



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 02:14 PM BST

PDB ID : 5A9E
EMDB ID: : EMD-3101
Title : Cryo-electron tomography and subtomogram averaging of Rous-Sarcoma-Virus deltaMBD virus-like particles
Authors : Schur, F.K.M.; Dick, R.A.; Hagen, W.J.H.; Vogt, V.M.; Briggs, J.A.G.
Deposited on : 2015-07-21
Resolution : 7.70 Å(reported)

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>

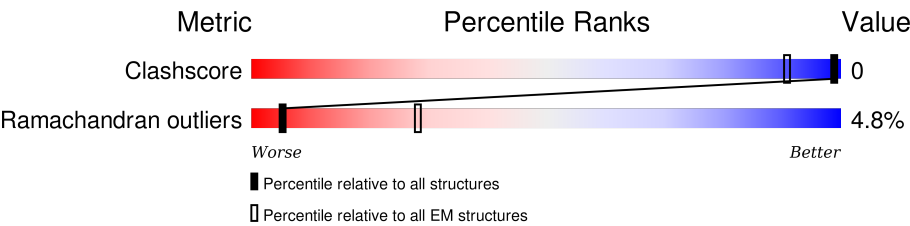
MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27241

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 7.70 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	114402	924
Ramachandran outliers	111179	726

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	495	<div><div>46%5%•48%</div></div>
1	B	495	<div><div>46%••48%</div></div>
1	C	495	<div><div>47%••48%</div></div>
1	D	495	<div><div>45%6%•48%</div></div>
1	E	495	<div><div>46%••48%</div></div>
1	F	495	<div><div>46%5%48%</div></div>
1	G	495	<div><div>46%5%•48%</div></div>
1	H	495	<div><div>46%5%•48%</div></div>
1	I	495	<div><div>46%5%•48%</div></div>
1	J	495	<div><div>45%6%•48%</div></div>
1	K	495	<div><div>44%6%•48%</div></div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	L	495	<div><div></div><div>45%5%•48%</div></div>
1	M	495	<div><div></div><div>40%•56%</div></div>
1	N	495	<div><div></div><div>40%•56%</div></div>
1	O	495	<div><div></div><div>41%••56%</div></div>
1	P	495	<div><div></div><div>41%••56%</div></div>
1	Q	495	<div><div></div><div>40%•56%</div></div>
1	R	495	<div><div></div><div>40%•56%</div></div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 17406 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 DELTAMBD GAG PROTEIN.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	255	Total	C	N	O	0	0
			1019	510	255	254		
1	B	255	Total	C	N	O	0	0
			1019	510	255	254		
1	C	255	Total	C	N	O	0	0
			1019	510	255	254		
1	D	255	Total	C	N	O	0	0
			1019	510	255	254		
1	E	255	Total	C	N	O	0	0
			1019	510	255	254		
1	F	255	Total	C	N	O	0	0
			1019	510	255	254		
1	G	255	Total	C	N	O	0	0
			1019	510	255	254		
1	H	255	Total	C	N	O	0	0
			1019	510	255	254		
1	I	255	Total	C	N	O	0	0
			1019	510	255	254		
1	J	255	Total	C	N	O	0	0
			1019	510	255	254		
1	K	255	Total	C	N	O	0	0
			1019	510	255	254		
1	L	255	Total	C	N	O	0	0
			1019	510	255	254		
1	M	216	Total	C	N	O	0	0
			863	432	216	215		
1	N	216	Total	C	N	O	0	0
			863	432	216	215		
1	O	216	Total	C	N	O	0	0
			863	432	216	215		
1	P	216	Total	C	N	O	0	0
			863	432	216	215		
1	Q	216	Total	C	N	O	0	0
			863	432	216	215		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				AltConf	Trace
1	R	216	Total 863	C 432	N 216	O 215	0	0

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	83	SER	-	EXPRESSION TAG	UNP P03322
A	573	GLN	PRO	CONFLICT	UNP P03322
B	83	SER	-	EXPRESSION TAG	UNP P03322
B	573	GLN	PRO	CONFLICT	UNP P03322
C	83	SER	-	EXPRESSION TAG	UNP P03322
C	573	GLN	PRO	CONFLICT	UNP P03322
D	83	SER	-	EXPRESSION TAG	UNP P03322
D	573	GLN	PRO	CONFLICT	UNP P03322
E	83	SER	-	EXPRESSION TAG	UNP P03322
E	573	GLN	PRO	CONFLICT	UNP P03322
F	83	SER	-	EXPRESSION TAG	UNP P03322
F	573	GLN	PRO	CONFLICT	UNP P03322
G	83	SER	-	EXPRESSION TAG	UNP P03322
G	573	GLN	PRO	CONFLICT	UNP P03322
H	83	SER	-	EXPRESSION TAG	UNP P03322
H	573	GLN	PRO	CONFLICT	UNP P03322
I	83	SER	-	EXPRESSION TAG	UNP P03322
I	573	GLN	PRO	CONFLICT	UNP P03322
J	83	SER	-	EXPRESSION TAG	UNP P03322
J	573	GLN	PRO	CONFLICT	UNP P03322
K	83	SER	-	EXPRESSION TAG	UNP P03322
K	573	GLN	PRO	CONFLICT	UNP P03322
L	83	SER	-	EXPRESSION TAG	UNP P03322
L	573	GLN	PRO	CONFLICT	UNP P03322
M	83	SER	-	EXPRESSION TAG	UNP P03322
M	573	GLN	PRO	CONFLICT	UNP P03322
N	83	SER	-	EXPRESSION TAG	UNP P03322
N	573	GLN	PRO	CONFLICT	UNP P03322
O	83	SER	-	EXPRESSION TAG	UNP P03322
O	573	GLN	PRO	CONFLICT	UNP P03322
P	83	SER	-	EXPRESSION TAG	UNP P03322
P	573	GLN	PRO	CONFLICT	UNP P03322
Q	83	SER	-	EXPRESSION TAG	UNP P03322
Q	573	GLN	PRO	CONFLICT	UNP P03322
R	83	SER	-	EXPRESSION TAG	UNP P03322
R	573	GLN	PRO	CONFLICT	UNP P03322

- Molecule 1: DELTAMBD GAG PROTEIN

[illegible]

- Molecule 1: DELTAMBD GAG PROTEIN

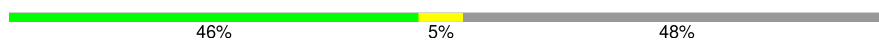
[illegible]

- Molecule 1: DELTAMBD GAG PROTEIN

Chain C:  47% .. 48%



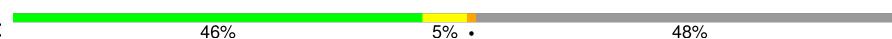
Chain F:



ARG	GLU	GLN	ASP	GLN	GLU	SER
GLU	ARG	GLY	GLN	SER	THR	ALA
GLU	CYS	ILE	ALA	ALA	THR	ALA
GLN	GLN	ALA	ALA	PRO	PRO	GLU
LEU	ALA	ALA	ALA	PRO	LYS	GLN
CYS	ASN	CYS	ALA	GLY	THR	VAL
ASN	GLN	MET	MET	HIS	VAL	THR
MET	GLY	SER	SER	A211	GLY	SER
GLY	GLY	ALA	ALA	L219	THR	GLU
HIS	GLN	ILE	ILE	T220	SER	GLN
ASN	GLN	GLN	GLN	E228	CYS	ALA
ALA	PRO	LEU	LEU	S231	THR	GLY
LYS	LYS	ILE	ILE	P234	ALA	LEU
GLN	GLN	MET	MET	M239	ILE	GLY
CYS	CYS	VAL	VAL	K244	GLY	GLY
ARG	ASP	ASN	ASN	T245	CYS	GLY
GLY	GLY	GLN	GLN	E246	ASN	ARG
GLN	GLY	GLN	GLY	G247	CYS	VAL
GLN	GLN	GLN	GLY	T267	THR	SER
ARG	ARG	GLN	GLN	K268	ALA	PRO
PRO	PRO	THR	THR	G269	PRO	GLY
GLY	GLY	GLY	GLY	L270	PRO	CYS
LYS	GLY	GLY	GLY	R271	PRO	ILE
LEU	LEU	GLY	GLY	S272	PRO	GLU
SER	SER	ARG	ARG	P273	TYR	LYS
SER	SER	ALA	ALA	M283	VAL	PRO
GLY	GLY	ARG	ARG	K283	GLY	ALA
PRO	PRO	GLY	GLY	A323	SER	ALA
TRP	TRP	LEU	LEU	E323	GLY	THR
PRO	PRO	CYS	CYS	LEU	GLY	GLU
GLY	GLY	TYR	TYR	P327	ARG	ARG
PRO	PRO	THR	THR	PRO	TYR	ILE
GLU	GLU	CYS	CYS	Q359	SER	ASP
GLN	GLN	GLY	GLY	LEU	SER	LYS
PRO	PRO	SER	SER	E387	ALA	GLY
ALA	ALA	PRO	PRO	P388	GLY	GLU
VAL	VAL	VAL	VAL	A389	VAL	GLU
SER	SER	HIS	HIS	G390	GLY	VAL
		THR	THR	P391	GLU	GLY
		GLN	GLN	M392	GLU	GLY
		ALA	ALA	Y460	GLN	THR
		GLN	GLN	Y460	GLY	THR
		CYS	CYS	D463	GLN	VAL
		PRO	PRO	R464	GLY	GLN
		LYS	LYS	Q465	ASP	ARG
		ARG	ARG	LYS	THR	GLY
		LYS	LYS	THR	PRO	LYS
		SER	SER	ALA	PRO	MET
		GLY	GLY	PRO	GLY	ALA
		ASN	ASN	LEU	ALA	PRO

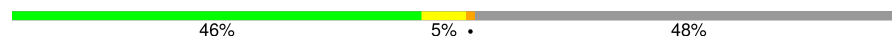
- Molecule 1: DELTAMBD GAG PROTEIN

Chain G:

[illegible]

- Molecule 1: DELTAMBD GAG PROTEIN

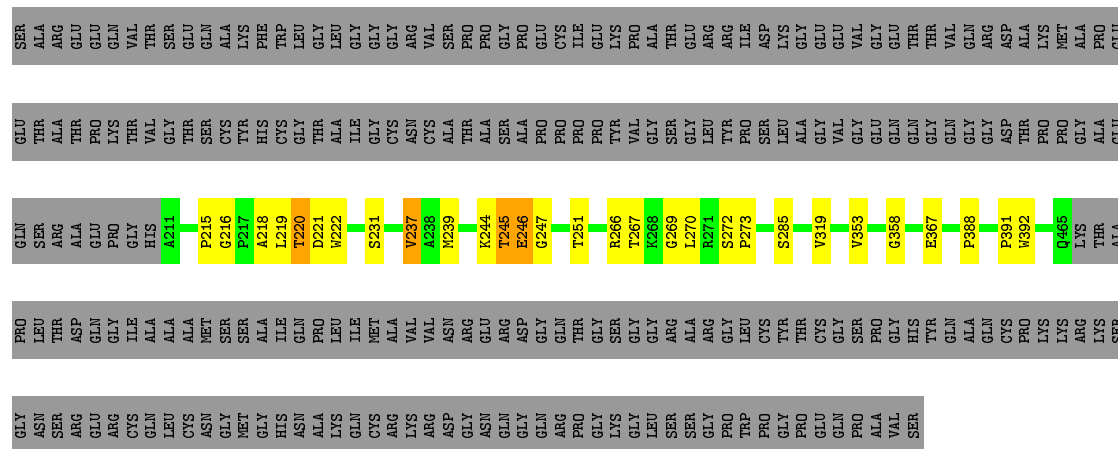
Chain H:



ARG	GLU	ASP	GLN	GLU	THR	GLU	THR	GLU	SER
GLU	ARG	GLN	SER	ARG	ALA	THR	ALA	ALA	ARG
CYS	GLN	ILE	ALA	ALA	THR	PRO	GLU	THR	GLU
LEU	ALA	ALA	PRO	GLY	THR	GLY	LYS	VAL	GLN
CYS	ASN	ALA	GLY	GLY	THR	VAL	THR	SER	THR
ASN	MET	SER	GLN	GLN	GLY	GLY	GLY	GLY	SER
GLY	GLY	SER	Q211	Q212	Q213	Q214	Q215	Q216	Q217
GLY	GLY	ILE	ALA	ALA	THR	THR	CYS	ALA	ALA
HIS	GLY	ILE	Q217	Q218	Q219	Q220	Q221	Q222	Q223
ASN	ASN	GLN	P217	P218	P219	P220	P221	P222	P223
ALA	ALA	PRO	L219	L220	L221	L222	L223	L224	L225
LYS	LYS	LEU	G218	G219	G220	G221	G222	G223	G224
GLN	GLN	ILE	T220	T221	T222	T223	T224	T225	T226
CYS	CYS	MET	E228	E229	E230	E231	E232	E233	E234
ARG	ARG	ALA	S231	S232	S233	S234	S235	S236	S237
LYS	LYS	VAL	ASN	ARG	ARG	K244	T245	E246	G247
ASP	GLY	ASN	ARG	ARG	GLU	T245	E246	G247	P248
ASN	ASN	GLU	T245	E246	G247	P248	P249	P250	P251
GLN	GLN	ARG	G247	P248	GLY	GLN	GLN	GLN	GLN
GLN	GLN	ARG	P248	P249	GLY	GLN	GLN	GLN	GLN
GLN	GLN	THR	P252	P253	THR	THR	THR	THR	THR
PRO	PRO	GLY	T267	T268	G269	L270	R271	S272	P273
GLY	LYS	SER	T267	T268	G269	L270	R271	S272	P273
GLY	GLY	GLY	G269	L270	TYR	VAL	VAL	GLY	SER
LEU	LEU	GLY	L270	TYR	TYR	VAL	VAL	GLY	SER
SER	SER	ALA	R271	S272	VAL	VAL	GLY	GLY	THR
SER	SER	ALA	S272	P273	VAL	GLY	GLY	GLY	THR
GLY	GLY	ARG	P273	P274	GLY	GLY	GLY	GLY	THR
PRO	PRO	LEU	P289	P290	LEU	LEU	LEU	LEU	ARG
PRO	PRO	CYS	P289	P290	LEU	LEU	LEU	LEU	ARG
PRO	PRO	THR	P290	P291	TYR	TYR	TYR	TYR	ILE
GLU	GLU	CYS	P290	P291	TYR	TYR	TYR	TYR	ILE
GLU	GLU	GLY	P291	P292	SER	SER	SER	SER	ASP
PRO	PRO	GLY	P292	P293	LEU	LEU	LEU	LEU	LYS
VAL	VAL	SER	P293	P294	ALA	ALA	ALA	ALA	GLY
SER	SER	GLY	P294	P295	VAL	VAL	VAL	VAL	GLY
SER	SER	HIS	P295	P296	GLY	GLY	GLY	GLY	VAL
THR	THR	THR	I411	K412	GLN	GLN	GLN	GLN	GLY
GLN	GLN	ALA	I411	K412	GLN	GLN	GLN	GLN	GLY
ALA	ALA	GLN	K412	A413	GLY	GLY	GLY	GLY	THR
CYS	CYS	CYS	A413	D418	GLY	GLY	GLY	GLY	THR
PRO	PRO	PRO	D418	Q465	GLY	GLY	GLY	GLY	THR
LYS	LYS	LYS	Q465	LYS	ASP	ASP	ASP	ASP	ARG
LYS	LYS	ARG	LYS	THR	THR	THR	THR	THR	ALA
SER	SER	SER	THR	ALA	PRO	PRO	PRO	PRO	LYS
GLY	GLY	GLY	ALA	PRO	GLY	GLY	GLY	GLY	ALA
ASN	ASN	ASN	PRO	LEU	ALA	ALA	ALA	ALA	PRO

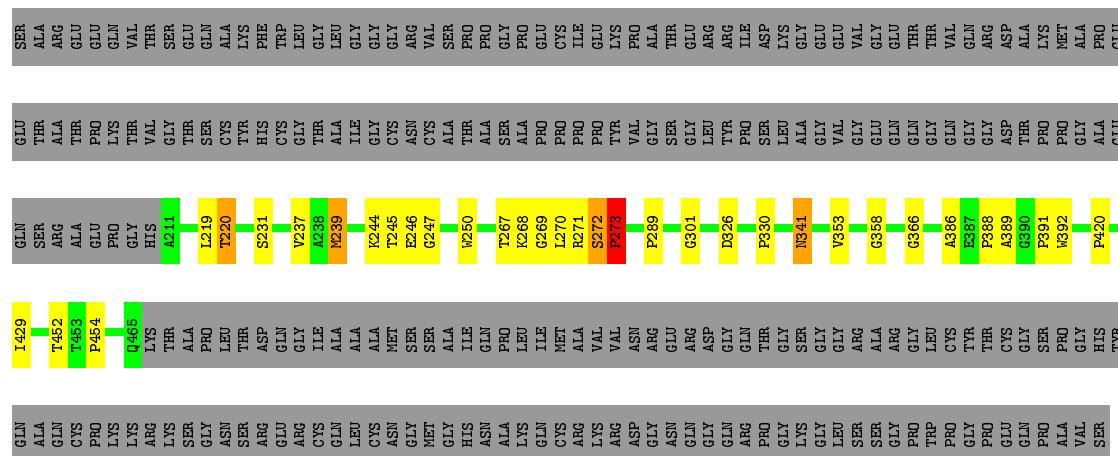
- Molecule 1: DELTAMBD GAG PROTEIN

Chain I:  46% 5% • 48%



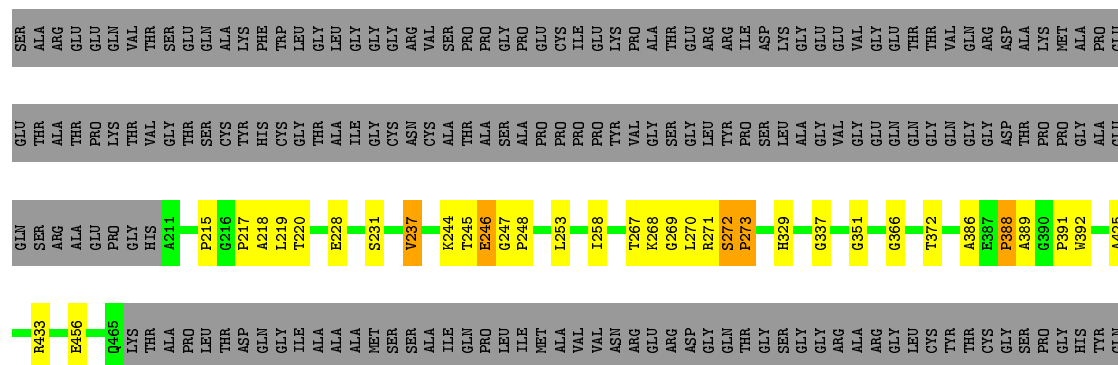
- Molecule 1: DELTAMBD GAG PROTEIN

Chain J: 45% 6% 48%



- Molecule 1: DELTAMBD GAG PROTEIN

Chain K:  44% 6% 48%



ALA	GLN	CYS	PRO	LYS	LYS	ARG	LYS	SER	GLY	ASN	SER	ASN	ARG	GLU	ARG	ARG	CYS	GLN	LEU	CYS	ASN	CYS	GLY	MET	GLY	HIS	ASN	ALA	LYS	GLN	CYS	ARG	LYS	ARG	ASP	GLY	GLY	ASN	GLN	ASN	GLY	GLY	LEU	SER	SER	PRO	TRP	PRO	GLY	GLY	PRO	GLU	GLN	PRO	ALA	VAL	SER
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Molecule 1: DELTAMBD GAG PROTEIN

Chain L:  45% 5% • 48%

SER	ALA	ARG	GLU	GLN	VAL	THR	SER	GLU	GLN	ALA	LYS	PHE	TRP	LEU	GLY	LEU	GLY	GLY	GLY	ARG	VAL	SER	PRO	PRO	GLY	GLY	PRO	CYS	ILE	GLU	LYS	PRO	ALA	THR	GLU	ARG	ARG	ILE	ASP	LYS	GLY	GLU	GLU	VAL	VAL	GLY	GLU	THR	THR	VAL	GLN	ARG	ASP	ALA	LYS	MET	ALA	ALA	PRO	CUA
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

GLU	THR	ALA	ALA	PRO	LYS	THR	VAL	GLY	THR	SER	CYS	TYR	HIS	CYS	GLY	THR	ALA	ILE	GLY	CYS	ASN	ALA	ALA	ALA	ALA	PRO	PRO	PRO	PRO	TYR	VAL	GLY	SER	GLY	LEU	TYR	PRO	SER	LEU	ALA	ALA	VAL	GLN	GLN	GLY	GLN	GLY	GLY	GLY	ASP	THR	PRO	PRO	ALA	GLU
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

GLN	SER	ARG	ALA	GLU	PRO	GLY	HIS	A211	A218	T219	T220	D221	D222	E228	S231	V237	A238	M239	K244	T245	E246	G247	L253	T267	K268	G269	L270	R271	S272	F273	P289	P300	G347	V353	P365	S374	A386	P391	K392	S436	A465	V465
-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

THR	ALA	ALA	PRO	LEU	THR	ASP	GLN	GLY	GLY	ILE	ALA	ALA	ALA	ALA	MET	SER	SER	SER	ALA	ALA	ILE	ILE	GLN	PRO	LEU	ILE	ILE	MET	GLU	VAL	ASN	ARG	GLU	ASP	ASP	GLY	GLN	THR	THR	GLY	GLY	SER	SER	GLY	GLY	GLY	ARG	ALA	ALA	ARG	GLY	GLY	LEU	CYS	TYR	THR	THR	CYS	GLY	GLY	SER	PRO	GLY	HIS	GLY	THR	TYR	GLN	GLN	ALA	ALA	GLN	CYS	PRO	LYS	LYS	ARG
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

LYS	SER	GLY	ASN	SER	ARG	GLU	ARG	CYS	GLN	LEU	CYS	ASN	GLY	MET	GLY	HIS	ASN	ALA	LYS	GLN	CYS	ARG	CYS	LYS	ARG	ASP	GLY	ASN	GLN	GLY	GLN	ARG	PRO	GLY	LYS	LEU	SER	GLY	PRO	TRP	PRO	GLY	PRO	GLN	PRO	ALA	VAL	SER
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Molecule 1: DELTAMBD GAG PROTEIN

Chain M:  40% . 56%

SER	ALA	ARG	GLU	GLY	GLN	VAL	THR	SER	GLU	GLN	ALA	LYS	PHE	TRP	LEU	GLY	LEU	GLY	GLY	ARG	VAL	SER	PRO	PRO	GLY	GLY	PRO	CYS	ILE	LYS	PRO	THR	GLU	ARG	ARG	ASP	ASP	LYS	GLY	GLU	GLU	VAL	VAL	GLY	THR	THR	VAL	GLN	ARG	ASP	ALA	LYS	MET	ALA	ALA	PRO	GLU
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

GLU	THR	ALA	ALA	PRO	LYS	THR	VAL	GLY	THR	SER	CYS	TYR	HIS	CYS	GLY	THR	ALA	ILE	GLY	CYS	ASN	ALA	ALA	PRO	PRO	PRO	PRO	TYR	VAL	GLY	SER	GLY	LEU	TYR	PRO	SER	LEU	ALA	ALA	GLY	VAL	GLN	GLN	GLN	GLN	GLY	GLY	GLY	ASP	THR	PRO	PRO	ALA	GLU
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

GLN	SER	ARG	ALA	GLU	PRO	GLY	HIS	ALA	GLY	GLN	ALA	PRO	GLY	PRO	ALA	LEU	THR	ASP	TRP	ALA	ALA	ARG	VAL	ARG	GLU	GLU	LEU	ALA	SER	THR	GLY	PRO	PRO	VAL	VAL	VAL	VAL	ILE	LYS	THR	GLU	GLY	PRO	PRO	ALA	T250	T251	T252	T253	T267	K268	G269	L270	S271	S272	P273
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------

L342
N355
V382
A363
R384
E387
P388
A389
W392
T446
Q465
LYS
THR
ALA
PRO
LEU
THR
ASP
GLN
GLY
IIE
ALA
ALA
ALA
MET
SER
SER
ALA
IIE
GLN
PRO
LEU
IIE
MET
ALA
VAL
VAL
ASN
ARG
ARG
GLU
ASP
ASP
GLY
GLN
THR
GLY
SER
GLY
ARG
ALA
ARG
GLY
LEU

CYS	TYR	THR	THR	CYS	GLY	SER	PRO	PRO	GLY	GLY	HIS	TYR	GLN	ALA	GLN	GLN	CYS	PRO	LYS	LYS	ARG	ARG	LYS	SER	GLY	ASN	SER	GLY	GLY	HIS	ASN	ALA	ALA	LYS	GLN	CYS	ARG	LYS	ASP	GLY	GLY	GLN	GLY	GLY	GLY	GLY	LEU	SER	GLY	PRO	TYR
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

PRO	GLY	PRO	GLU	GLN	PRO	ALA	VAL	SER
-----	-----	-----	-----	-----	-----	-----	-----	-----

- Molecule 1: DELTAMBD GAG PROTEIN

Chain N: 40% 0% 56%

SER	ALA	ARG	GLU	GLN	VAL	THR	SER	GLU	GLN	ALA	LYS	TRP	LEU	GLY	LEU	GLY	GLY	ARG	VAL	SER	PRO	PRO	GLY	GLU	CYS	ILE	GLU	ARG	ARG	ILE	ASP	LYS	GLY	GLU	GLU	VAL	GLY	GLU	THR	THR	VAL	GLN	ASP	ALA	LYS	MET	ALA	PRO	GLU
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

GLU	THR	ALA	ALA	THR	PRO	LYS	THR	VAL	GLY	GLY	THR	SER	CYS	THR	HIS	CYS	GLY	THR	ALA	ALA	ALA	ALA	PRO	PRO	PRO	PRO	TYR	VAL	GLY	SER	GLY	GLY	LEU	TYR	PRO	SER	SER	LEU	ALA	ALA	VAL	GLY	GLY	GLU	GLN	GLN	GLY	GLN	GLY	GLY	GLY	GLY	ASP	PRO	THR	PRO	PRO	GLY	GLY	GLY	THR	ALA	THR
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

4 Experimental information

Property	Value	Source
Reconstruction method	TOMOGRAPHY	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	PHASE-FLIPPING OF INDIVIDUAL MICROGRAPHS	Depositor
Microscope	OTHER	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	34	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	81000	Depositor
Image detector	GATAN MULTISCAN	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 > 2	RMSZ	# Z > 2
1	A	1.43	1/1018 (0.1%)	1.70	8/1271 (0.6%)
1	B	1.40	2/1018 (0.2%)	1.62	3/1271 (0.2%)
1	C	1.45	0/1018	1.64	3/1271 (0.2%)
1	D	1.44	4/1018 (0.4%)	1.73	14/1271 (1.1%)
1	E	1.44	3/1018 (0.3%)	1.60	4/1271 (0.3%)
1	F	1.46	1/1018 (0.1%)	1.70	9/1271 (0.7%)
1	G	1.44	0/1018	1.72	6/1271 (0.5%)
1	H	1.51	1/1018 (0.1%)	1.63	5/1271 (0.4%)
1	I	1.49	2/1018 (0.2%)	1.68	7/1271 (0.6%)
1	J	1.50	5/1018 (0.5%)	1.70	7/1271 (0.6%)
1	K	1.47	4/1018 (0.4%)	1.69	14/1271 (1.1%)
1	L	1.49	2/1018 (0.2%)	1.67	4/1271 (0.3%)
1	M	1.47	1/862 (0.1%)	1.65	6/1076 (0.6%)
1	N	1.42	2/862 (0.2%)	1.66	7/1076 (0.7%)
1	O	1.47	3/862 (0.3%)	1.63	2/1076 (0.2%)
1	P	1.39	0/862	1.62	6/1076 (0.6%)
1	Q	1.49	3/862 (0.3%)	1.65	5/1076 (0.5%)
1	R	1.42	2/862 (0.2%)	1.57	2/1076 (0.2%)
All	All	1.46	36/17388 (0.2%)	1.66	112/21708 (0.5%)

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	A	0	11
1	B	0	10
1	C	0	10
1	D	0	9
1	E	0	12
1	F	0	11
1	G	0	13

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
1	H	0	11
1	I	0	9
1	J	0	13
1	K	0	11
1	L	0	11
1	M	0	3
1	N	0	4
1	O	0	5
1	P	0	4
1	Q	0	6
1	R	0	5
All	All	0	158

The worst 5 of 36 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	390	GLY	CA-C	-6.71	1.41	1.51
1	R	437	GLN	C-N	6.15	1.46	1.34
1	A	301	GLY	C-N	-6.07	1.22	1.34
1	J	326	ASP	C-N	-6.00	1.22	1.34
1	Q	333	GLY	CA-C	-5.99	1.42	1.51

The worst 5 of 112 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	N	389	ALA	C-N-CA	7.78	138.63	122.30
1	H	217	PRO	C-N-CA	7.34	140.04	121.70
1	N	414	VAL	O-C-N	-7.06	111.41	122.70
1	P	330	PRO	N-CA-C	6.85	129.91	112.10
1	D	337	GLY	O-C-N	-6.65	112.06	122.70

There are no chirality outliers.

5 of 158 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	219	LEU	Peptide
1	A	220	THR	Peptide
1	A	221	ASP	Peptide
1	A	244	LYS	Peptide
1	A	245	THR	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	1019	0	266	1	0
1	B	1019	0	266	1	0
1	C	1019	0	266	0	0
1	D	1019	0	266	0	0
1	E	1019	0	266	0	0
1	F	1019	0	266	0	0
1	G	1019	0	266	0	0
1	H	1019	0	266	0	0
1	I	1019	0	266	0	0
1	J	1019	0	266	0	0
1	K	1019	0	266	0	0
1	L	1019	0	266	0	0
1	M	863	0	225	0	0
1	N	863	0	225	0	0
1	O	863	0	225	0	0
1	P	863	0	225	0	0
1	Q	863	0	225	0	0
1	R	863	0	225	0	0
All	All	17406	0	4542	2	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 0.

All (2) 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:382:VAL:C	1:B:384:ARG:H	2.21	0.43
1:A:351:GLY:O	1:A:358:GLY:HA3	2.20	0.42

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 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	253/495 (51%)	210 (83%)	28 (11%)	15 (6%)	2	27
1	B	253/495 (51%)	216 (85%)	25 (10%)	12 (5%)	3	32
1	C	253/495 (51%)	218 (86%)	20 (8%)	15 (6%)	2	27
1	D	253/495 (51%)	220 (87%)	22 (9%)	11 (4%)	3	34
1	E	253/495 (51%)	224 (88%)	18 (7%)	11 (4%)	3	34
1	F	253/495 (51%)	222 (88%)	20 (8%)	11 (4%)	3	34
1	G	253/495 (51%)	221 (87%)	17 (7%)	15 (6%)	2	27
1	H	253/495 (51%)	212 (84%)	27 (11%)	14 (6%)	2	29
1	I	253/495 (51%)	218 (86%)	20 (8%)	15 (6%)	2	27
1	J	253/495 (51%)	218 (86%)	19 (8%)	16 (6%)	2	25
1	K	253/495 (51%)	224 (88%)	16 (6%)	13 (5%)	2	30
1	L	253/495 (51%)	214 (85%)	22 (9%)	17 (7%)	1	24
1	M	214/495 (43%)	190 (89%)	17 (8%)	7 (3%)	5	40
1	N	214/495 (43%)	188 (88%)	17 (8%)	9 (4%)	3	34
1	O	214/495 (43%)	195 (91%)	11 (5%)	8 (4%)	4	38
1	P	214/495 (43%)	191 (89%)	18 (8%)	5 (2%)	8	48
1	Q	214/495 (43%)	188 (88%)	19 (9%)	7 (3%)	5	40
1	R	214/495 (43%)	191 (89%)	15 (7%)	8 (4%)	4	38
All	All	4320/8910 (48%)	3760 (87%)	351 (8%)	209 (5%)	5	32

5 of 209 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	246	GLU
1	A	267	THR
1	A	271	ARG
1	A	273	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	327	PRO

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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](#)

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.