



wwPDB X-ray Structure Validation Summary Report ⓘ

May 13, 2020 – 10:02 am BST

PDB ID : 4Q3L
Title : Crystal structure of MGS-M2, an alpha/beta hydrolase enzyme from a Medee basin deep-sea metagenome library
Authors : Stogios, P.J.; Xu, X.; Cui, H.; Alcaide, M.; Ferrer, M.; Savchenko, A.
Deposited on : 2014-04-11
Resolution : 3.01 Å(reported)

This is a wwPDB X-ray Structure 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/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

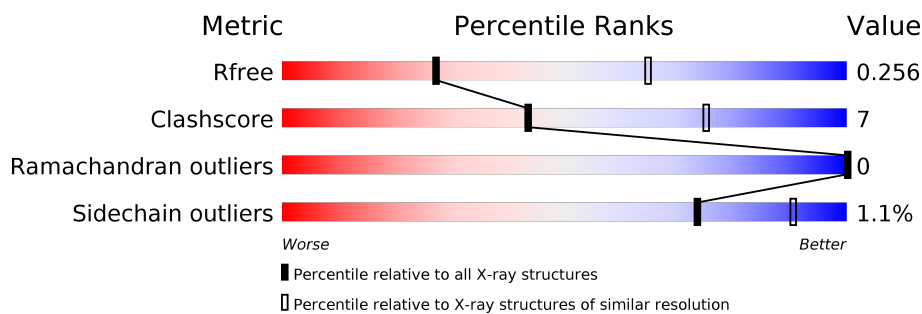
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.01 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2399 (3.04-3.00)
Clashscore	141614	2734 (3.04-3.00)
Ramachandran outliers	138981	2640 (3.04-3.00)
Sidechain outliers	138945	2643 (3.04-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower 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	297	76% 15% 7%
1	B	297	80% 14% 6%
1	C	297	78% 15% 6%
1	D	297	77% 14% 7%
1	E	297	81% 11% 7%
1	F	297	76% 16% 7%
1	G	297	75% 18% 6%

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Mol	Chain	Length	Quality of chain
1	H	297	<div><div></div><div>80%</div><div>13%</div><div>• 6%</div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 18226 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 MGS-M2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	275	Total	C	N	O	S	0	0	0
			2223	1439	355	420	9			
1	B	280	Total	C	N	O	S	0	0	0
			2266	1469	361	427	9			
1	C	278	Total	C	N	O	S	0	0	0
			2243	1451	359	424	9			
1	D	275	Total	C	N	O	S	0	1	0
			2231	1444	358	420	9			
1	E	275	Total	C	N	O	S	0	0	0
			2223	1439	355	420	9			
1	F	275	Total	C	N	O	S	0	0	0
			2223	1439	355	420	9			
1	G	278	Total	C	N	O	S	0	0	0
			2243	1451	359	424	9			
1	H	280	Total	C	N	O	S	0	0	0
			2266	1469	361	427	9			

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			6	3	3		
2	G	1	Total	C	O	0	0
			6	3	3		

- Molecule 3 is water.

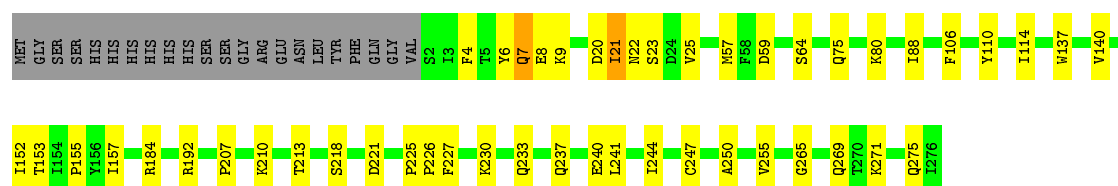
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	43	Total	O	0	0
			43	43		
3	B	33	Total	O	0	0
			33	33		
3	C	38	Total	O	0	0
			38	38		
3	D	37	Total	O	0	0
			37	37		
3	E	38	Total	O	0	3
			41	41		
3	F	30	Total	O	0	1
			31	31		
3	G	36	Total	O	0	0
			36	36		
3	H	37	Total	O	0	0
			37	37		

3 Residue-property plots [i](#)


These plots are drawn for all protein, RNA and DNA 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. 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. 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.

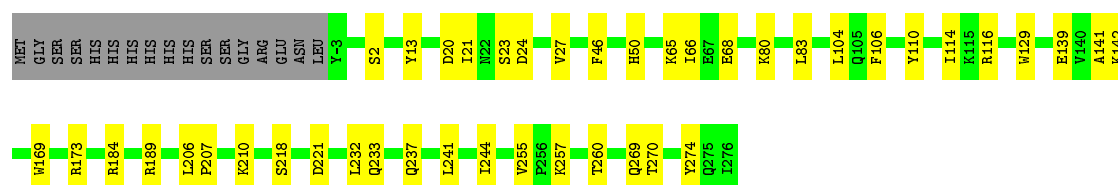
• Molecule 1: MGS-M2

Chain A: 




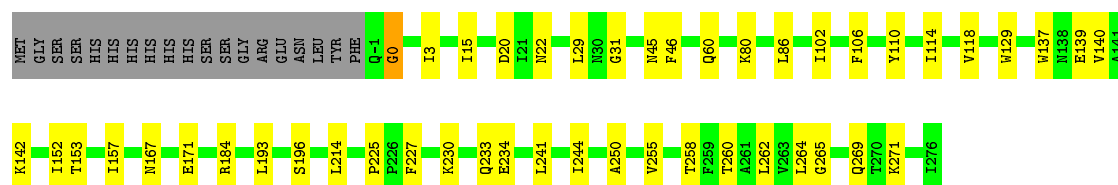
• Molecule 1: MGS-M2

Chain B: 




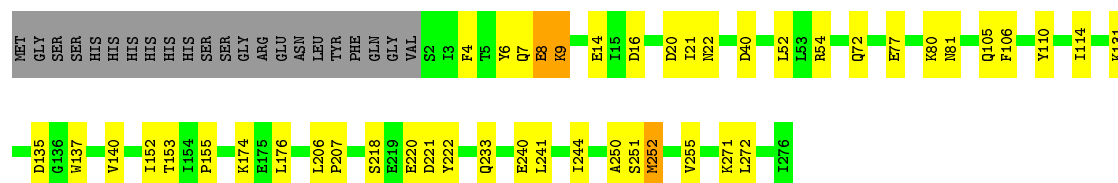
• Molecule 1: MGS-M2

Chain C: 

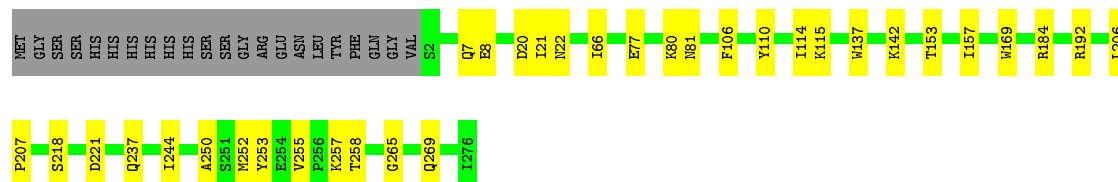



• Molecule 1: MGS-M2

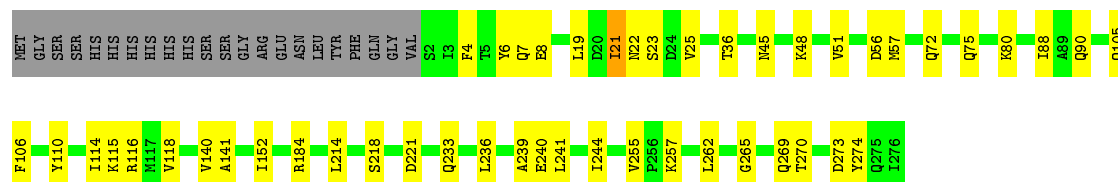

Chain D: 



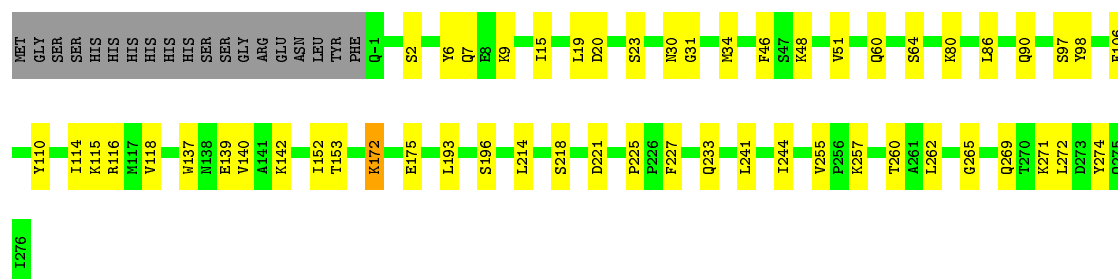
• Molecule 1: MGS-M2

Chain E: 

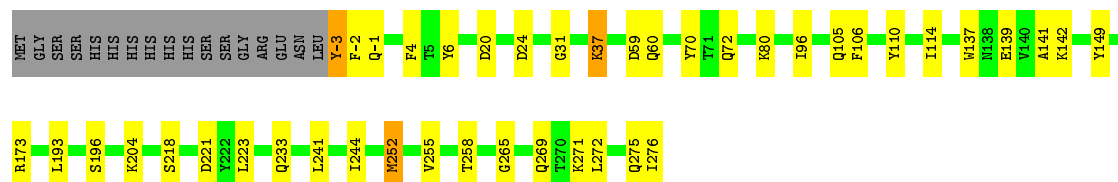
• Molecule 1: MGS-M2

Chain F: 

• Molecule 1: MGS-M2

Chain G: 

• Molecule 1: MGS-M2

Chain H: 

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	105.57Å 139.13Å 111.11Å 90.00° 89.94° 90.00°	Depositor
Resolution (Å)	31.67 – 3.01 31.67 – 3.01	Depositor EDS
% Data completeness (in resolution range)	99.2 (31.67-3.01) 80.4 (31.67-3.01)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.66 (at 3.00Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1631)	Depositor
R, R_{free}	0.201 , 0.255 0.203 , 0.256	Depositor DCC
R_{free} test set	1996 reflections (3.16%)	wwPDB-VP
Wilson B-factor (Å ²)	42.2	Xtriage
Anisotropy	0.475	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 100.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.060 for -l,k,h 0.397 for h,-k,-l 0.069 for -l,-k,-h	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	18226	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.22% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	0/2276	0.42	0/3090
1	B	0.25	0/2321	0.41	0/3151
1	C	0.22	0/2296	0.39	0/3117
1	D	0.28	0/2287	0.42	0/3104
1	E	0.26	0/2276	0.40	0/3090
1	F	0.28	0/2276	0.42	0/3090
1	G	0.30	0/2296	0.44	0/3117
1	H	0.26	0/2321	0.42	0/3151
All	All	0.27	0/18349	0.41	0/24910

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1
1	H	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	0	GLY	Peptide
1	H	-3	TYR	Peptide

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	2223	0	2210	34	0
1	B	2266	0	2251	26	0
1	C	2243	0	2233	26	0
1	D	2231	0	2223	45	0
1	E	2223	0	2210	20	0
1	F	2223	0	2210	30	0
1	G	2243	0	2233	32	0
1	H	2266	0	2251	38	0
2	B	6	0	8	0	0
2	G	6	0	8	1	0
3	A	43	0	0	1	0
3	B	33	0	0	0	0
3	C	38	0	0	0	0
3	D	37	0	0	0	0
3	E	41	0	0	1	0
3	F	31	0	0	0	0
3	G	36	0	0	0	0
3	H	37	0	0	0	0
All	All	18226	0	17837	238	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 7.

The worst 5 of 238 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:7:GLN:OE1	1:F:8:GLU:N	1.87	1.08
1:A:8:GLU:OE1	1:A:8:GLU:N	2.00	0.94
1:E:7:GLN:O	1:E:8:GLU:HB2	1.68	0.91
1:D:250:ALA:HA	1:D:252:MET:HE1	1.58	0.85
1:A:20:ASP:OD1	1:A:22:ASN:HB3	1.79	0.82

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	273/297 (92%)	263 (96%)	10 (4%)	0	100	100
1	B	278/297 (94%)	270 (97%)	8 (3%)	0	100	100
1	C	276/297 (93%)	266 (96%)	10 (4%)	0	100	100
1	D	274/297 (92%)	260 (95%)	14 (5%)	0	100	100
1	E	273/297 (92%)	261 (96%)	12 (4%)	0	100	100
1	F	273/297 (92%)	260 (95%)	13 (5%)	0	100	100
1	G	276/297 (93%)	267 (97%)	9 (3%)	0	100	100
1	H	278/297 (94%)	266 (96%)	12 (4%)	0	100	100
All	All	2201/2376 (93%)	2113 (96%)	88 (4%)	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 X-ray entries followed by that with respect to entries of similar resolution.

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	247/266 (93%)	244 (99%)	3 (1%)	71	89
1	B	251/266 (94%)	250 (100%)	1 (0%)	91	97
1	C	249/266 (94%)	249 (100%)	0	100	100
1	D	248/266 (93%)	245 (99%)	3 (1%)	71	89
1	E	247/266 (93%)	244 (99%)	3 (1%)	71	89
1	F	247/266 (93%)	244 (99%)	3 (1%)	71	89

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	249/266 (94%)	245 (98%)	4 (2%)	62	86
1	H	251/266 (94%)	247 (98%)	4 (2%)	62	86
All	All	1989/2128 (94%)	1968 (99%)	21 (1%)	73	90

5 of 21 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	252	MET
1	F	22	ASN
1	H	20	ASP
1	E	22	ASN
1	H	24	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	121	ASN
1	D	269	GLN
1	F	121	ASN
1	D	81	ASN
1	G	62	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	GOL	G	301	-	5,5,5	0.37	0	5,5,5	0.29	0
2	GOL	B	301	-	5,5,5	0.36	0	5,5,5	0.30	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GOL	G	301	-	-	2/4/4/4	-
2	GOL	B	301	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	G	301	GOL	O1-C1-C2-C3
2	G	301	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	301	GOL	1	0

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 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.