



Full wwPDB EM Validation Report ⓘ

Jun 28, 2026 – 12:53 AM JST

PDB ID : 9VXZ / pdb_00009vxz
EMDB ID : EMD-65446
Title : Cryo-EM structure of Measles Virus L Protein bound by Phosphoprotein Tetramer
Authors : Xue, L.; Gui, J.; Chang, T.; Pan, H.; Xiong, X.
Deposited on : 2025-07-20
Resolution : 2.68 Å(reported)

This is a Full wwPDB EM Validation 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 : **FAILED**
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

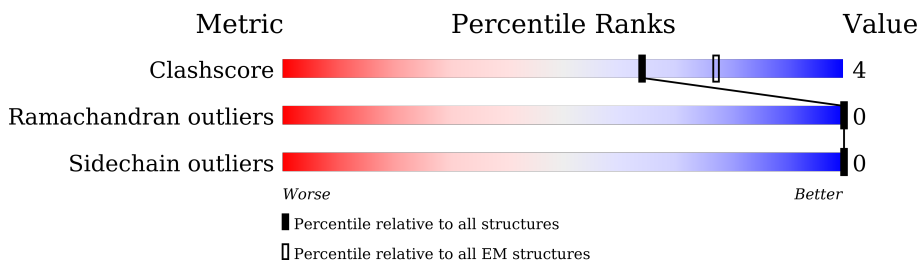
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.68 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	2183	
2	B	507	
2	C	507	
2	D	507	
2	E	507	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12553 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 RNA-directed RNA polymerase L.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1255	Total	C	N	O	S	0	0
			10082	6445	1743	1839	55		

- Molecule 2 is a protein called Phosphoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	148	Total	C	N	O	S	0	0
			1159	736	208	210	5		
2	C	47	Total	C	N	O	S	0	0
			372	233	65	73	1		
2	D	67	Total	C	N	O	S	0	0
			514	322	87	104	1		
2	E	55	Total	C	N	O	S	0	0
			425	269	74	81	1		

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
3	A	1	Total	Zn	0
			1	1	



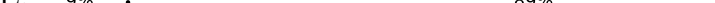
PRO	LEU	GLU	THR	ASP	LYS
ASP	LYS	GLU	GLY	VAL	GLY
THR	PRO	GLY	ILE	GLU	GLN
GLY	ILE	GLY	ASP	ALA	ASP
PRO	ILE	GLY	TYR	LEU	ALA
ALA	ARG	TYR	ASP	GLY	ASP
SER	ARG	ASP	THR	LEU	ASP
ARG	ASP	ASP	THR	GLY	SER
SER	SER	GLY	GLY	ILE	MET
VAL	GLY	GLU	ASP	ILE	MET
ILE	ARG	LEU	PHE	HIS	VAL
ARG	ALA	PHE	SER	GLU	GLN
SER	LEU	SER	GLN	LEU	SER
ILE	ALA	ASP	CYS	LEU	SER
ILE	GLY	VAL	ALA	LYS	LEU
LYS	VAL	GLN	ARG	ASP	ASP
VAL	LEU	ASP	LYS	GLN	GLY
SER	LYS	ILE	SER	SER	GLY
SER	LYS	LYS	PRO	ARG	SER
ARG	LYS	THR	SER	GLY	THR
GLU	VAL	ALA	GLU	ASN	LEU
GLU	ALA	LEU	PRO	ASN	SER
ASP	SER	ALA	SER	PHE	GLY
ARG	ARG	LYS	PRO	GLY	GLY
LYS	GLN	1825	PRO	LYS	ASP
ARG	LEU	D828	GLY	LEU	GLU
TYR	GLN		ALA	GLY	ASP
LEU	GLY	K331	PRO	LYS	GLU
MET	MET	1332	ALA	THR	GLU
THR	THR		GLY	LEU	ASN
LEU	ASN	1363	ASN	ASN	SER
GLY	GLY		VAL	ASP	ASP
ASP	ARG	L363	PRO	PRO	VAL
ARG	THR		GLU	PRO	ASP
ILE	SER	L367	CYS	PRO	ILE
LYS	SER		VAL	PRO	GLY
GLY	ARG	M371	SER	ASN	GLU
ALA	GLY		ASN	GLU	PRO
ASN	GLN	ILE	ALA	SER	ASP
ASP	LEU	ALA	ALA	THR	ARG
LEU	LEU	ILE	LEU	ALA	GLU
ALA	LYS	PRO	ILE	SER	GLY
LYS	GLU	GLY	GLN	SER	TYR
PHE	PHE	LEU	GLU	THR	THR
HIS	GLN	GLY	TRP	GLU	ILE
GLN	LEU	LYS	THR	THR	THR
MET	LYS	ASP	PRO	PRO	ASP
LEU	LEU	PRO	GLU	ILE	ARG
MET	ILE	ASN	SER	LYS	GLY
MET	LYS	ASP	GLY	SER	ALA
ILE	LYS	PRO	THR	THR	ALA
ILE	LYS	THR	THR	THR	PRO
MET	VAL	ALA	ILE	ASP	ILE
LYS	SER	ASP	SER	ALA	SER
	SER	VAL	PRO	ARG	MET
	ALA	GLU	ARG	LEU	GLY
	VAL	LEU	ARG	ALA	PHE
	GLY	ASN	SER	ALA	ARG
	GLY	ASN	GLN	SER	ASN
	PHE	PRO	ASN	PHE	ALA
	VAL	ASP	THR	GLY	SER

- Molecule 2: Phosphoprotein

Chain D: 11% . 87%

ARG	SER	ALA	GLU	THR	ASP	LYS	SER	MET
SER	ILE	LEU	GLU	GLU	VAL	GLY	LYS	ALA
ILE	GLY	ALA	ILE	ILE	THR	ILE	PRO	GLU
LYS	VAL	GLY	SER	SER	ALA	ASP	GLN	CYS
SER	LEU	LEU	TYR	LEU	GLU	ALA	SER	LEU
SER	LYS	TYR	TYR	LEU	GLY	ASP	ALA	SER
ARG	LEU	ASP	ASP	THR	GLY	SER	ILE	ARG
LEU	PRO	ASP	ASP	GLY	GLU	ILE	GLY	VAL
GLU	VAL	GLY	GLU	GLY	ILE	VAL	THR	ASN
ALA	ALA	LEU	PHE	THR	GLU	GLN	GLY	GLY
SER	SER	SER	SER	GLN	LEU	SER	GLY	LEU
ARG	ARG	ARG	SER	THR	LEU	GLY	GLY	LEU
LYS	LYS	GLN	ASP	CYS	LEU	GLY	GLY	CYS
ARG	ARG	LEU	VAL	ALA	LYS	LEU	ALA	ALA
TYR	TYR	GLN	GLN	ARG	LEU	ASP	PRO	ILE
LEU	LEU	ASP	ASP	LYS	GLN	GLY	ARG	ARG
MET	MET	ILE	ILE	SER	SER	ASP	ILE	ALA
THR	THR	THR	LYS	PRO	ARG	SER	ARG	LEU
LEU	LEU	ASN	THR	SER	GLY	THR	GLY	LYS
LEU	LEU	GLY	ALA	GLU	ASN	LEU	GLN	ALA
ASP	ASP	ARG	LEU	PRO	ASN	SER	GLY	GLU
THR	THR	THR	ALA	SER	PHE	GLY	SER	PRO
ILE	ILE	SER	LYS	GLY	PRO	ASP	GLY	ILE
LYS	LYS	SER	I325	PRO	LYS	ASP	GLU	GLY
GLY	GLY	ALA	I332	GLY	LEU	ASP	SER	SER
ASN	ASN	GLN	E347	PRO	LYS	SER	ASP	ALA
ASP	ASP	LEU	E347	ALA	THR	GLU	ASP	VAL
LEU	LEU	LEU	K351	GLY	LEU	ASN	ALA	GLU
ALA	LYS	LYS	Q352	ASN	ASN	SER	GLU	GLU
LYS	LYS	PHE	Q352	VAL	VAL	ASP	THR	ALA
PHE	PHE	GLN	R355	PRO	PRO	VAL	LEU	MET
HIS	HIS	GLN	R355	GLU	PRO	ASP	GLY	ALA
GLN	GLN	LEU	L363	CYS	PRO	ILE	ILE	ALA
MET	MET	LYS	L363	VAL	PRO	GLY	PRO	TRP
LEU	LEU	PRO	L367	SER	ASN	GLU	SER	SER
MET	MET	ILE	L367	ASN	PRO	PRO	ARG	GLU
LYS	LYS	GLY	I372	ALA	SER	ASN	ILE	ILE
ILE	ILE	LYS	I372	ALA	ARG	THR	LEU	SER
LYS	LYS	LYS	G376	LEU	ALA	GLU	GLN	ASP
MET	MET	VAL	G376	ILE	SER	GLY	ALA	ASN
LYS	LYS	SER	LYS	THR	THR	TYR	PRO	PRO
SER	SER	SER	ASP	GLN	THR	GLY	SER	GLY
ALA	ALA	ALA	PRO	GLU	GLU	ALA	GLY	GLY
VAL	VAL	VAL	R382	THR	THR	THR	THR	ASP
GLY	GLY	PHE	V388	PRO	PRO	ASP	LEU	ARG
PHE	PHE	VAL	V388	GLU	ILE	ARG	GLN	ALA
VAL	VAL	VAL	L394	SER	LYS	GLY	CYS	THR
PRO	PRO	PRO	L394	GLY	LYS	SER	TYR	GLY
THR	THR	THR	PRO	THR	GLY	ALA	HIS	CYS
GLY	GLY	ILE	ILE	ILE	ASP	ILE	VAL	GLU
PRO	PRO	ILE	ILE	SER	ALA	SER	TYR	GLU
ALA	ALA	GLY	GLY	PRO	ARG	MET	HIS	ALA
SER	SER	ARG	ARG	ARG	LEU	GLY	SER	ALA
ARG	ARG	ASP	ASP	ALA	ALA	PHE	GLY	SER
SER	SER	SER	SER	GLN	SER	ARG	GLY	SER
VAL	VAL	GLY	GLY	ASN	PHE	THR	GLU	GLY
ILE	ILE	THR	ARG	ASN	CYS	SER	ALA	THR

- Molecule 2: Phosphoprotein

Chain E:  9% . 89%

[illegible]

GLY	THR	ASP
PRO	VAL	THR
ALA	ILE	GLY
ARG	GLY	ALA
ARG	THR	THR
VAL	ALA	ASP
ILE	LEU	ASP
ARG	LEU	TYR
ARG	THR	TYR
ALA	THR	ASP
LEU	GLY	ASP
ILE	GLY	LEU
ILE	ALA	LEU
ILE	ALA	PHE
LYS	THR	SER
SER	GLN	ASP
SER	LEU	VAL
ARG	LYS	GLN
LEU	ARG	ASP
LEU	LYS	ASP
GLU	GLN	ILE
GLU	SER	ILE
ASP	PRO	LYS
GLY	THR	THR
ARG	SER	ALA
LYS	GLU	ALA
ARG	PRO	LEU
TYR	SER	ALA
LEU	GLY	LYS
MET	PRO	GLY
THR	GLY	I325
LEU	ALA	N329
LEU	PRO	I332
ASP	ALA	I333
ASP	GLY	L336
ILE	ASN	Q356
LYS	VAL	L363
GLY	PRO	I370
ALA	ASN	I374
LYS	ALA	P375
PHE	LEU	K379
HIS	THR	ASP
GLN	SER	PRO
LEU	GLU	ASN
LYS	THR	ASP
PRO	TRP	PRO
ILE	THR	ASN
GLY	PRO	ASP
LYS	PRO	PRO
VAL	ILE	PRO
SER	GLY	THR
SER	THR	ALA
ALA	ILE	ASP
VAL	ASP	PRO
GLY	ARG	PRO
PHE	LEU	ASP
VAL	SER	LEU
PRO	GLN	LYS
ASP	ASN	THR
THR	GLY	ASN

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	4035198	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	TFS FALCON 4i (4k x 4k)	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.13	0/10307	0.32	0/13966
2	B	0.13	0/1168	0.34	0/1556
2	C	0.17	0/373	0.35	0/497
2	D	0.16	0/517	0.35	0/696
2	E	0.18	0/427	0.43	0/570
All	All	0.13	0/12792	0.32	0/17285

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	10082	0	10102	76	0
2	B	1159	0	1261	21	0
2	C	372	0	398	7	0
2	D	514	0	535	8	0
2	E	425	0	462	9	0
3	A	1	0	0	0	0
All	All	12553	0	12758	103	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 4.

All (103) 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:1180:CYS:SG	1:A:1364:HIS:HE1	2.11	0.71
2:B:356:GLN:HE21	2:E:356:GLN:HE22	1.37	0.69
2:B:434:LEU:HD23	2:B:436:GLU:H	1.60	0.67
2:B:342:LEU:HA	2:B:345:GLU:HG2	1.76	0.66
1:A:1397:LEU:HD12	1:A:1398:ILE:HG23	1.76	0.66
1:A:989:SER:H	1:A:1147:ARG:HH22	1.45	0.63
2:D:352:GLN:HG2	2:D:355:ARG:HH22	1.63	0.63
1:A:933:LEU:HD12	1:A:934:PRO:HD2	1.80	0.62
1:A:1081:THR:HG22	1:A:1085:LEU:HD23	1.81	0.62
1:A:1190:PHE:HB2	1:A:1361:LEU:HB3	1.83	0.60
2:C:363:LEU:HD23	2:D:363:LEU:HD22	1.86	0.58
1:A:1109:GLU:HG2	1:A:1112:ARG:HH21	1.68	0.57
1:A:530:LEU:HB3	1:A:705:LEU:HD22	1.86	0.57
1:A:457:ASP:HA	1:A:1029:MET:HE1	1.86	0.57
2:E:329:ASN:HA	2:E:332:ILE:HG12	1.86	0.57
1:A:197:THR:HA	1:A:202:GLU:HG2	1.87	0.56
1:A:1057:PRO:HG2	1:A:1157:LEU:HD11	1.88	0.56
2:B:339:LEU:HA	2:B:342:LEU:HD23	1.88	0.56
1:A:266:ASP:HA	1:A:269:PHE:HD2	1.71	0.54
1:A:1269:VAL:HG21	1:A:1274:LEU:HD13	1.88	0.53
1:A:1302:THR:HG22	1:A:1304:LEU:H	1.73	0.53
1:A:456:LEU:HD13	1:A:510:PRO:HB2	1.91	0.52
1:A:1009:ILE:HG23	1:A:1103:LEU:HD22	1.91	0.52
1:A:14:VAL:HG11	1:A:856:TRP:HB2	1.92	0.52
1:A:27:ALA:HB2	1:A:45:LEU:HD21	1.92	0.51
1:A:1392:LEU:HD23	1:A:1394:THR:H	1.75	0.51
1:A:656:VAL:HG21	1:A:792:LYS:HB3	1.93	0.51
1:A:929:ARG:HH12	1:A:1118:LEU:HB3	1.75	0.51
1:A:289:ALA:HB2	1:A:304:PHE:HD2	1.76	0.50
2:B:488:ILE:HG22	2:B:494:LEU:HD12	1.92	0.50
1:A:681:GLN:HG2	2:D:372:ILE:HD13	1.94	0.50
1:A:30:GLU:HB3	1:A:49:ILE:HG21	1.94	0.49
1:A:1166:MET:HG2	1:A:1365:VAL:HG22	1.93	0.49
1:A:16:LEU:HD22	1:A:230:MET:HB2	1.95	0.49
1:A:307:HIS:ND1	1:A:821:ASN:HB3	2.27	0.49
2:E:333:ILE:HA	2:E:336:LEU:HG	1.95	0.49
1:A:460:LEU:HD21	1:A:1029:MET:HG2	1.93	0.49
2:C:328:ASP:O	2:C:332:ILE:HG12	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:762:SER:HB3	1:A:806:ILE:HD12	1.95	0.49
1:A:853:CYS:HB2	1:A:874:THR:HG21	1.94	0.49
1:A:333:ALA:O	1:A:337:ILE:HG13	2.13	0.49
1:A:1062:GLU:HG2	1:A:1244:VAL:HG21	1.94	0.48
2:C:367:LEU:HD21	2:D:367:LEU:HD11	1.95	0.48
2:B:375:PRO:HD2	2:B:438:GLN:HE22	1.78	0.48
1:A:193:PRO:HB2	1:A:204:LEU:HD11	1.95	0.48
1:A:781:LYS:HD2	1:A:799:VAL:HG11	1.96	0.48
1:A:752:ILE:HA	1:A:755:LEU:HD12	1.95	0.47
1:A:832:TYR:HE1	1:A:837:TYR:HB2	1.80	0.47
2:B:345:GLU:O	2:B:349:ILE:HG12	2.15	0.47
1:A:371:ARG:HH12	1:A:728:ASP:HA	1.78	0.47
1:A:142:ARG:HB2	1:A:145:ILE:HG13	1.96	0.47
1:A:152:LEU:HD11	1:A:891:LEU:HD13	1.95	0.47
1:A:331:ILE:HG21	2:B:462:SER:HB3	1.96	0.47
2:B:396:PRO:HG2	2:E:370:ILE:HA	1.96	0.47
2:C:367:LEU:HG	2:D:367:LEU:HD21	1.95	0.47
2:B:333:ILE:HD13	2:B:336:LEU:HD12	1.98	0.46
1:A:1171:ILE:HG23	1:A:1175:GLU:HB3	1.97	0.46
1:A:291:LEU:HB2	1:A:346:THR:HG21	1.98	0.46
1:A:836:ILE:HB	1:A:843:VAL:HB	1.98	0.45
1:A:286:LEU:HD22	1:A:290:TYR:HE2	1.81	0.45
1:A:801:ARG:HD2	2:B:450:VAL:HG13	1.98	0.45
2:C:331:LYS:HG3	2:D:332:ILE:HD12	1.99	0.45
1:A:1099:VAL:O	1:A:1103:LEU:HG	2.17	0.45
1:A:497:ARG:HB3	1:A:500:ASP:HB2	1.99	0.45
1:A:920:LEU:HD23	1:A:926:LEU:HD23	1.99	0.45
1:A:1029:MET:HE3	1:A:1397:LEU:HD23	1.99	0.45
1:A:1013:LEU:HD12	1:A:1013:LEU:HA	1.80	0.44
1:A:916:VAL:HA	1:A:1115:MET:HE1	1.98	0.44
1:A:1171:ILE:HD11	1:A:1177:CYS:HB2	1.98	0.44
1:A:171:VAL:HG22	1:A:203:LEU:HD21	1.99	0.44
1:A:201:VAL:HG12	1:A:214:SER:HA	1.97	0.44
1:A:403:ARG:HD2	1:A:571:TYR:HE1	1.81	0.44
1:A:674:GLU:HB2	2:E:374:ILE:HD11	2.00	0.44
1:A:286:LEU:HD11	1:A:312:ILE:HD11	1.99	0.44
1:A:411:LEU:HD11	1:A:446:VAL:HG22	1.99	0.44
1:A:685:GLU:HA	2:D:388:VAL:HG13	2.00	0.44
1:A:462:MET:HA	1:A:465:LYS:HE3	1.99	0.43
1:A:400:TYR:HB3	1:A:409:PRO:HD3	1.99	0.43
1:A:94:LEU:HB3	1:A:168:TRP:HZ2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:347:GLU:HG2	2:D:351:LYS:HE3	2.00	0.43
1:A:379:VAL:HG21	2:B:433:LEU:HD11	2.01	0.43
1:A:109:LEU:HD23	1:A:109:LEU:HA	1.91	0.43
1:A:272:LEU:HB3	1:A:276:THR:OG1	2.19	0.43
2:B:332:ILE:O	2:B:336:LEU:HG	2.19	0.43
2:B:488:ILE:HG23	2:B:493:ASP:HB3	2.01	0.43
2:B:364:GLU:HA	2:E:363:LEU:HD21	2.01	0.42
1:A:810:ARG:HA	1:A:810:ARG:HD3	1.84	0.42
1:A:120:VAL:HG11	1:A:928:ILE:HG21	2.01	0.42
1:A:871:ILE:HD13	1:A:895:LYS:HB3	2.01	0.42
2:B:371:MET:HB3	2:B:394:LEU:HD12	2.03	0.41
2:B:332:ILE:HD11	2:C:332:ILE:HG23	2.02	0.41
1:A:1388:LEU:HD23	1:A:1388:LEU:HA	1.92	0.41
1:A:973:MET:HE2	1:A:973:MET:HB3	1.92	0.41
2:B:405:ALA:HB2	2:E:375:PRO:HD3	2.03	0.41
1:A:653:TYR:HD2	1:A:782:ARG:HG2	1.86	0.41
1:A:1304:LEU:HD12	1:A:1345:GLU:HG3	2.02	0.41
2:B:349:ILE:HG23	2:C:353:ILE:HD13	2.03	0.41
2:B:360:ILE:HD13	2:B:360:ILE:HA	1.94	0.41
2:B:367:LEU:HD13	2:E:363:LEU:HD22	2.03	0.41
1:A:291:LEU:HD12	1:A:346:THR:HB	2.03	0.40
1:A:657:SER:HB2	1:A:780:THR:HG22	2.03	0.40
1:A:672:ARG:HD2	2:E:374:ILE:HG21	2.03	0.40
1:A:42:ASP:HB2	1:A:364:VAL:HG21	2.03	0.40

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	1241/2183 (57%)	1199 (97%)	42 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	142/507 (28%)	136 (96%)	6 (4%)	0	100	100
2	C	45/507 (9%)	45 (100%)	0	0	100	100
2	D	63/507 (12%)	63 (100%)	0	0	100	100
2	E	53/507 (10%)	53 (100%)	0	0	100	100
All	All	1544/4211 (37%)	1496 (97%)	48 (3%)	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 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	1114/1945 (57%)	1114 (100%)	0	100	100
2	B	132/416 (32%)	132 (100%)	0	100	100
2	C	45/416 (11%)	45 (100%)	0	100	100
2	D	61/416 (15%)	61 (100%)	0	100	100
2	E	50/416 (12%)	50 (100%)	0	100	100
All	All	1402/3609 (39%)	1402 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	313	HIS
1	A	358	HIS
2	B	326	HIS
2	B	356	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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.