



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>

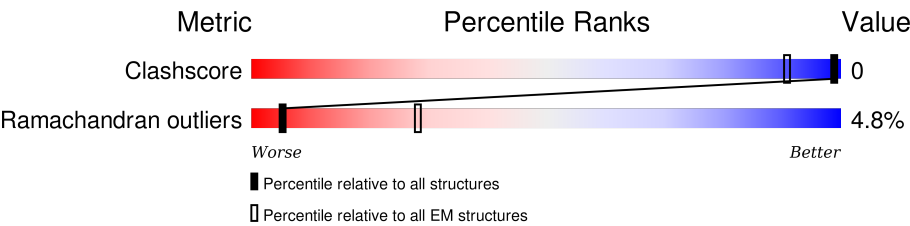
MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27241

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%•</div><div>48%</div></div>
1	B	495	<div><div>46%••</div><div>48%</div></div>
1	C	495	<div><div>47%••</div><div>48%</div></div>
1	D	495	<div><div>45%6%•</div><div>48%</div></div>
1	E	495	<div><div>46%••</div><div>48%</div></div>
1	F	495	<div><div>46%5%</div><div>48%</div></div>
1	G	495	<div><div>46%5%•</div><div>48%</div></div>
1	H	495	<div><div>46%5%•</div><div>48%</div></div>
1	I	495	<div><div>46%5%•</div><div>48%</div></div>
1	J	495	<div><div>45%6%•</div><div>48%</div></div>
1	K	495	<div><div>44%6%•</div><div>48%</div></div>

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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		

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

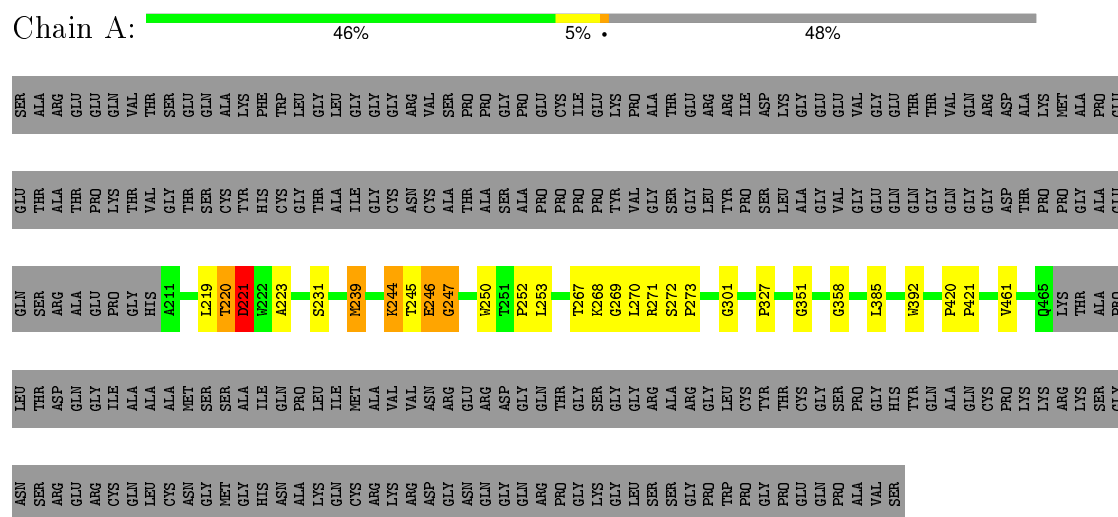
There are 36 discrepancies between the modelled and reference sequences:

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

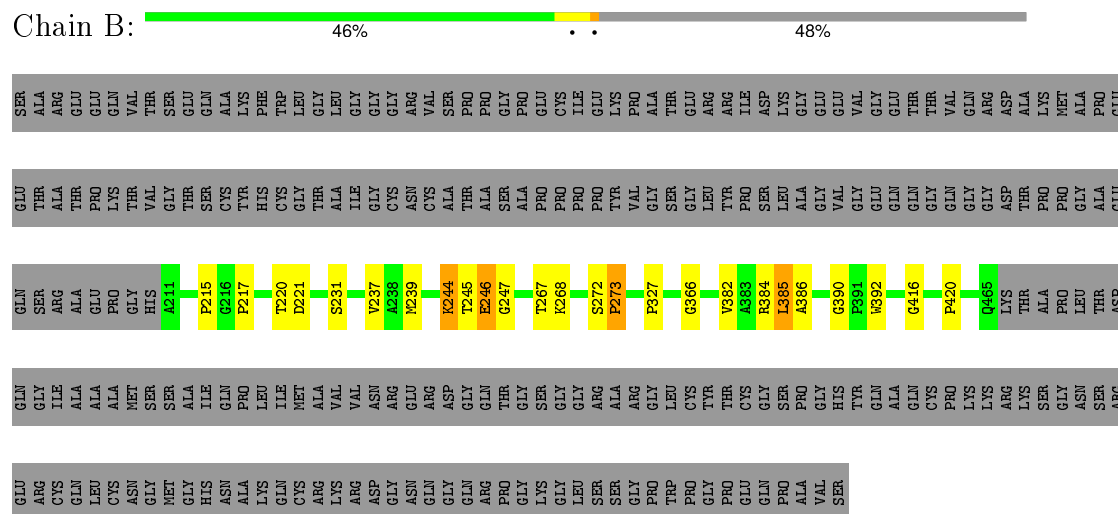
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: DELTAMBD GAG PROTEIN

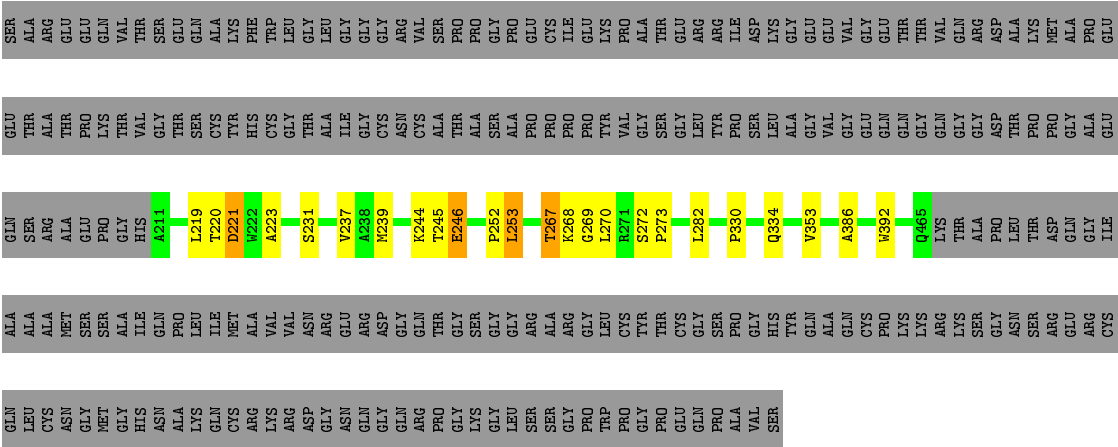


• Molecule 1: DELTAMBD GAG PROTEIN

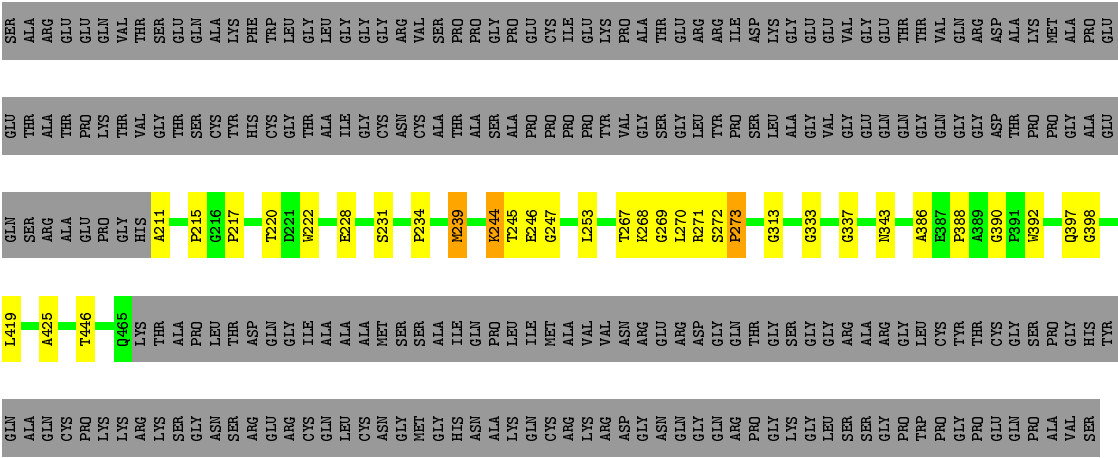


• Molecule 1: DELTAMBD GAG PROTEIN

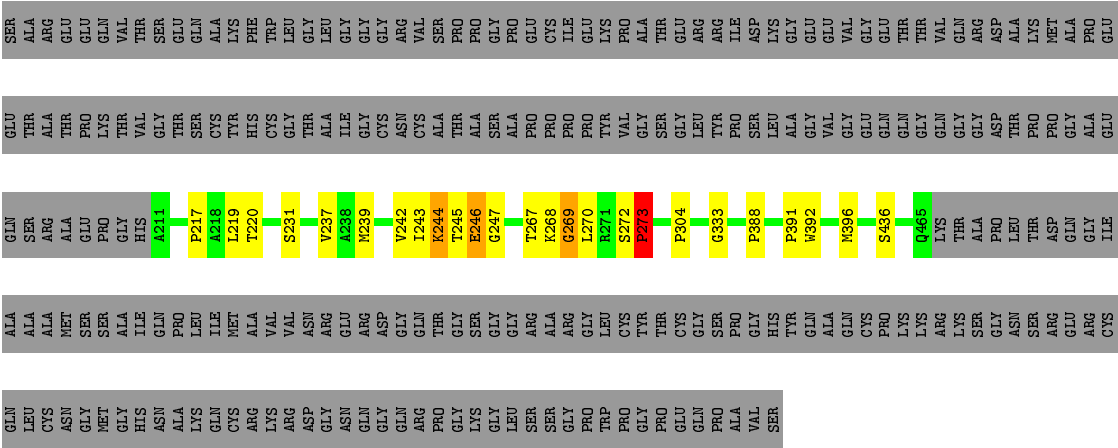




• Molecule 1: DELTAMBD GAG PROTEIN

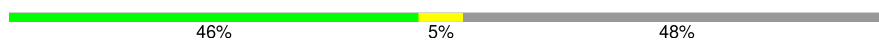


• Molecule 1: DELTAMBD GAG PROTEIN



• Molecule 1: DELTAMBD GAG PROTEIN

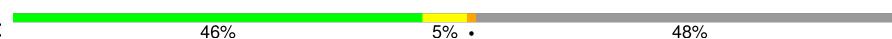
Chain F:



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
GLY	GLY	SER	SER	A211	GLY	SER
MET	GLY	ALA	ALA	L219	THR	GLU
HIS	GLY	ILE	ILE	T220	SER	GLN
ASN	ASN	GLN	GLN	E228	CYS	ALA
ALA	ALA	PRO	PRO	E228	HIS	LYS
LYS	LYS	LEU	LEU	S231	CYS	PHE
GLN	GLN	ILE	ILE	S231	GLY	TRP
CYS	CYS	MET	MET	P234	THR	LEU
ARG	ARG	ALA	ALA	P234	ALA	GLY
LYS	LYS	VAL	VAL	M239	ILE	LEU
ASP	ASP	VAL	VAL	M239	GLY	GLY
ASN	ASN	ASN	ASN	K244	CYS	GLY
ASN	ASN	GLU	GLU	T245	ASN	ARG
GLN	GLN	ARG	ARG	E246	CYS	VAL
GLY	GLY	ARG	ARG	G247	ALA	VAL
GLN	GLN	GLY	GLY	G247	THR	SER
ARG	ARG	GLN	GLN	T267	ALA	PRO
PRO	PRO	THR	THR	T267	SER	GLY
GLY	GLY	GLY	GLY	K268	ALA	PRO
LYS	LYS	GLY	GLY	G269	PRO	GLY
GLY	GLY	GLY	GLY	L270	PRO	CYS
LEU	LEU	GLY	GLY	R271	PRO	ILE
SER	SER	ARG	ARG	S272	PRO	GLU
SER	SER	ALA	ALA	P273	TYR	LYS
GLY	GLY	ARG	ARG	M283	VAL	PRO
PRO	PRO	GLY	GLY	M283	GLY	ALA
TRP	TRP	LEU	LEU	A223	SER	ALA
PRO	PRO	CYS	CYS	A223	GLY	THR
GLY	GLY	TYR	TYR	P227	LEU	GLU
PRO	PRO	THR	THR	P227	TYR	ARG
GLU	GLU	CYS	CYS	Q259	PRO	ILE
GLN	GLN	GLY	GLY	Q259	SER	ASP
PRO	PRO	SER	SER	E387	LEU	LYS
ALA	ALA	PRO	PRO	E387	ALA	GLY
VAL	VAL	VAL	VAL	A389	GLY	GLU
SER	SER	HIS	HIS	G390	VAL	GLU
		THR	THR	P281	GLY	VAL
		GLN	GLN	M392	GLU	GLY
		ALA	ALA	M392	THR	GLY
		GLN	GLN	Y460	GLN	THR
		CYS	CYS	Y460	GLN	VAL
		PRO	PRO	D463	GLY	GLN
		LYS	LYS	R464	GLY	GLN
		ARG	ARG	Q465	ASP	ARG
		LYS	LYS	LYS	THR	ASP
		SER	SER	ALA	PRO	LYS
		GLY	GLY	PRO	PRO	MET
		ASN	ASN	LEU	GLY	ALA
					ALA	PRO

- Molecule 1: DELTAMBD GAG PROTEIN

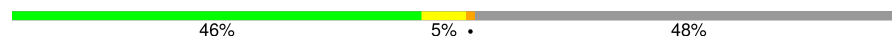
Chain G:



THR	GLN	GLU	THR	SER
GLN	ASP	THR	ALA	ARG
GLU	GLN	THR	ALA	ARG
ILE	GLY	PRO	PRO	GLU
ALA	PRO	LYS	THR	GLN
ALA	GLY	THR	VAL	THR
ALA	HIS	VAL	THR	SER
MET	A211	GLY	GLY	SER
SER	T220	SER	CYS	GLU
SER	D221	CYS	CYS	GLN
ALA	D222	THR	LYS	ALA
ILE	E228	HIS	LYS	ALA
GLN	E228	CYS	TRP	PHE
PRO	E228	CYS	LEU	TRP
LEU	S231	GLY	LEU	GLY
ILE	S231	THR	ALA	LEU
MET	P244	ILE	ILE	GLY
ALA	T245	GLY	GLY	GLY
VAL	T245	CYS	CYS	GLY
VAL	E246	ASN	ASN	ARG
ASN	G247	CYS	CYS	VAL
ARG	L283	CYS	CYS	VAL
GLU	L283	ALA	SER	SER
ARG	T267	THR	PRO	PRO
ASP	K268	ALA	PRO	PRO
GLY	G269	SER	GLY	GLY
GLN	G269	ALA	ALA	PRO
THR	L270	PRO	PRO	GLU
GLY	R271	PRO	PRO	CYS
LYS	S272	PRO	ILE	GLU
GLY	P273	PRO	GLU	GLU
ARG	I274	TYR	LYS	LYS
GLY	I274	VAL	PRO	PRO
ALA	S284	GLY	ALA	ALA
ARG	S284	GLY	ALA	ALA
GLY	A311	SER	THR	THR
PRO	A311	GLY	GLU	GLU
TRP	LEU	LEU	ARG	ARG
PRO	V353	TYR	ARG	ARG
GLY	V353	PRO	ILE	ILE
THR	S974	SER	ASP	ASP
CYS	S974	LEU	LYS	LYS
GLY	A386	ALA	GLY	GLY
PRO	E387	GLY	GLY	GLY
ALA	P388	VAL	GLU	GLU
VAL	P388	VAL	VAL	VAL
SER	P391	GLY	GLY	VAL
HIS	P391	GLU	GLY	GLY
THR	W392	GLN	GLU	GLU
ALA	P399	GLN	THR	THR
GLN	P399	GLY	GLY	VAL
CYS	L451	GLY	GLY	GLN
PRO	L451	GLY	GLY	GLN
LYS	R464	ASP	ASP	ARG
LYS	Q465	THR	THR	ALA
ARG	Q465	PRO	PRO	LYS
LYS	THR	PRO	PRO	MET
SER	ALA	GLY	GLY	ALA
GLY	PRO	ALA	ALA	PRO

- Molecule 1: DELTAMBD GAG PROTEIN

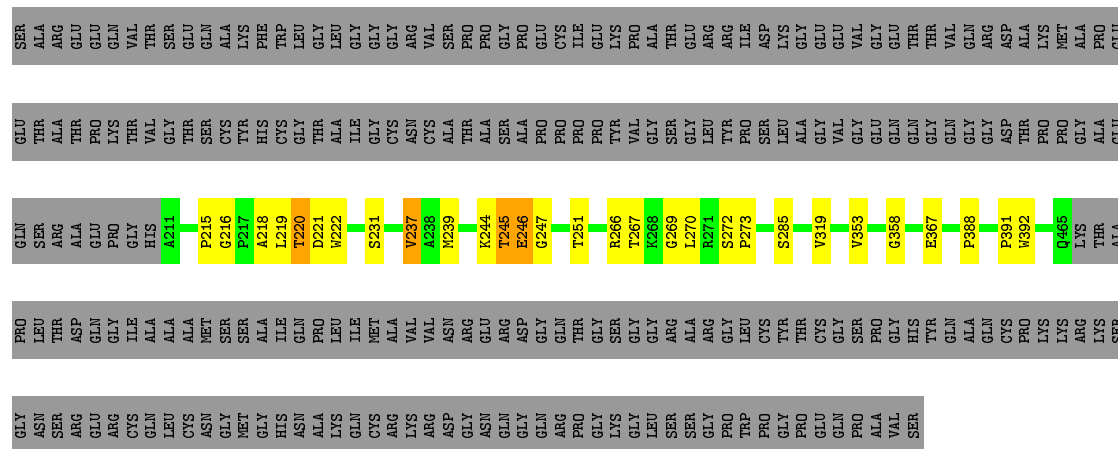
Chain H:



ARG	GLU	ASP	GLN	GLU	THR	SER
GLU	ARG	GLN	SER	ARG	ALA	ALA
CYS	GLY	ILE	ALA	THR	THR	ALA
GLN	ALA	ALA	GLU	PRO	PRO	GLU
LEU	ALA	ALA	GLY	GLY	THR	GLN
CYS	ASN	ALA	HIS	THR	VAL	VAL
ASN	GLY	SER	A211	A212	A213	SER
MET	GLY	SER	Q212	Q213	Q213	GLY
GLY	GLY	ILE	P217	P218	P219	THR
HIS	GLY	ILE	P217	P218	P219	GLN
ASN	ASN	GLN	L219	L219	L219	ALA
ALA	ALA	PRO	A218	A218	A218	GLY
LYS	LYS	LEU	T220	T220	T220	THR
GLN	GLN	ILE	T220	T220	T220	ALA
CYS	CYS	MET	E228	E228	E228	LEU
ARG	ARG	ALA	S231	S231	S231	GLY
LYS	LYS	VAL	S231	S231	S231	GLY
ASP	ASP	ASN	K244	K244	K244	GLY
GLY	GLY	ARG	T245	T245	T245	VAL
ASN	ASN	GLU	E246	E246	E246	ASN
GLN	GLN	ARG	Q247	Q247	Q247	SER
GLY	GLY	GLY	P248	P248	P248	PRO
GLN	GLN	ARG	P248	P248	P248	GLY
ARG	ARG	THR	P252	P252	P252	PRO
PRO	PRO	THR	P252	P252	P252	ALA
GLY	GLY	GLY	T267	T267	T267	PRO
LYS	LYS	SER	K268	K268	K268	GLU
GLY	GLY	GLY	G269	G269	G269	ILE
LEU	LEU	GLY	L270	L270	L270	GLU
SER	SER	ARG	R271	R271	R271	LYS
SER	SER	ALA	S272	S272	S272	PRO
GLY	GLY	ARG	P273	P273	P273	ALA
PRO	PRO	GLY	P289	P289	P289	THR
THR	THR	LEU	P289	P289	P289	SER
CYS	CYS	THR	T289	T289	T289	ARG
THR	THR	THR	P230	P230	P230	ILE
GLU	GLU	CYS	P230	P230	P230	ASP
PRO	PRO	GLY	V383	V383	V383	LYS
PRO	PRO	SER	P388	P388	P388	GLY
ALA	ALA	PRO	P388	P388	P388	GLY
VAL	VAL	GLY	W392	W392	W392	GLU
SER	SER	HIS	I411	I411	I411	VAL
THR	THR	THR	K412	K412	K412	GLY
GLN	GLN	GLN	A413	A413	A413	GLU
ALA	ALA	GLN	A413	A413	A413	THR
CYS	CYS	CYS	D418	D418	D418	VAL
PRO	PRO	PRO	D418	D418	D418	GLN
LYS	LYS	LYS	Q465	Q465	Q465	ARG
LYS	LYS	ARG	LYS	LYS	LYS	ASP
ARG	ARG	THR	THR	THR	THR	ALA
LYS	LYS	THR	THR	THR	THR	ALA
SER	SER	ALA	ALA	ALA	ALA	MET
GLY	GLY	GLY	PRO	PRO	PRO	ALA
ASN	ASN	LEU	LEU	LEU	LEU	PRO

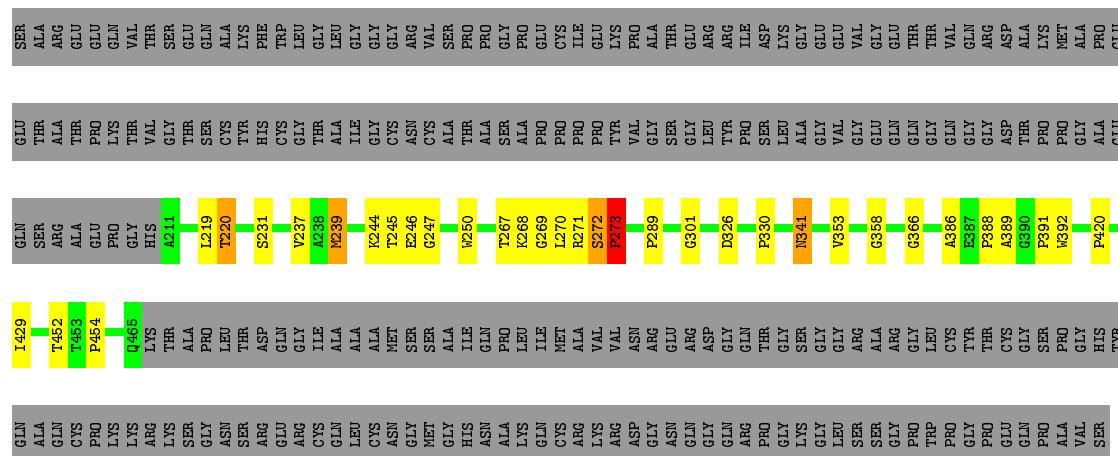
- Molecule 1: DELTAMBD GAG PROTEIN

Chain I:  46% 5% • 48%



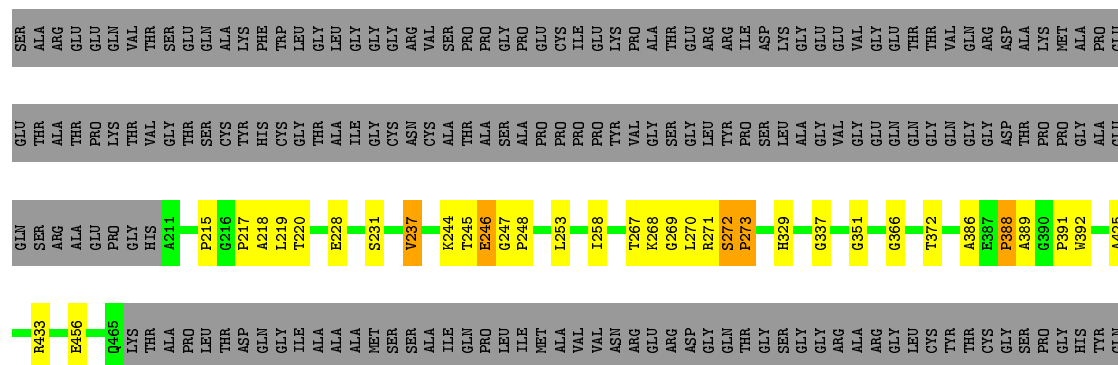
- Molecule 1: DELTAMBD GAG PROTEIN

Chain J: 45% 6% 48%



- Molecule 1: DELTAMBD GAG PROTEIN

Chain K:  44% 6% 48%



ALA	GLN	CYS	PRO	LYS	LYS	ARG	LYS	GLY	ASN	SER	SER	ARG	GLU	ARG	CYS	GLN	LEU	CYS	ASN	GLY	MET	GLY	HIS	ALA	LYS	GLN	CYS	ARG	LYS	ASP	GLY	ASN	GLN	GLY	GLN	ARG	ARG	PRO	GLY	LYS	TRP	PRO	GLY	GLU	GLN	ALA	VAL.
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- 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	PRO	PRO	CYS	ILE	GLU	GLY	LYS	THR	GLU	GLU	ARG	ARG	ILE	ASP	LYS	GLY	GLU	GLU	VAL	VAL	GLY	GLU	THR	THR	VAL	GLN	ARG	ASP	ALA	LYS	MET	ALA	PRO
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GLU	THR	ALA	ALA	PRO	THR	LYS	VAL	GLY	THR	SER	CYS	TYR	HIS	CYS	GLY	THR	ALA	ALA	ILE	GLY	GLY	ASN	CYS	ALA	ALA	THR	SER	SER	PRO	PRO	PRO	TYR	VAL	GLY	SER	LEU	TYR	PRO	SER	LEU	ALA	GLY	VAL	GLY	GLN	GLN	GLY	GLY	GLU	GLN	ASP	THR	PRO	PRO	GLY	ALA	THR
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GLN	SER	ARG	ALA	GLU	PRO	GLY	HIS	A211	A218	L219	L220	D221	D222	E228	S231	A237	W238	W239	K244	T245	E246	G247	L253	T267	K268	G269	L270	R271	S272	P273	P289	P330	G347	V353	P365	S374	A386	P391	K392	S436	G465
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[illegible]

LVS	SER	GLN	ASN	SER	ARG	GLU	ARG	CYS	GLN	LEU	CYS	ASN	GLY	GLY	HIS	ASN	ALA	LVS	GLN	CYS	ARG	LVS	ASP	GLY	ASN	GLN	GLY	GLN	ARG	PRO	GLY	LVS	GLY	LEU	SER	SER	GLY	PRO	TRP	PRO	PRO	GLY	GLU	GLN	PRO	ALA	VAL	SER
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- Molecule 1: DELTAMBD GAG PROTEIN

Chain M:  40% . 56%

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

GLN	SER	ARG	ALA	GLU	PRO	GLY	HIS	ALA	GLY	GLN	ALA	PRO	GLY	PRO	PRO	ALA	LEU	THR	ASP	TRP	ALA	ARG	VAL	ARG	GLU	GLU	LEU	ALA	SER	THR	GLY	PRO	PRO	VAL	VAL	VAL	ILE	LYS	THR	GLU	GLY	PRO	PRO	ALA	T250	T251	L253	T267	K268	T269	L270	R271	S272	P273
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[illegible]

CYS	TYR	THR	THR	CYS	GLY	SER	PRO	GLY	GLY	HIS	TYR	GLN	ALA	GLN	CYS	PRO	LYS	LYS	ARG	LYS	LYS	SER	SER	GLY	ASN	ARG	GLU	ARG	CYS	GLN	LEU	CYS	ASN	ALA	LYS	GLN	CYS	ARG	LYS	ASP	ASP	ARG	PRO	PRO	GLY	GLY	LYS	GLY	LEU	SER	SER	GLY	PRO
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PRO	GLY	PRO	GLU	GLN	PRO	ALA	VAL	SER
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- Molecule 1: DELTAMBD GAG PROTEIN

Chain N: 40% 0% 56%

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

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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

All (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
1	E	333	GLY	N-CA	5.98	1.55	1.46
1	M	355	ASN	N-CA	-5.93	1.34	1.46
1	K	337	GLY	CA-C	-5.90	1.42	1.51
1	O	354	GLY	CA-C	-5.89	1.42	1.51
1	J	454	PRO	N-CA	-5.84	1.37	1.47
1	E	304	PRO	CA-C	-5.59	1.41	1.52
1	H	252	PRO	CA-C	5.58	1.64	1.52
1	I	215	PRO	C-N	5.58	1.43	1.33
1	J	452	THR	N-CA	5.56	1.57	1.46
1	D	313	GLY	CA-C	-5.56	1.43	1.51
1	B	366	GLY	CA-C	-5.51	1.43	1.51
1	D	397	GLN	CA-C	-5.48	1.38	1.52
1	J	429	ILE	N-CA	-5.43	1.35	1.46
1	I	358	GLY	CA-C	-5.42	1.43	1.51
1	J	366	GLY	N-CA	-5.40	1.38	1.46
1	O	366	GLY	CA-C	-5.40	1.43	1.51
1	L	365	PRO	CA-C	-5.36	1.42	1.52
1	O	362	LEU	N-CA	-5.35	1.35	1.46
1	E	269	GLY	N-CA	-5.32	1.38	1.46
1	D	343	ASN	N-CA	-5.30	1.35	1.46
1	K	389	ALA	N-CA	-5.30	1.35	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	N	313	GLY	N-CA	5.29	1.53	1.46
1	K	433	ARG	N-CA	-5.28	1.35	1.46
1	F	359	GLN	CA-C	5.25	1.66	1.52
1	L	347	GLY	CA-C	-5.25	1.43	1.51
1	R	398	GLY	CA-C	-5.22	1.43	1.51
1	Q	347	GLY	CA-C	-5.20	1.43	1.51
1	N	337	GLY	CA-C	-5.08	1.43	1.51
1	D	333	GLY	CA-C	-5.07	1.43	1.51
1	Q	416	GLY	CA-C	-5.04	1.43	1.51
1	K	366	GLY	N-CA	-5.02	1.38	1.46

All (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
1	K	329	HIS	N-CA-C	6.64	128.94	111.00
1	B	385	LEU	N-CA-C	6.64	128.93	111.00
1	O	444	ILE	O-C-N	-6.46	112.36	122.70
1	H	212	GLY	C-N-CA	6.42	137.76	121.70
1	D	217	PRO	O-C-N	-6.41	112.44	122.70
1	J	239	MET	CA-C-N	6.33	134.84	117.10
1	K	215	PRO	C-N-CA	6.27	135.46	122.30
1	E	217	PRO	C-N-CA	6.25	137.34	121.70
1	B	217	PRO	C-N-CA	6.25	137.32	121.70
1	J	358	GLY	O-C-N	-6.23	112.72	122.70
1	G	284	SER	O-C-N	-6.22	112.75	122.70
1	M	384	ARG	O-C-N	-6.18	112.81	122.70
1	K	217	PRO	O-C-N	-6.17	112.82	122.70
1	D	273	PRO	N-CA-C	6.17	128.14	112.10
1	D	239	MET	CA-C-N	6.16	134.35	117.10
1	G	399	PRO	C-N-CA	6.13	137.03	121.70
1	G	253	LEU	N-CA-C	6.11	127.50	111.00
1	K	258	ILE	O-C-N	-6.11	112.93	122.70
1	F	463	ASP	O-C-N	-6.03	113.05	122.70
1	G	374	SER	O-C-N	-6.03	113.06	122.70
1	F	220	THR	C-N-CA	6.01	136.73	121.70
1	M	382	VAL	O-C-N	-5.93	113.22	122.70
1	I	319	VAL	O-C-N	-5.89	113.27	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	396	MET	O-C-N	-5.88	113.29	122.70
1	N	390	GLY	CA-C-N	5.80	133.35	117.10
1	P	396	MET	N-CA-C	-5.80	95.34	111.00
1	B	416	GLY	O-C-N	-5.78	113.45	122.70
1	H	289	PRO	N-CA-C	5.78	127.13	112.10
1	L	289	PRO	N-CA-C	5.78	127.11	112.10
1	Q	261	LEU	O-C-N	-5.76	113.48	122.70
1	K	237	VAL	N-CA-C	5.76	126.55	111.00
1	A	220	THR	C-N-CA	5.74	136.06	121.70
1	K	351	GLY	O-C-N	-5.73	113.53	122.70
1	D	211	ALA	CA-C-N	5.72	127.64	116.20
1	M	342	LEU	O-C-N	-5.71	113.56	122.70
1	M	387	GLU	CA-C-N	5.68	133.00	117.10
1	A	239	MET	O-C-N	-5.67	110.32	121.10
1	C	253	LEU	N-CA-C	5.65	126.26	111.00
1	Q	271	ARG	N-CA-C	-5.64	95.76	111.00
1	Q	434	GLN	O-C-N	-5.63	113.69	122.70
1	J	341	ASN	N-CA-C	5.62	126.17	111.00
1	G	311	ALA	O-C-N	-5.61	113.73	122.70
1	D	390	GLY	N-CA-C	-5.59	99.12	113.10
1	A	461	VAL	C-N-CA	5.55	135.59	121.70
1	K	388	PRO	N-CA-C	5.55	126.53	112.10
1	D	398	GLY	N-CA-C	-5.54	99.25	113.10
1	I	367	GLU	O-C-N	-5.54	113.84	122.70
1	D	215	PRO	O-C-N	-5.51	113.83	123.20
1	I	216	GLY	CA-C-O	-5.51	110.69	120.60
1	I	237	VAL	N-CA-C	5.50	125.86	111.00
1	N	383	ALA	N-CA-C	5.50	125.86	111.00
1	K	425	ALA	CA-C-N	5.46	132.39	117.10
1	F	390	GLY	N-CA-C	-5.46	99.46	113.10
1	F	234	PRO	CA-C-N	5.41	132.25	117.10
1	F	246	GLU	O-C-N	-5.40	114.02	123.20
1	I	251	THR	O-C-N	-5.39	110.86	121.10
1	K	372	THR	O-C-N	-5.38	114.08	122.70
1	N	265	VAL	C-N-CA	5.36	135.10	121.70
1	C	282	LEU	O-C-N	-5.36	114.13	122.70
1	I	220	THR	C-N-CA	5.36	135.09	121.70
1	M	446	THR	O-C-N	-5.35	114.14	122.70
1	L	237	VAL	N-CA-C	5.32	125.36	111.00
1	A	221	ASP	N-CA-C	5.32	125.35	111.00
1	R	275	THR	CA-C-O	5.30	131.24	120.10
1	N	333	GLY	N-CA-C	5.29	126.33	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	Q	402	SER	O-C-N	-5.29	114.24	122.70
1	K	456	GLU	O-C-N	-5.27	114.26	122.70
1	A	239	MET	CA-C-N	5.27	131.86	117.10
1	D	211	ALA	O-C-N	-5.25	114.28	123.20
1	D	222	TRP	N-CA-C	5.25	125.17	111.00
1	L	239	MET	CA-C-N	5.24	131.76	117.10
1	I	266	ARG	C-N-CA	5.22	134.76	121.70
1	J	220	THR	O-C-N	-5.20	114.38	122.70
1	Q	350	ASP	C-N-CA	5.19	133.20	122.30
1	R	425	ALA	CA-C-N	5.19	131.63	117.10
1	J	289	PRO	CA-C-N	5.19	128.61	117.20
1	K	215	PRO	CA-C-N	5.19	126.58	116.20
1	P	378	ALA	O-C-N	-5.18	114.41	122.70
1	N	275	THR	O-C-N	5.17	130.97	122.70
1	A	421	PRO	C-N-CA	5.16	134.61	121.70
1	L	374	SER	O-C-N	-5.16	114.44	122.70
1	J	273	PRO	N-CA-C	5.16	125.51	112.10
1	P	264	THR	O-C-N	-5.16	114.45	122.70
1	C	267	THR	O-C-N	-5.15	114.47	122.70
1	A	244	LYS	O-C-N	-5.14	114.47	122.70
1	E	243	ILE	C-N-CA	5.14	134.54	121.70
1	P	289	PRO	O-C-N	-5.13	114.48	122.70
1	H	413	ALA	O-C-N	-5.13	114.49	122.70
1	E	273	PRO	N-CA-C	5.12	125.42	112.10
1	K	246	GLU	O-C-N	-5.12	114.49	123.20
1	K	218	ALA	N-CA-C	5.12	124.82	111.00
1	D	446	THR	O-C-N	-5.10	114.54	122.70
1	J	389	ALA	CA-C-N	5.09	126.39	116.20
1	D	425	ALA	CA-C-N	5.09	131.34	117.10
1	H	411	ILE	O-C-N	-5.08	114.58	122.70
1	A	247	GLY	CA-C-N	5.07	131.29	117.10
1	O	349	ALA	O-C-N	-5.07	114.59	122.70
1	F	246	GLU	CA-C-N	5.06	126.33	116.20
1	F	460	TYR	O-C-N	-5.06	114.61	122.70
1	F	323	ALA	O-C-N	-5.05	114.62	122.70
1	D	419	LEU	O-C-N	-5.05	111.51	121.10
1	K	389	ALA	N-CA-C	-5.03	97.43	111.00
1	G	274	ILE	O-C-N	-5.02	114.67	122.70
1	F	389	ALA	O-C-N	-5.02	114.67	123.20
1	M	389	ALA	N-CA-C	-5.02	97.45	111.00
1	P	308	TRP	O-C-N	-5.02	114.67	122.70
1	D	234	PRO	CA-C-O	-5.01	108.17	120.20

There are no chirality outliers.

All (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
1	A	246	GLU	Peptide
1	A	247	GLY	Peptide
1	A	268	LYS	Peptide
1	A	269	GLY	Peptide
1	A	270	LEU	Peptide
1	A	272	SER	Peptide
1	B	220	THR	Peptide
1	B	221	ASP	Peptide
1	B	244	LYS	Peptide
1	B	245	THR	Peptide
1	B	246	GLU	Peptide
1	B	247	GLY	Peptide
1	B	268	LYS	Peptide
1	B	272	SER	Peptide
1	B	273	PRO	Peptide
1	B	386	ALA	Peptide
1	C	219	LEU	Peptide
1	C	220	THR	Peptide
1	C	221	ASP	Peptide
1	C	244	LYS	Peptide
1	C	245	THR	Peptide
1	C	246	GLU	Peptide
1	C	268	LYS	Peptide
1	C	269	GLY	Peptide
1	C	270	LEU	Peptide
1	C	272	SER	Peptide
1	D	220	THR	Peptide
1	D	244	LYS	Peptide
1	D	245	THR	Peptide
1	D	246	GLU	Peptide
1	D	247	GLY	Peptide
1	D	268	LYS	Peptide
1	D	269	GLY	Peptide
1	D	270	LEU	Peptide
1	D	272	SER	Peptide

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Mol	Chain	Res	Type	Group
1	E	219	LEU	Peptide
1	E	220	THR	Peptide
1	E	242	VAL	Peptide
1	E	244	LYS	Peptide
1	E	245	THR	Peptide
1	E	246	GLU	Peptide
1	E	247	GLY	Peptide
1	E	268	LYS	Peptide
1	E	269	GLY	Peptide
1	E	270	LEU	Peptide
1	E	272	SER	Peptide
1	E	273	PRO	Peptide
1	F	219	LEU	Peptide
1	F	220	THR	Peptide
1	F	244	LYS	Peptide
1	F	245	THR	Peptide
1	F	246	GLU	Peptide
1	F	247	GLY	Peptide
1	F	268	LYS	Peptide
1	F	269	GLY	Peptide
1	F	270	LEU	Peptide
1	F	272	SER	Peptide
1	F	283	MET	Mainchain
1	G	220	THR	Peptide
1	G	244	LYS	Peptide
1	G	245	THR	Peptide
1	G	246	GLU	Peptide
1	G	247	GLY	Peptide
1	G	268	LYS	Peptide
1	G	269	GLY	Mainchain
1	G	270	LEU	Peptide
1	G	272	SER	Peptide
1	G	273	PRO	Peptide
1	G	386	ALA	Peptide
1	G	388	PRO	Mainchain
1	G	464	ARG	Mainchain
1	H	220	THR	Peptide
1	H	244	LYS	Peptide
1	H	245	THR	Mainchain,Peptide
1	H	246	GLU	Peptide
1	H	247	GLY	Peptide
1	H	268	LYS	Peptide

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Mol	Chain	Res	Type	Group
1	H	269	GLY	Peptide
1	H	270	LEU	Peptide
1	H	272	SER	Peptide
1	H	273	PRO	Peptide
1	I	220	THR	Peptide
1	I	244	LYS	Peptide
1	I	245	THR	Peptide
1	I	246	GLU	Peptide
1	I	247	GLY	Peptide
1	I	269	GLY	Peptide
1	I	270	LEU	Peptide
1	I	272	SER	Peptide
1	I	285	SER	Mainchain
1	J	219	LEU	Mainchain
1	J	220	THR	Mainchain,Peptide
1	J	244	LYS	Peptide
1	J	245	THR	Peptide
1	J	246	GLU	Peptide
1	J	247	GLY	Peptide
1	J	268	LYS	Peptide
1	J	269	GLY	Mainchain
1	J	270	LEU	Peptide
1	J	272	SER	Peptide
1	J	273	PRO	Peptide
1	J	301	GLY	Mainchain
1	K	219	LEU	Peptide
1	K	220	THR	Peptide
1	K	244	LYS	Peptide
1	K	245	THR	Peptide
1	K	246	GLU	Peptide
1	K	247	GLY	Peptide
1	K	268	LYS	Peptide
1	K	269	GLY	Peptide
1	K	270	LEU	Peptide
1	K	272	SER	Peptide
1	K	273	PRO	Peptide
1	L	219	LEU	Peptide
1	L	220	THR	Peptide
1	L	244	LYS	Peptide
1	L	245	THR	Peptide
1	L	246	GLU	Peptide
1	L	247	GLY	Peptide

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Mol	Chain	Res	Type	Group
1	L	268	LYS	Peptide
1	L	269	GLY	Peptide
1	L	270	LEU	Peptide
1	L	272	SER	Peptide
1	L	273	PRO	Peptide
1	M	269	GLY	Peptide
1	M	270	LEU	Peptide
1	M	272	SER	Peptide
1	N	268	LYS	Peptide
1	N	269	GLY	Peptide
1	N	272	SER	Peptide
1	N	273	PRO	Peptide
1	O	268	LYS	Peptide
1	O	269	GLY	Peptide
1	O	270	LEU	Peptide
1	O	272	SER	Peptide
1	O	273	PRO	Peptide
1	P	269	GLY	Peptide
1	P	270	LEU	Peptide
1	P	272	SER	Peptide
1	P	273	PRO	Peptide
1	Q	268	LYS	Peptide
1	Q	269	GLY	Mainchain
1	Q	270	LEU	Peptide
1	Q	272	SER	Peptide
1	Q	273	PRO	Peptide
1	Q	386	ALA	Peptide
1	R	269	GLY	Peptide
1	R	270	LEU	Peptide
1	R	272	SER	Peptide
1	R	288	LEU	Mainchain
1	R	386	ALA	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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 [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	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

All (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
1	A	327	PRO
1	A	392	TRP
1	B	246	GLU
1	B	267	THR
1	B	273	PRO
1	B	385	LEU
1	C	253	LEU
1	C	267	THR
1	C	386	ALA
1	C	392	TRP

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Mol	Chain	Res	Type
1	D	273	PRO
1	D	386	ALA
1	E	267	THR
1	E	273	PRO
1	F	246	GLU
1	F	273	PRO
1	F	392	TRP
1	G	221	ASP
1	G	245	THR
1	G	253	LEU
1	G	273	PRO
1	H	246	GLU
1	H	273	PRO
1	I	237	VAL
1	I	245	THR
1	I	273	PRO
1	I	353	VAL
1	I	388	PRO
1	I	392	TRP
1	J	237	VAL
1	J	273	PRO
1	J	353	VAL
1	J	388	PRO
1	K	237	VAL
1	K	267	THR
1	K	392	TRP
1	L	237	VAL
1	L	267	THR
1	L	273	PRO
1	L	386	ALA
1	M	273	PRO
1	M	392	TRP
1	N	273	PRO
1	N	392	TRP
1	O	273	PRO
1	O	392	TRP
1	P	267	THR
1	P	273	PRO
1	P	392	TRP
1	Q	386	ALA
1	Q	392	TRP
1	R	253	LEU

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Mol	Chain	Res	Type
1	R	267	THR
1	R	273	PRO
1	R	392	TRP
1	R	419	LEU
1	A	221	ASP
1	A	250	TRP
1	A	253	LEU
1	A	420	PRO
1	B	215	PRO
1	B	237	VAL
1	B	392	TRP
1	C	221	ASP
1	C	223	ALA
1	C	237	VAL
1	C	273	PRO
1	C	334	GLN
1	C	353	VAL
1	D	267	THR
1	D	392	TRP
1	E	237	VAL
1	E	392	TRP
1	E	436	SER
1	F	267	THR
1	F	271	ARG
1	F	327	PRO
1	F	388	PRO
1	G	267	THR
1	G	271	ARG
1	G	272	SER
1	G	392	TRP
1	H	267	THR
1	H	353	VAL
1	H	388	PRO
1	H	392	TRP
1	H	418	ASP
1	I	218	ALA
1	I	221	ASP
1	I	222	TRP
1	I	231	SER
1	J	267	THR
1	J	271	ARG
1	J	272	SER

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Mol	Chain	Res	Type
1	J	341	ASN
1	J	392	TRP
1	J	420	PRO
1	L	218	ALA
1	L	271	ARG
1	L	272	SER
1	M	253	LEU
1	M	267	THR
1	M	269	GLY
1	N	253	LEU
1	N	267	THR
1	O	252	PRO
1	O	267	THR
1	P	269	GLY
1	Q	267	THR
1	R	386	ALA
1	R	449	SER
1	A	231	SER
1	A	252	PRO
1	A	385	LEU
1	B	244	LYS
1	B	327	PRO
1	B	420	PRO
1	C	252	PRO
1	D	228	GLU
1	D	244	LYS
1	E	244	LYS
1	F	387	GLU
1	G	388	PRO
1	H	231	SER
1	I	267	THR
1	J	250	TRP
1	K	271	ARG
1	K	272	SER
1	K	391	PRO
1	L	222	TRP
1	L	231	SER
1	L	253	LEU
1	L	391	PRO
1	L	392	TRP
1	L	436	SER
1	M	252	PRO

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Mol	Chain	Res	Type
1	N	252	PRO
1	N	387	GLU
1	N	390	GLY
1	O	253	LEU
1	O	270	LEU
1	O	272	SER
1	P	330	PRO
1	Q	387	GLU
1	Q	390	GLY
1	B	231	SER
1	D	271	ARG
1	D	388	PRO
1	E	231	SER
1	E	246	GLU
1	F	231	SER
1	G	222	TRP
1	G	451	LEU
1	H	228	GLU
1	H	248	PRO
1	H	272	SER
1	I	246	GLU
1	J	231	SER
1	K	228	GLU
1	K	231	SER
1	K	273	PRO
1	K	386	ALA
1	L	228	GLU
1	L	353	VAL
1	M	268	LYS
1	Q	449	SER
1	A	223	ALA
1	C	246	GLU
1	C	330	PRO
1	D	253	LEU
1	F	239	MET
1	G	228	GLU
1	G	231	SER
1	G	353	VAL
1	H	213	GLN
1	H	330	PRO
1	J	386	ALA
1	K	248	PRO

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Mol	Chain	Res	Type
1	K	253	LEU
1	K	388	PRO
1	N	386	ALA
1	O	449	SER
1	R	452	THR
1	A	239	MET
1	C	231	SER
1	D	231	SER
1	E	239	MET
1	E	388	PRO
1	E	391	PRO
1	F	228	GLU
1	H	218	ALA
1	I	219	LEU
1	J	330	PRO
1	L	330	PRO
1	N	286	PRO
1	D	239	MET
1	G	391	PRO
1	Q	333	GLY
1	B	239	MET
1	I	391	PRO
1	J	239	MET
1	C	239	MET
1	J	391	PRO
1	L	239	MET
1	I	239	MET

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.