	0.49	0/4520
1	V	0.26	0/3320	0.47	0/4483
1	W	0.26	0/3318	0.48	0/4480
1	X	0.26	0/3330	0.48	0/4496
1	Y	0.26	0/3330	0.48	0/4496
1	Z	0.26	0/3330	0.48	0/4496
1	a	0.26	0/3330	0.48	0/4496
1	b	0.26	0/3330	0.48	0/4496
All	All	0.27	0/93145	0.48	0/125771

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

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	412/477 (86%)	400 (97%)	12 (3%)	0	100	100
1	B	411/477 (86%)	399 (97%)	12 (3%)	0	100	100
1	C	413/477 (87%)	403 (98%)	10 (2%)	0	100	100
1	D	410/477 (86%)	399 (97%)	11 (3%)	0	100	100
1	E	409/477 (86%)	396 (97%)	13 (3%)	0	100	100
1	F	411/477 (86%)	401 (98%)	10 (2%)	0	100	100
1	G	411/477 (86%)	399 (97%)	12 (3%)	0	100	100
1	H	409/477 (86%)	395 (97%)	14 (3%)	0	100	100
1	I	410/477 (86%)	397 (97%)	13 (3%)	0	100	100
1	J	408/477 (86%)	393 (96%)	15 (4%)	0	100	100
1	K	413/477 (87%)	402 (97%)	11 (3%)	0	100	100
1	L	410/477 (86%)	397 (97%)	13 (3%)	0	100	100
1	M	404/477 (85%)	386 (96%)	18 (4%)	0	100	100
1	N	409/477 (86%)	395 (97%)	14 (3%)	0	100	100
1	O	409/477 (86%)	398 (97%)	11 (3%)	0	100	100
1	P	415/477 (87%)	403 (97%)	12 (3%)	0	100	100
1	Q	409/477 (86%)	400 (98%)	9 (2%)	0	100	100
1	R	409/477 (86%)	401 (98%)	8 (2%)	0	100	100
1	S	409/477 (86%)	397 (97%)	12 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	T	410/477 (86%)	403 (98%)	7 (2%)	0	100	100
1	U	412/477 (86%)	401 (97%)	11 (3%)	0	100	100
1	V	409/477 (86%)	395 (97%)	14 (3%)	0	100	100
1	W	409/477 (86%)	403 (98%)	6 (2%)	0	100	100
1	X	411/477 (86%)	401 (98%)	10 (2%)	0	100	100
1	Y	411/477 (86%)	404 (98%)	7 (2%)	0	100	100
1	Z	411/477 (86%)	399 (97%)	12 (3%)	0	100	100
1	a	411/477 (86%)	401 (98%)	10 (2%)	0	100	100
1	b	411/477 (86%)	403 (98%)	8 (2%)	0	100	100
All	All	11486/13356 (86%)	11171 (97%)	315 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	348/398 (87%)	345 (99%)	3 (1%)	78	94
1	B	347/398 (87%)	345 (99%)	2 (1%)	86	96
1	C	349/398 (88%)	340 (97%)	9 (3%)	46	79
1	D	346/398 (87%)	343 (99%)	3 (1%)	78	94
1	E	345/398 (87%)	341 (99%)	4 (1%)	71	92
1	F	347/398 (87%)	343 (99%)	4 (1%)	71	92
1	G	347/398 (87%)	338 (97%)	9 (3%)	46	79
1	H	345/398 (87%)	338 (98%)	7 (2%)	55	84
1	I	346/398 (87%)	340 (98%)	6 (2%)	60	87
1	J	344/398 (86%)	337 (98%)	7 (2%)	55	84
1	K	349/398 (88%)	342 (98%)	7 (2%)	55	84
1	L	346/398 (87%)	343 (99%)	3 (1%)	78	94

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	M	343/398 (86%)	343 (100%)	0	100	100
1	N	345/398 (87%)	343 (99%)	2 (1%)	86	96
1	O	345/398 (87%)	339 (98%)	6 (2%)	60	87
1	P	351/398 (88%)	346 (99%)	5 (1%)	67	90
1	Q	345/398 (87%)	339 (98%)	6 (2%)	60	87
1	R	345/398 (87%)	339 (98%)	6 (2%)	60	87
1	S	345/398 (87%)	339 (98%)	6 (2%)	60	87
1	T	346/398 (87%)	341 (99%)	5 (1%)	67	90
1	U	348/398 (87%)	343 (99%)	5 (1%)	67	90
1	V	346/398 (87%)	342 (99%)	4 (1%)	71	92
1	W	345/398 (87%)	338 (98%)	7 (2%)	55	84
1	X	347/398 (87%)	340 (98%)	7 (2%)	55	84
1	Y	347/398 (87%)	342 (99%)	5 (1%)	67	90
1	Z	347/398 (87%)	343 (99%)	4 (1%)	71	92
1	a	347/398 (87%)	343 (99%)	4 (1%)	71	92
1	b	347/398 (87%)	339 (98%)	8 (2%)	50	82
All	All	9698/11144 (87%)	9554 (98%)	144 (2%)	66	89

All (144) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	GLN
1	A	45	ASP
1	A	158	PHE
1	B	33	LYS
1	B	453	GLU
1	C	15	GLN
1	C	35	LYS
1	C	72	SER
1	C	106	MET
1	C	211	MET
1	C	233	LYS
1	C	272	ASP
1	C	346	ARG
1	C	461	LYS
1	D	15	GLN

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Mol	Chain	Res	Type
1	D	272	ASP
1	D	453	GLU
1	E	102	GLU
1	E	154	SER
1	E	265	MET
1	E	348	ARG
1	F	15	GLN
1	F	106	MET
1	F	220	HIS
1	F	224	THR
1	G	15	GLN
1	G	67	LYS
1	G	77	MET
1	G	224	THR
1	G	265	MET
1	G	281	MET
1	G	453	GLU
1	G	457	GLU
1	G	461	LYS
1	H	15	GLN
1	H	35	LYS
1	H	67	LYS
1	H	77	MET
1	H	224	THR
1	H	265	MET
1	H	336	GLU
1	I	15	GLN
1	I	35	LYS
1	I	77	MET
1	I	90	GLU
1	I	272	ASP
1	I	457	GLU
1	J	15	GLN
1	J	41	MET
1	J	50	GLU
1	J	58	PHE
1	J	77	MET
1	J	272	ASP
1	J	453	GLU
1	K	15	GLN
1	K	44	ARG
1	K	74	MET

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Mol	Chain	Res	Type
1	K	220	HIS
1	K	224	THR
1	K	340	MET
1	K	348	ARG
1	L	33	LYS
1	L	77	MET
1	L	224	THR
1	N	224	THR
1	N	346	ARG
1	O	37	GLN
1	O	106	MET
1	O	151	SER
1	O	265	MET
1	O	272	ASP
1	O	281	MET
1	P	33	LYS
1	P	106	MET
1	P	151	SER
1	P	281	MET
1	P	371	ASP
1	Q	35	LYS
1	Q	77	MET
1	Q	106	MET
1	Q	151	SER
1	Q	157	MET
1	Q	272	ASP
1	R	77	MET
1	R	151	SER
1	R	157	MET
1	R	265	MET
1	R	272	ASP
1	R	281	MET
1	S	44	ARG
1	S	151	SER
1	S	224	THR
1	S	273	ASN
1	S	340	MET
1	S	371	ASP
1	T	67	LYS
1	T	106	MET
1	T	157	MET
1	T	224	THR

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Mol	Chain	Res	Type
1	T	272	ASP
1	U	41	MET
1	U	77	MET
1	U	106	MET
1	U	151	SER
1	U	340	MET
1	V	106	MET
1	V	281	MET
1	V	469	LEU
1	V	472	ASP
1	W	35	LYS
1	W	157	MET
1	W	224	THR
1	W	272	ASP
1	W	281	MET
1	W	469	LEU
1	W	472	ASP
1	X	45	ASP
1	X	56	LYS
1	X	77	MET
1	X	106	MET
1	X	277	MET
1	X	281	MET
1	X	472	ASP
1	Y	41	MET
1	Y	106	MET
1	Y	224	THR
1	Y	227	GLN
1	Y	472	ASP
1	Z	106	MET
1	Z	157	MET
1	Z	272	ASP
1	Z	457	GLU
1	a	41	MET
1	a	106	MET
1	a	151	SER
1	a	472	ASP
1	b	33	LYS
1	b	35	LYS
1	b	41	MET
1	b	106	MET
1	b	224	THR

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Mol	Chain	Res	Type
1	b	265	MET
1	b	281	MET
1	b	472	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	218	HIS
1	J	218	HIS
1	K	198	HIS
1	S	15	GLN
1	Y	218	HIS
1	Z	218	HIS
1	a	36	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

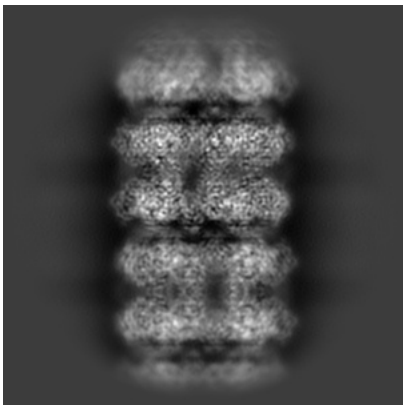
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-28965. These allow visual inspection of the internal detail of the map and identification of artifacts.

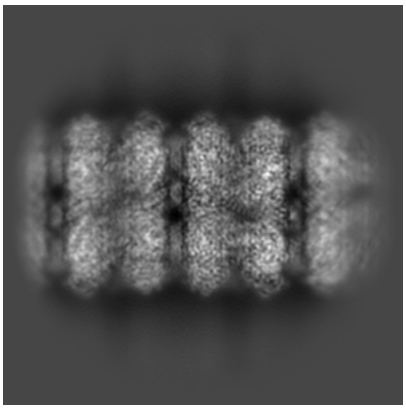
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

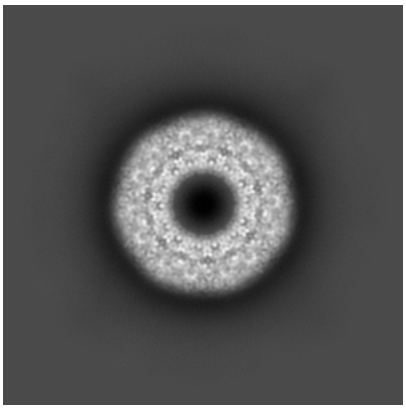
6.1.1 Primary map



X

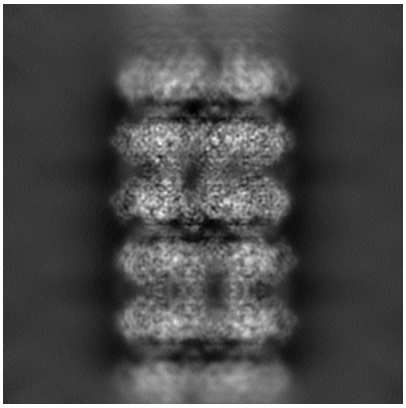


Y

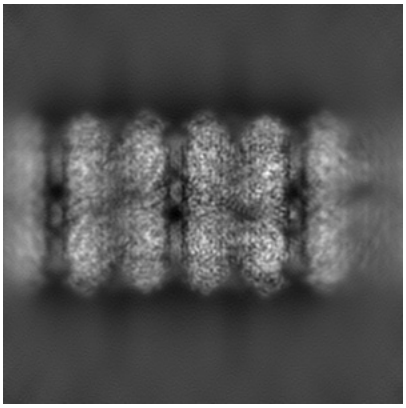


Z

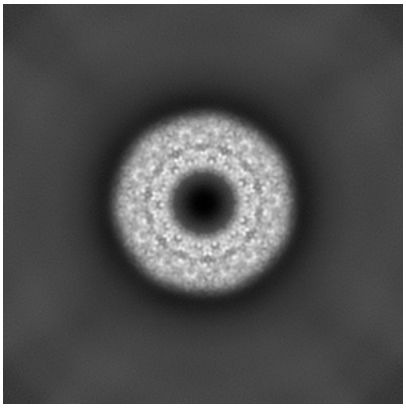
6.1.2 Raw map



X



Y

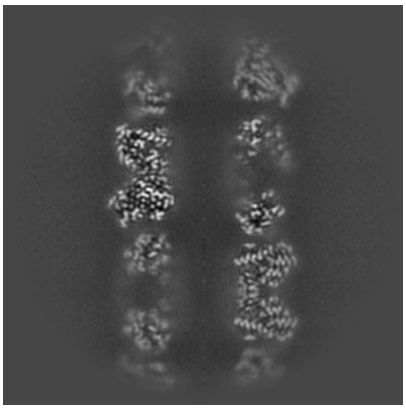


Z

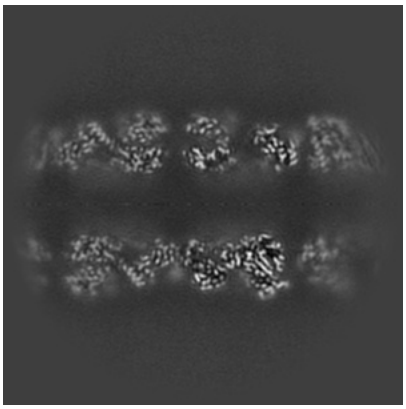
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

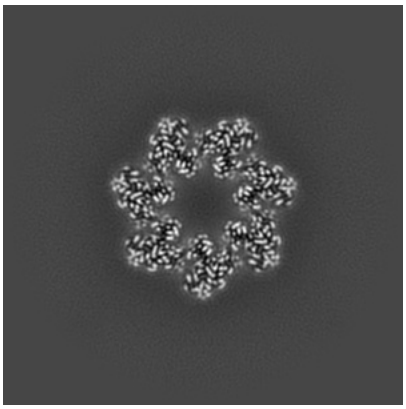
6.2.1 Primary map



X Index: 128

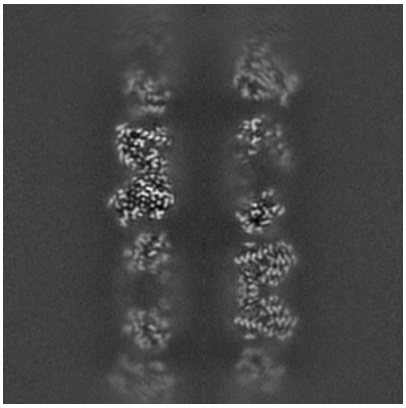


Y Index: 128

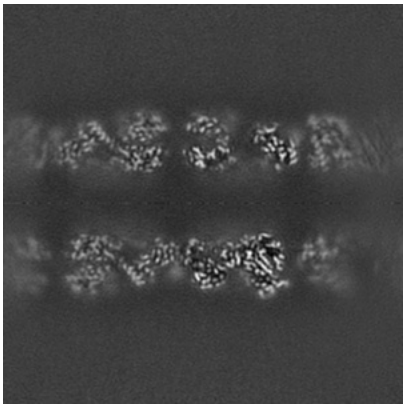


Z Index: 128

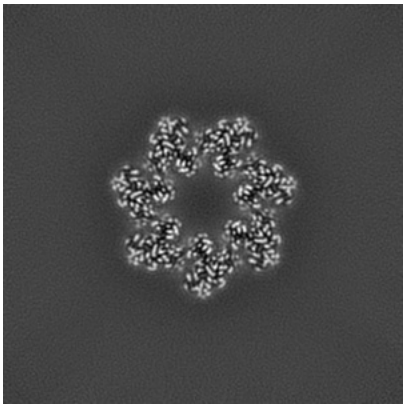
6.2.2 Raw map



X Index: 128



Y Index: 128

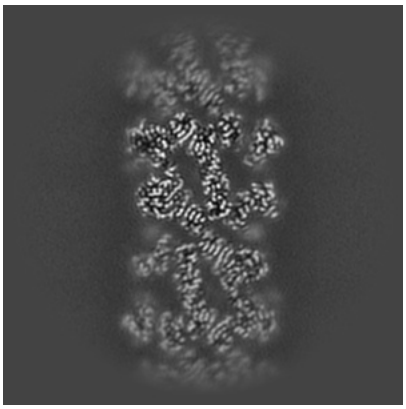


Z Index: 128

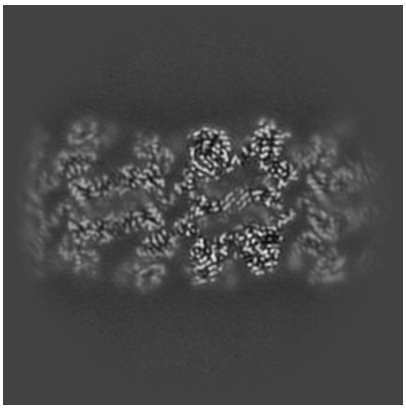
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

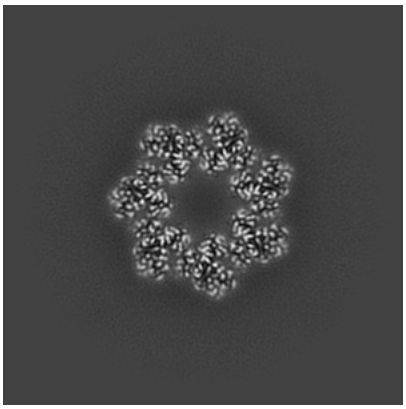
6.3.1 Primary map



X Index: 97

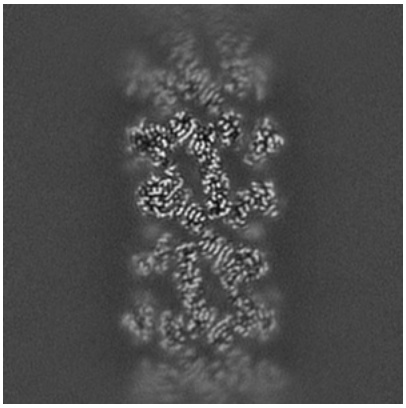


Y Index: 103

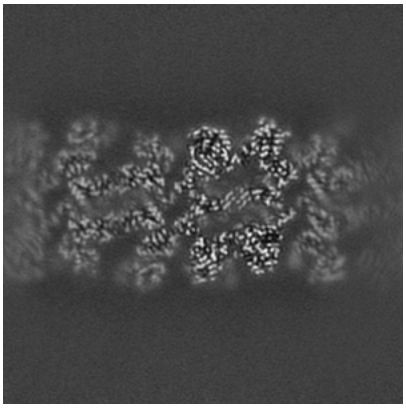


Z Index: 170

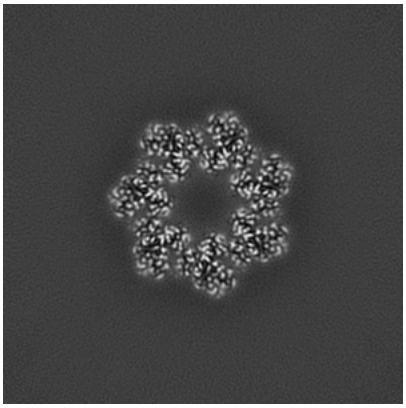
6.3.2 Raw map



X Index: 97



Y Index: 103

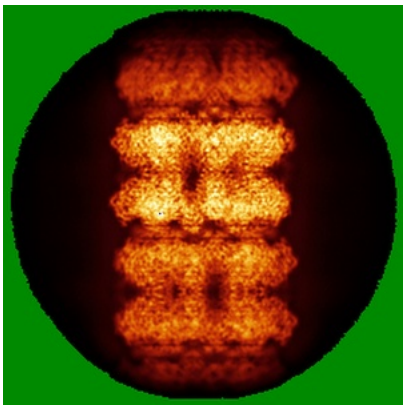


Z Index: 170

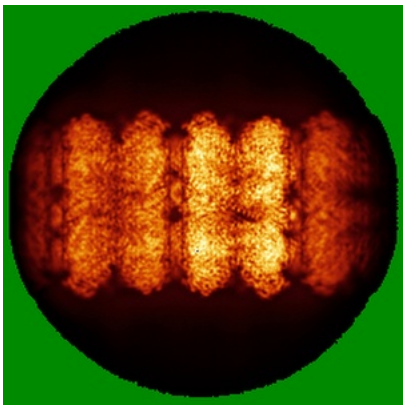
The images above show the largest variance slices of the map in three orthogonal directions.

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

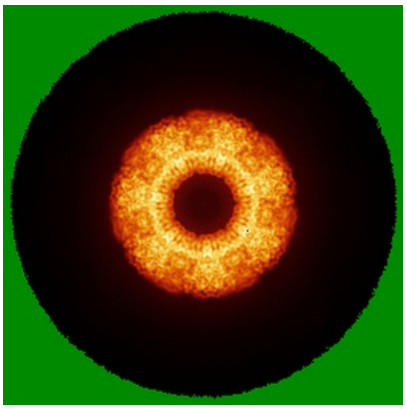
6.4.1 Primary map



X

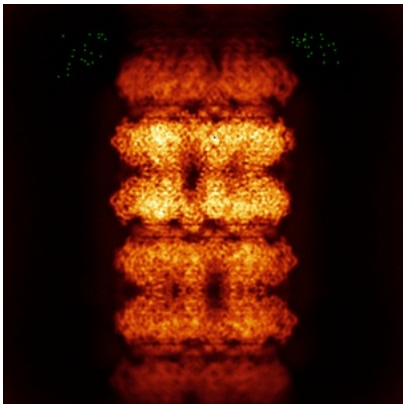


Y

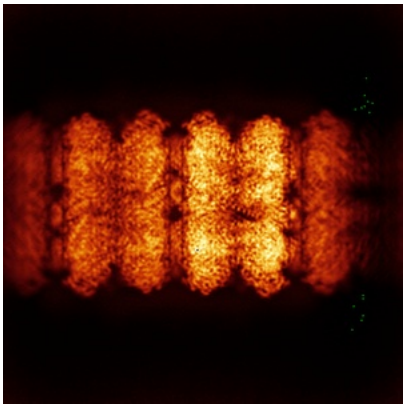


Z

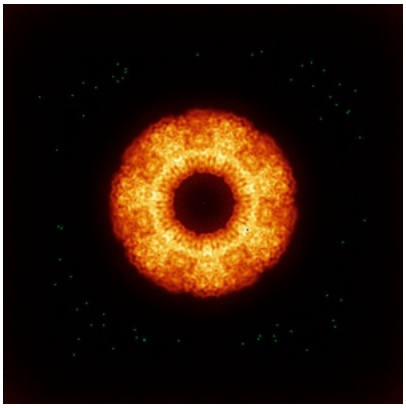
6.4.2 Raw map



X



Y

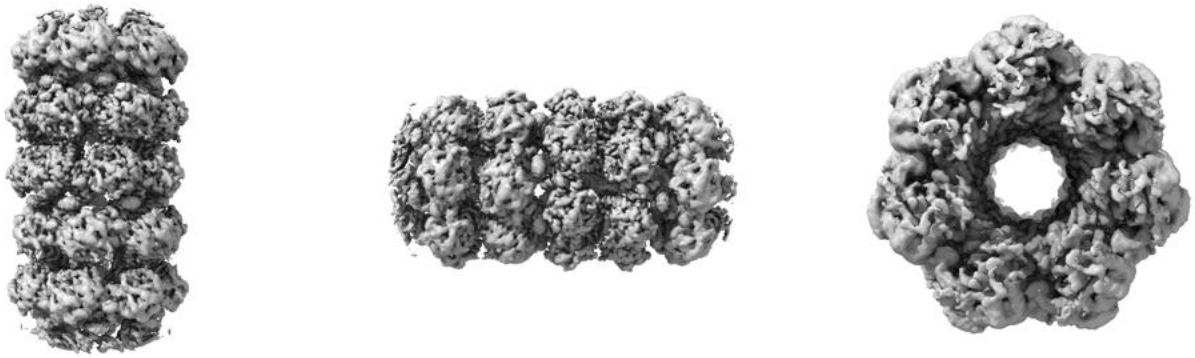


Z

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)

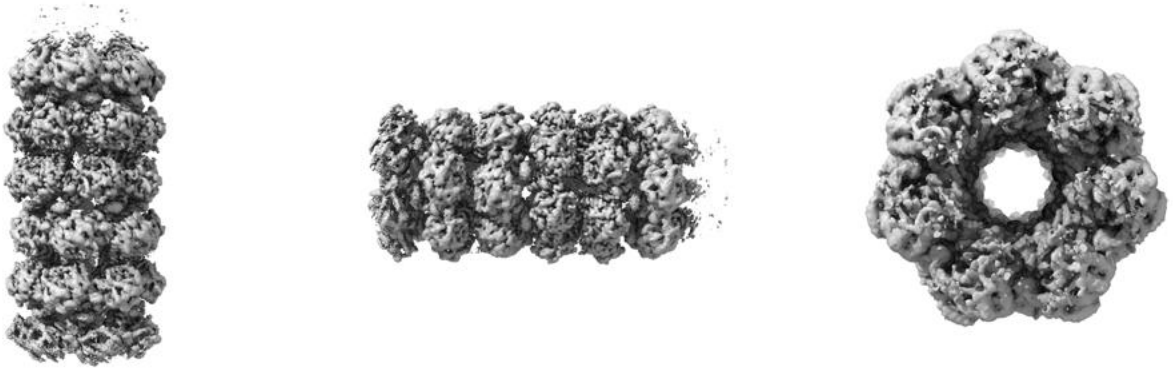
6.5.1 Primary map



X Y Z

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

6.5.2 Raw map



X Y Z

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.

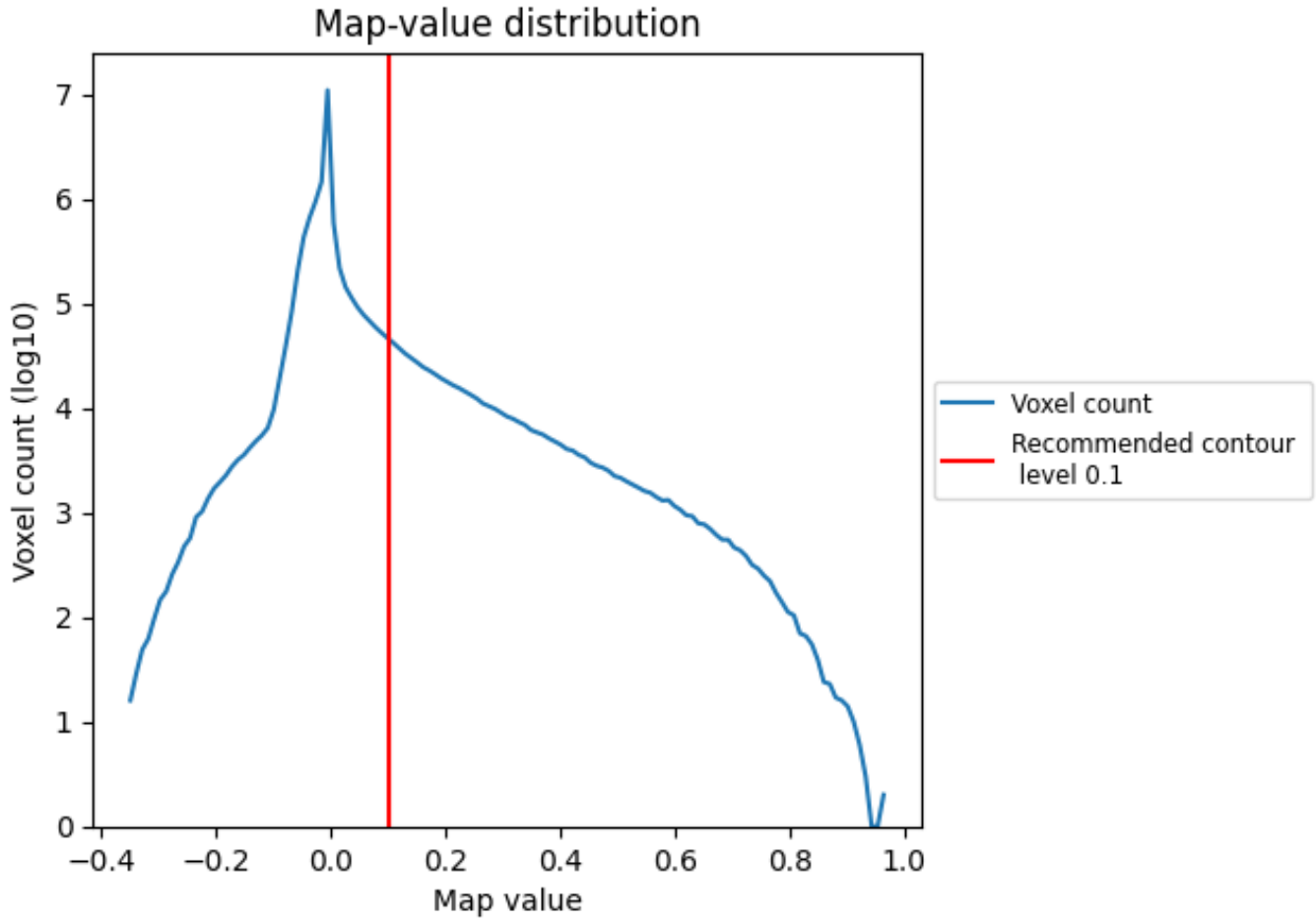
6.6 Mask visualisation (i)

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

7 Map analysis

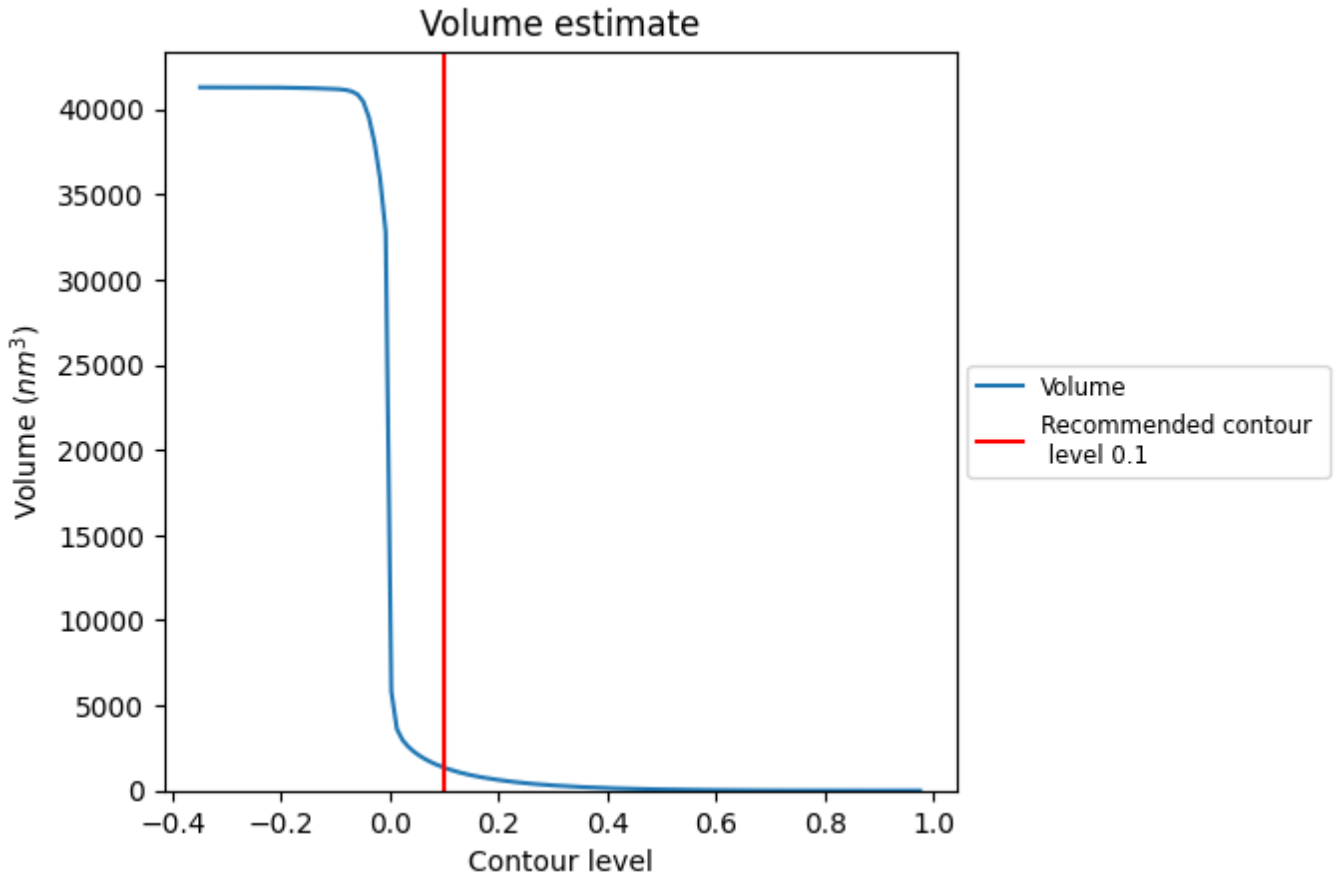
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

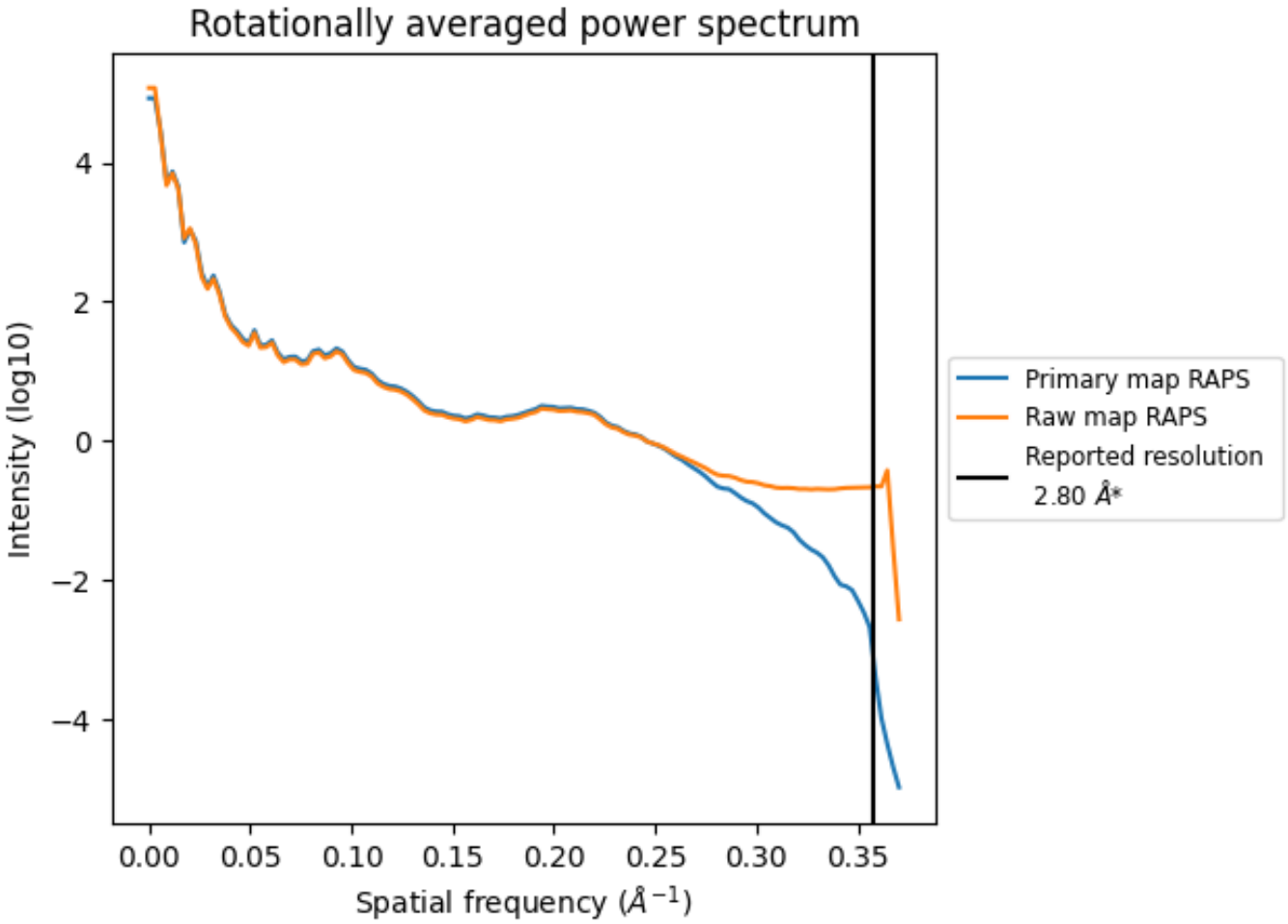
7.2 Volume estimate



The volume at the recommended contour level is 1343 nm^3; this corresponds to an approximate mass of 1213 kDa.

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

7.3 Rotationally averaged power spectrum (i)

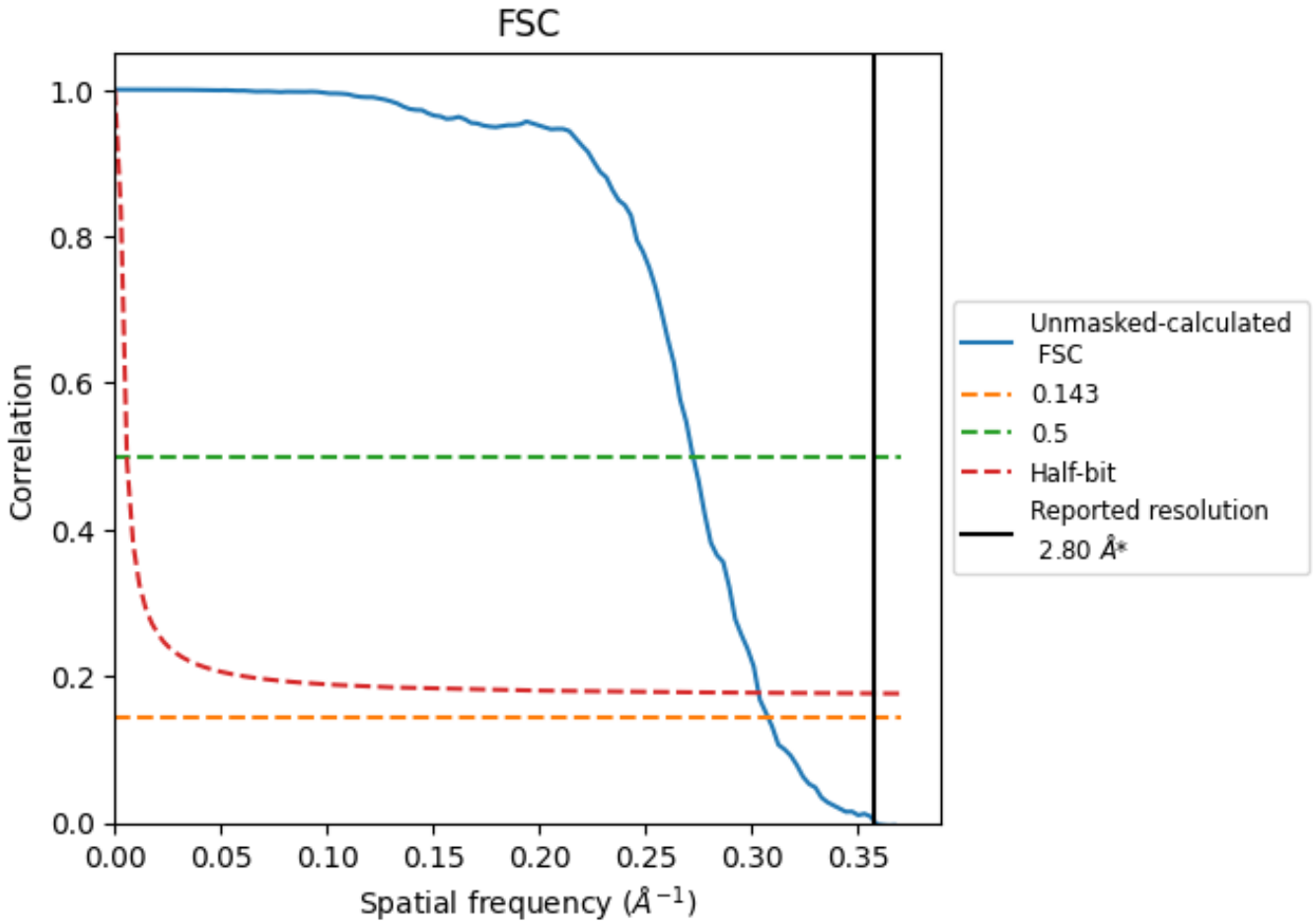


*Reported resolution corresponds to spatial frequency of 0.357 Å^{-1}

8 Fourier-Shell correlation

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



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

8.2 Resolution estimates (i)

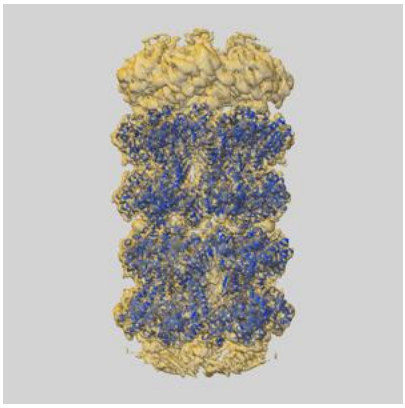
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.25	3.67	3.30

*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 3.25 differs from the reported value 2.8 by more than 10 %

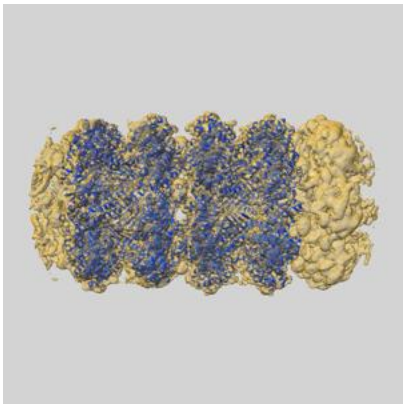
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-28965 and PDB model 8FBP. Per-residue inclusion information can be found in section 3 on page 11.

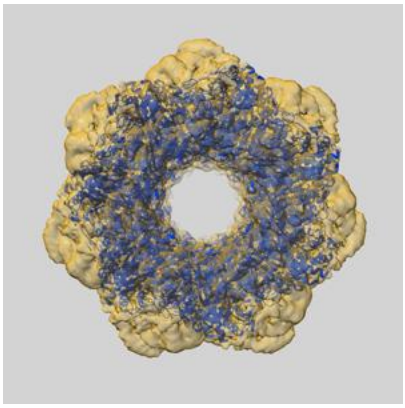
9.1 Map-model overlay



X



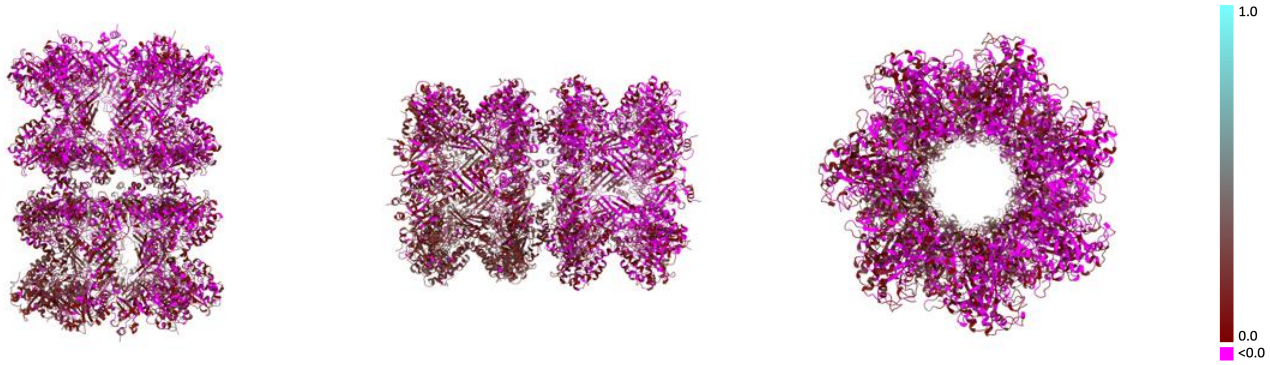
Y



Z

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

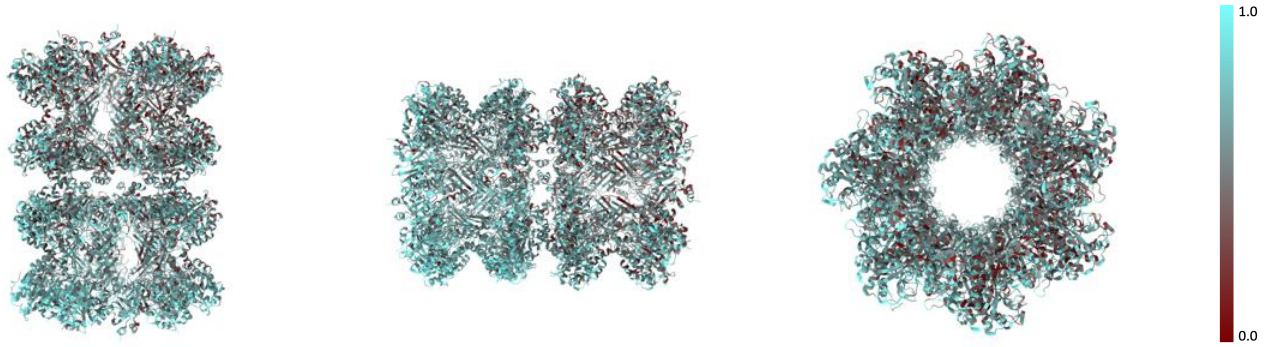
9.2 Q-score mapped to coordinate model



X Y Z

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

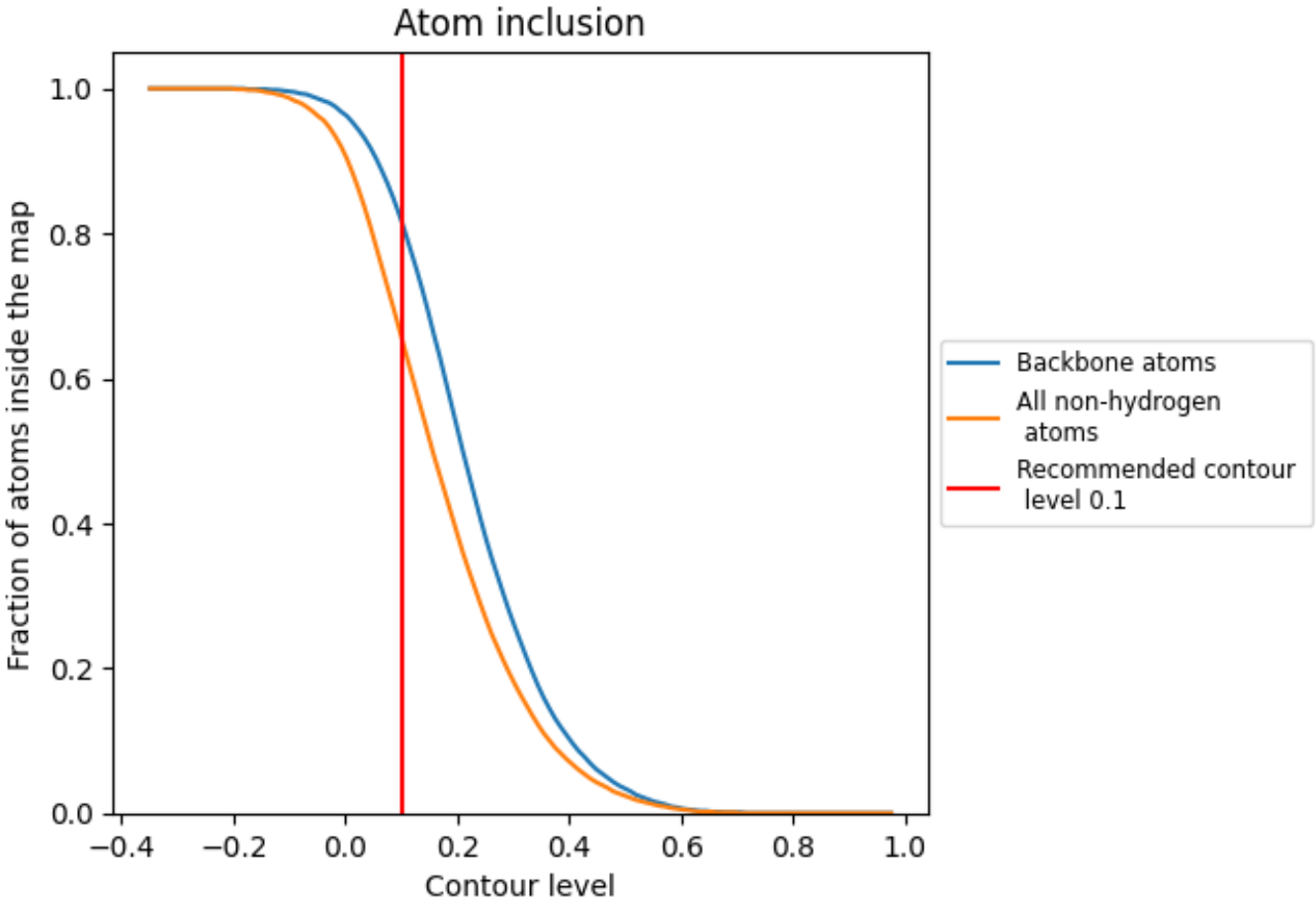
9.3 Atom inclusion mapped to coordinate model



X Y Z

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

9.4 Atom inclusion (i)



At the recommended contour level, 82% of all backbone atoms, 66% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.6560	0.0820
A	0.5510	-0.0080
B	0.5950	0.0200
C	0.6210	0.0460
D	0.5680	-0.0040
E	0.5850	0.0230
F	0.5520	-0.0080
G	0.5590	-0.0220
H	0.5630	0.0010
I	0.6330	0.0710
J	0.6850	0.1250
K	0.5700	0.0160
L	0.6590	0.0790
M	0.6080	0.0320
N	0.5720	0.0060
O	0.6610	0.0760
P	0.7680	0.2240
Q	0.7400	0.1750
R	0.7350	0.1790
S	0.6890	0.1100
T	0.6500	0.0400
U	0.6260	0.0190
V	0.6700	0.0670
W	0.7530	0.1770
X	0.7800	0.2060
Y	0.7040	0.1130
Z	0.7930	0.2340
a	0.7680	0.2050
b	0.6980	0.1050