



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 01:41 AM UTC

PDB ID : 8EAX / pdb_00008eax
EMDB ID : EMD-27989
Title : Octameric prenyltransferase domain of fusicoccadiene Synthase with C2 symmetry sans transiently associating cyclase domains
Authors : Faylo, J.L.; van Eeuwen, T.; Christianson, D.W.
Deposited on : 2022-08-29
Resolution : 3.73 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : **NOT EXECUTED**
MapQ : **FAILED**
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

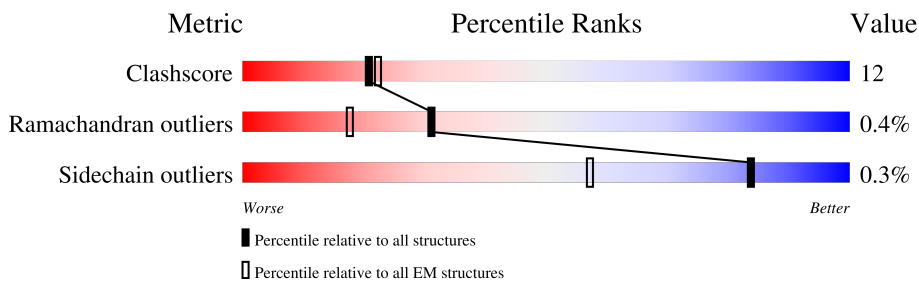
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.73 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	229148	23984
Ramachandran outliers	224038	23583
Sidechain outliers	223484	23102

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	739	31% 9% 60%
1	B	739	28% 11% 61%
1	C	739	29% 10% 60%
1	D	739	28% 11% 61%
1	E	739	31% 9% 60%
1	F	739	29% 11% 61%
1	G	739	29% 10% 60%
1	H	739	28% 12% 61%

2 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 18458 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 Fusicoccadiene synthase.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	294	2333	1481	406	431	15	0	0
1	B	289	2293	1460	393	425	15	1	0
1	C	294	2329	1478	402	434	15	0	0
1	D	289	2274	1450	386	423	15	1	0
1	E	294	2333	1481	406	431	15	0	0
1	F	289	2293	1460	393	425	15	1	0
1	G	294	2329	1478	402	434	15	0	0
1	H	289	2274	1450	386	423	15	1	0

There are 176 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP A2PZA5
A	-18	GLY	-	expression tag	UNP A2PZA5
A	-17	SER	-	expression tag	UNP A2PZA5
A	-16	SER	-	expression tag	UNP A2PZA5
A	-15	HIS	-	expression tag	UNP A2PZA5
A	-14	HIS	-	expression tag	UNP A2PZA5
A	-13	HIS	-	expression tag	UNP A2PZA5
A	-12	HIS	-	expression tag	UNP A2PZA5
A	-11	HIS	-	expression tag	UNP A2PZA5
A	-10	HIS	-	expression tag	UNP A2PZA5
A	-9	SER	-	expression tag	UNP A2PZA5
A	-8	SER	-	expression tag	UNP A2PZA5
A	-7	GLY	-	expression tag	UNP A2PZA5
A	-6	LEU	-	expression tag	UNP A2PZA5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	VAL	-	expression tag	UNP A2PZA5
A	-4	PRO	-	expression tag	UNP A2PZA5
A	-3	ARG	-	expression tag	UNP A2PZA5
A	-2	GLY	-	expression tag	UNP A2PZA5
A	-1	SER	-	expression tag	UNP A2PZA5
A	0	HIS	-	expression tag	UNP A2PZA5
A	53	ARG	GLY	conflict	UNP A2PZA5
A	604	CYS	ARG	conflict	UNP A2PZA5
B	-19	MET	-	initiating methionine	UNP A2PZA5
B	-18	GLY	-	expression tag	UNP A2PZA5
B	-17	SER	-	expression tag	UNP A2PZA5
B	-16	SER	-	expression tag	UNP A2PZA5
B	-15	HIS	-	expression tag	UNP A2PZA5
B	-14	HIS	-	expression tag	UNP A2PZA5
B	-13	HIS	-	expression tag	UNP A2PZA5
B	-12	HIS	-	expression tag	UNP A2PZA5
B	-11	HIS	-	expression tag	UNP A2PZA5
B	-10	HIS	-	expression tag	UNP A2PZA5
B	-9	SER	-	expression tag	UNP A2PZA5
B	-8	SER	-	expression tag	UNP A2PZA5
B	-7	GLY	-	expression tag	UNP A2PZA5
B	-6	LEU	-	expression tag	UNP A2PZA5
B	-5	VAL	-	expression tag	UNP A2PZA5
B	-4	PRO	-	expression tag	UNP A2PZA5
B	-3	ARG	-	expression tag	UNP A2PZA5
B	-2	GLY	-	expression tag	UNP A2PZA5
B	-1	SER	-	expression tag	UNP A2PZA5
B	0	HIS	-	expression tag	UNP A2PZA5
B	53	ARG	GLY	conflict	UNP A2PZA5
B	604	CYS	ARG	conflict	UNP A2PZA5
C	-19	MET	-	initiating methionine	UNP A2PZA5
C	-18	GLY	-	expression tag	UNP A2PZA5
C	-17	SER	-	expression tag	UNP A2PZA5
C	-16	SER	-	expression tag	UNP A2PZA5
C	-15	HIS	-	expression tag	UNP A2PZA5
C	-14	HIS	-	expression tag	UNP A2PZA5
C	-13	HIS	-	expression tag	UNP A2PZA5
C	-12	HIS	-	expression tag	UNP A2PZA5
C	-11	HIS	-	expression tag	UNP A2PZA5
C	-10	HIS	-	expression tag	UNP A2PZA5
C	-9	SER	-	expression tag	UNP A2PZA5
C	-8	SER	-	expression tag	UNP A2PZA5

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-7	GLY	-	expression tag	UNP A2PZA5
C	-6	LEU	-	expression tag	UNP A2PZA5
C	-5	VAL	-	expression tag	UNP A2PZA5
C	-4	PRO	-	expression tag	UNP A2PZA5
C	-3	ARG	-	expression tag	UNP A2PZA5
C	-2	GLY	-	expression tag	UNP A2PZA5
C	-1	SER	-	expression tag	UNP A2PZA5
C	0	HIS	-	expression tag	UNP A2PZA5
C	53	ARG	GLY	conflict	UNP A2PZA5
C	604	CYS	ARG	conflict	UNP A2PZA5
D	-19	MET	-	initiating methionine	UNP A2PZA5
D	-18	GLY	-	expression tag	UNP A2PZA5
D	-17	SER	-	expression tag	UNP A2PZA5
D	-16	SER	-	expression tag	UNP A2PZA5
D	-15	HIS	-	expression tag	UNP A2PZA5
D	-14	HIS	-	expression tag	UNP A2PZA5
D	-13	HIS	-	expression tag	UNP A2PZA5
D	-12	HIS	-	expression tag	UNP A2PZA5
D	-11	HIS	-	expression tag	UNP A2PZA5
D	-10	HIS	-	expression tag	UNP A2PZA5
D	-9	SER	-	expression tag	UNP A2PZA5
D	-8	SER	-	expression tag	UNP A2PZA5
D	-7	GLY	-	expression tag	UNP A2PZA5
D	-6	LEU	-	expression tag	UNP A2PZA5
D	-5	VAL	-	expression tag	UNP A2PZA5
D	-4	PRO	-	expression tag	UNP A2PZA5
D	-3	ARG	-	expression tag	UNP A2PZA5
D	-2	GLY	-	expression tag	UNP A2PZA5
D	-1	SER	-	expression tag	UNP A2PZA5
D	0	HIS	-	expression tag	UNP A2PZA5
D	53	ARG	GLY	conflict	UNP A2PZA5
D	604	CYS	ARG	conflict	UNP A2PZA5
E	-19	MET	-	initiating methionine	UNP A2PZA5
E	-18	GLY	-	expression tag	UNP A2PZA5
E	-17	SER	-	expression tag	UNP A2PZA5
E	-16	SER	-	expression tag	UNP A2PZA5
E	-15	HIS	-	expression tag	UNP A2PZA5
E	-14	HIS	-	expression tag	UNP A2PZA5
E	-13	HIS	-	expression tag	UNP A2PZA5
E	-12	HIS	-	expression tag	UNP A2PZA5
E	-11	HIS	-	expression tag	UNP A2PZA5
E	-10	HIS	-	expression tag	UNP A2PZA5

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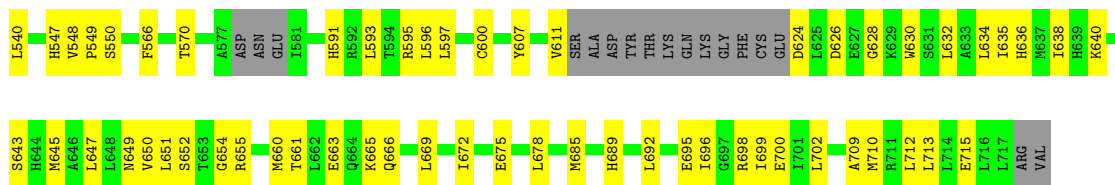
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Chain	Residue	Modelled	Actual	Comment	Reference
E	-9	SER	-	expression tag	UNP A2PZA5
E	-8	SER	-	expression tag	UNP A2PZA5
E	-7	GLY	-	expression tag	UNP A2PZA5
E	-6	LEU	-	expression tag	UNP A2PZA5
E	-5	VAL	-	expression tag	UNP A2PZA5
E	-4	PRO	-	expression tag	UNP A2PZA5
E	-3	ARG	-	expression tag	UNP A2PZA5
E	-2	GLY	-	expression tag	UNP A2PZA5
E	-1	SER	-	expression tag	UNP A2PZA5
E	0	HIS	-	expression tag	UNP A2PZA5
E	53	ARG	GLY	conflict	UNP A2PZA5
E	604	CYS	ARG	conflict	UNP A2PZA5
F	-19	MET	-	initiating methionine	UNP A2PZA5
F	-18	GLY	-	expression tag	UNP A2PZA5
F	-17	SER	-	expression tag	UNP A2PZA5
F	-16	SER	-	expression tag	UNP A2PZA5
F	-15	HIS	-	expression tag	UNP A2PZA5
F	-14	HIS	-	expression tag	UNP A2PZA5
F	-13	HIS	-	expression tag	UNP A2PZA5
F	-12	HIS	-	expression tag	UNP A2PZA5
F	-11	HIS	-	expression tag	UNP A2PZA5
F	-10	HIS	-	expression tag	UNP A2PZA5
F	-9	SER	-	expression tag	UNP A2PZA5
F	-8	SER	-	expression tag	UNP A2PZA5
F	-7	GLY	-	expression tag	UNP A2PZA5
F	-6	LEU	-	expression tag	UNP A2PZA5
F	-5	VAL	-	expression tag	UNP A2PZA5
F	-4	PRO	-	expression tag	UNP A2PZA5
F	-3	ARG	-	expression tag	UNP A2PZA5
F	-2	GLY	-	expression tag	UNP A2PZA5
F	-1	SER	-	expression tag	UNP A2PZA5
F	0	HIS	-	expression tag	UNP A2PZA5
F	53	ARG	GLY	conflict	UNP A2PZA5
F	604	CYS	ARG	conflict	UNP A2PZA5
G	-19	MET	-	initiating methionine	UNP A2PZA5
G	-18	GLY	-	expression tag	UNP A2PZA5
G	-17	SER	-	expression tag	UNP A2PZA5
G	-16	SER	-	expression tag	UNP A2PZA5
G	-15	HIS	-	expression tag	UNP A2PZA5
G	-14	HIS	-	expression tag	UNP A2PZA5
G	-13	HIS	-	expression tag	UNP A2PZA5
G	-12	HIS	-	expression tag	UNP A2PZA5

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Chain	Residue	Modelled	Actual	Comment	Reference
G	-11	HIS	-	expression tag	UNP A2PZA5
G	-10	HIS	-	expression tag	UNP A2PZA5
G	-9	SER	-	expression tag	UNP A2PZA5
G	-8	SER	-	expression tag	UNP A2PZA5
G	-7	GLY	-	expression tag	UNP A2PZA5
G	-6	LEU	-	expression tag	UNP A2PZA5
G	-5	VAL	-	expression tag	UNP A2PZA5
G	-4	PRO	-	expression tag	UNP A2PZA5
G	-3	ARG	-	expression tag	UNP A2PZA5
G	-2	GLY	-	expression tag	UNP A2PZA5
G	-1	SER	-	expression tag	UNP A2PZA5
G	0	HIS	-	expression tag	UNP A2PZA5
G	53	ARG	GLY	conflict	UNP A2PZA5
G	604	CYS	ARG	conflict	UNP A2PZA5
H	-19	MET	-	initiating methionine	UNP A2PZA5
H	-18	GLY	-	expression tag	UNP A2PZA5
H	-17	SER	-	expression tag	UNP A2PZA5
H	-16	SER	-	expression tag	UNP A2PZA5
H	-15	HIS	-	expression tag	UNP A2PZA5
H	-14	HIS	-	expression tag	UNP A2PZA5
H	-13	HIS	-	expression tag	UNP A2PZA5
H	-12	HIS	-	expression tag	UNP A2PZA5
H	-11	HIS	-	expression tag	UNP A2PZA5
H	-10	HIS	-	expression tag	UNP A2PZA5
H	-9	SER	-	expression tag	UNP A2PZA5
H	-8	SER	-	expression tag	UNP A2PZA5
H	-7	GLY	-	expression tag	UNP A2PZA5
H	-6	LEU	-	expression tag	UNP A2PZA5
H	-5	VAL	-	expression tag	UNP A2PZA5
H	-4	PRO	-	expression tag	UNP A2PZA5
H	-3	ARG	-	expression tag	UNP A2PZA5
H	-2	GLY	-	expression tag	UNP A2PZA5
H	-1	SER	-	expression tag	UNP A2PZA5
H	0	HIS	-	expression tag	UNP A2PZA5
H	53	ARG	GLY	conflict	UNP A2PZA5
H	604	CYS	ARG	conflict	UNP A2PZA5



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	151710	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	52	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON III (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	0.20	0/2375	0.47	0/3207
1	B	0.20	0/2337	0.43	0/3157
1	C	0.21	0/2371	0.42	0/3204
1	D	0.20	0/2318	0.44	0/3134
1	E	0.20	0/2375	0.47	0/3207
1	F	0.20	0/2337	0.43	0/3157
1	G	0.21	0/2371	0.42	0/3204
1	H	0.20	0/2318	0.44	0/3134
All	All	0.20	0/18802	0.44	0/25404

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	2333	0	2330	60	0
1	B	2293	0	2291	53	0
1	C	2329	0	2317	55	0
1	D	2274	0	2259	64	0
1	E	2333	0	2330	59	0
1	F	2293	0	2291	51	0
1	G	2329	0	2317	54	0
1	H	2274	0	2259	64	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	18458	0	18394	442	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 12.

The worst 5 of 442 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:A:699:ILE:HA	1:A:702:LEU:HD21	1.30	1.12
1:E:699:ILE:HA	1:E:702:LEU:HD21	1.30	1.11
1:A:699:ILE:HA	1:A:702:LEU:CD2	1.90	1.02
1:E:699:ILE:HA	1:E:702:LEU:CD2	1.90	1.00
1:E:698:ARG:O	1:E:702:LEU:HD23	1.80	0.82

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	290/739 (39%)	255 (88%)	33 (11%)	2 (1%)	18	50
1	B	284/739 (38%)	259 (91%)	24 (8%)	1 (0%)	30	60
1	C	290/739 (39%)	261 (90%)	27 (9%)	2 (1%)	18	50
1	D	284/739 (38%)	256 (90%)	28 (10%)	0	100	100
1	E	290/739 (39%)	255 (88%)	33 (11%)	2 (1%)	18	50
1	F	284/739 (38%)	259 (91%)	24 (8%)	1 (0%)	30	60
1	G	290/739 (39%)	261 (90%)	27 (9%)	2 (1%)	18	50
1	H	284/739 (38%)	256 (90%)	28 (10%)	0	100	100
All	All	2296/5912 (39%)	2062 (90%)	224 (10%)	10 (0%)	31	60

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	655	ARG
1	F	655	ARG
1	A	578	ASP
1	C	481	PRO
1	E	578	ASP

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	255/652 (39%)	254 (100%)	1 (0%)	84	81
1	B	252/652 (39%)	251 (100%)	1 (0%)	84	81
1	C	255/652 (39%)	254 (100%)	1 (0%)	84	81
1	D	248/652 (38%)	248 (100%)	0	100	100
1	E	255/652 (39%)	254 (100%)	1 (0%)	84	81
1	F	252/652 (39%)	251 (100%)	1 (0%)	84	81
1	G	255/652 (39%)	254 (100%)	1 (0%)	84	81
1	H	248/652 (38%)	248 (100%)	0	100	100
All	All	2020/5216 (39%)	2014 (100%)	6 (0%)	84	83

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	702	LEU
1	F	657	HIS
1	G	586	ILE
1	B	657	HIS
1	A	702	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 66 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	591	HIS
1	G	657	HIS
1	H	641	GLN
1	C	591	HIS
1	C	560	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 oligosaccharides 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

This section contains visualisations of the EMDB entry EMD-27989. 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

This section was not generated.

6.2 Central slices

This section was not generated.

6.3 Largest variance slices

This section was not generated.

6.4 Orthogonal standard-deviation projections (False-color)

This section was not generated.

6.5 Orthogonal surface views

This section was not generated.

6.6 Mask visualisation

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.