



wwPDB EM Validation Summary Report ⓘ

Jun 3, 2024 – 09:36 PM JST

PDB ID : 7V4K
EMDB ID : EMD-31714
Title : Cryo-EM Structure of Camellia sinensis glutamine synthetase CsGS1b inactive Pentamer State II
Authors : Xu, W.; Chen, Y.; Xing, Q.; Huang, C.
Deposited on : 2021-08-13
Resolution : Not provided

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

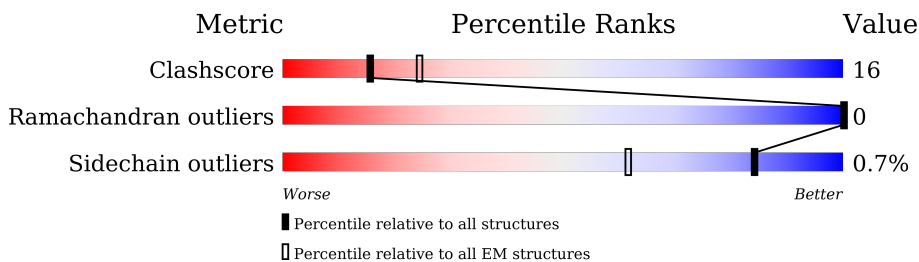
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is unknown.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	356	
1	B	356	
1	C	356	
1	D	356	
1	E	356	

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 9260 atoms, of which 0 are hydrogens and 0 are deuteriums.

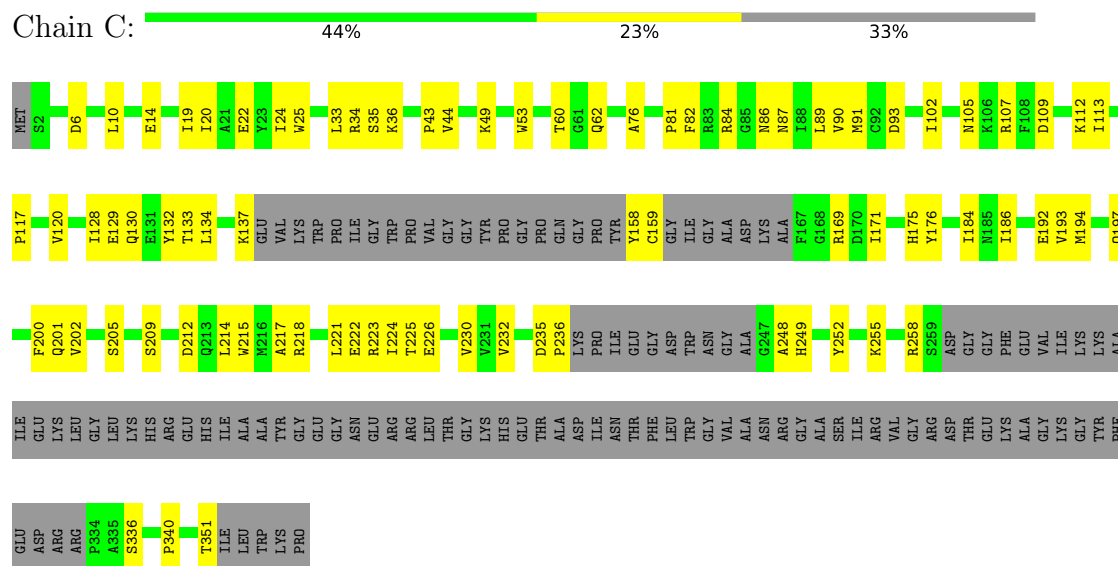
In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Glutamine synthetase.

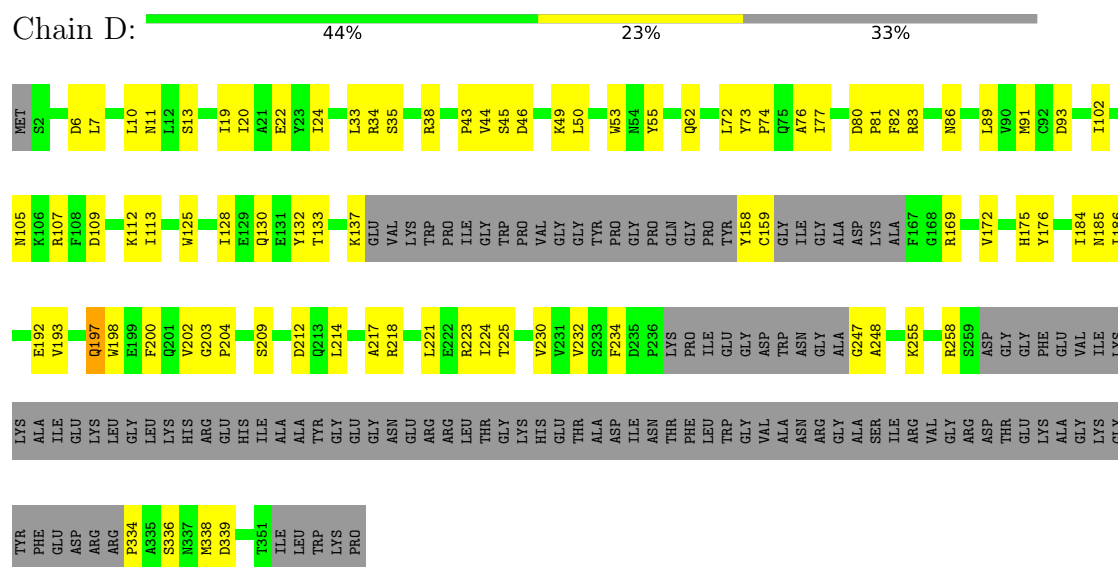
Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	239	Total	C	N	O	S	0	0
			1852	1173	306	362	11		
1	B	239	Total	C	N	O	S	0	0
			1852	1173	306	362	11		
1	C	239	Total	C	N	O	S	0	0
			1852	1173	306	362	11		
1	D	239	Total	C	N	O	S	0	0
			1852	1173	306	362	11		
1	E	239	Total	C	N	O	S	0	0
			1852	1173	306	362	11		

There are 10 discrepancies between the modelled and reference sequences:

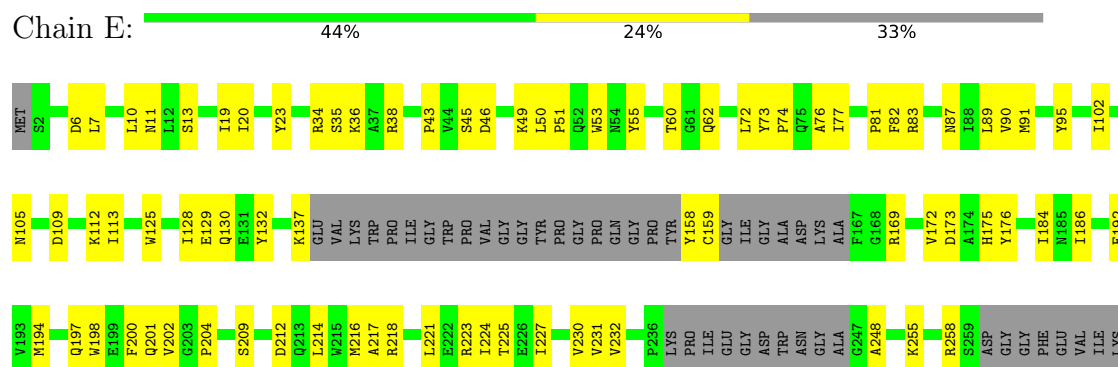
Chain	Residue	Modelled	Actual	Comment	Reference
A	278	ARG	LYS	conflict	UNP Q762D2
A	342	ILE	VAL	conflict	UNP Q762D2
B	278	ARG	LYS	conflict	UNP Q762D2
B	342	ILE	VAL	conflict	UNP Q762D2
C	278	ARG	LYS	conflict	UNP Q762D2
C	342	ILE	VAL	conflict	UNP Q762D2
D	278	ARG	LYS	conflict	UNP Q762D2
D	342	ILE	VAL	conflict	UNP Q762D2
E	278	ARG	LYS	conflict	UNP Q762D2
E	342	ILE	VAL	conflict	UNP Q762D2



- Molecule 1: Glutamine synthetase



- Molecule 1: Glutamine synthetase



LYS
ALA
ILE
GLU
ASP
LYS
LEU
GLY
LEU
LYS
HIS
ARG
GLU
HIS
ILE
ALA
ALA
TYR
GLY
GLY
GLY
ASN
GLU
ARG
ARG
LEU
THR
GLY
LYS
HIS
GLU
THR
ALA
ASP
ILE
ASN
THR
PHE
LEU
TRP
GLY
VAL
ALA
ASN
ARG
GLY
ALA
SER
ILE
ARG
VAL
GLY
ARG
ASP
THR
GLU
LYS
ALA
GLY
LYS
GLY

TYR
PHE
GLU
ASP
ARG
ARG
P334
A335
S336
HIS
Y341
GLU
T344
T351
ILE
LEU
TRP
LYS
PRO

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	96758	Depositor
Resolution determination method	Not provided	
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	51	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.29	0/1895	0.50	0/2573
1	B	0.28	0/1895	0.51	0/2573
1	C	0.28	0/1895	0.51	0/2573
1	D	0.28	0/1895	0.51	0/2573
1	E	0.28	0/1895	0.49	0/2573
All	All	0.28	0/9475	0.50	0/12865

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1852	0	1784	68	0
1	B	1852	0	1784	59	0
1	C	1852	0	1784	65	0
1	D	1852	0	1784	61	0
1	E	1852	0	1784	64	0
All	All	9260	0	8920	296	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 16.

The worst 5 of 296 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:B:158:TYR:HB3	1:E:34:ARG:HH22	1.35	0.91
1:B:130:GLN:OE1	1:B:218:ARG:NH1	2.11	0.83
1:D:125:TRP:HB3	1:D:204:PRO:HB3	1.66	0.77
1:E:129:GLU:HG2	1:E:201:GLN:HG3	1.69	0.75
1:E:125:TRP:HB3	1:E:204:PRO:HB3	1.71	0.72

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	229/356 (64%)	219 (96%)	10 (4%)	0	100	100
1	B	229/356 (64%)	223 (97%)	6 (3%)	0	100	100
1	C	229/356 (64%)	221 (96%)	8 (4%)	0	100	100
1	D	229/356 (64%)	220 (96%)	9 (4%)	0	100	100
1	E	229/356 (64%)	219 (96%)	10 (4%)	0	100	100
All	All	1145/1780 (64%)	1102 (96%)	43 (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	202/289 (70%)	201 (100%)	1 (0%)	88	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	202/289 (70%)	200 (99%)	2 (1%)	76	76
1	C	202/289 (70%)	201 (100%)	1 (0%)	88	88
1	D	202/289 (70%)	200 (99%)	2 (1%)	76	76
1	E	202/289 (70%)	201 (100%)	1 (0%)	88	88
All	All	1010/1445 (70%)	1003 (99%)	7 (1%)	84	84

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	137	LYS
1	D	137	LYS
1	E	137	LYS
1	D	197	GLN
1	B	197	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	87	ASN
1	D	130	GLN
1	E	87	ASN
1	D	197	GLN
1	A	197	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 [i](#)

There are no ligands in this entry.

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-31714. These allow visual inspection of the internal detail of the map and identification of artifacts.

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

6.1 Orthogonal projections [i](#)

This section was not generated.

6.2 Central slices [i](#)

This section was not generated.

6.3 Largest variance slices [i](#)

This section was not generated.

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

This section was not generated.

6.5 Orthogonal surface views [i](#)

This section was not generated.

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 ⓘ

This section was not generated.

7.2 Volume estimate versus contour level ⓘ

This section was not generated.

7.3 Rotationally averaged power spectrum ⓘ

This section was not generated. The rotationally averaged power spectrum had issues being displayed.

8 Fourier-Shell correlation ⓘ

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

9 Map-model fit

This section was not generated.