



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:00 PM UTC

PDB ID : 8W52 / pdb_00008w52
Title : p17 protein structure of HIV2 when OLA1 existing
Authors : Dang, L.L.
Deposited on : 2023-08-25
Resolution : 2.38 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp>

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:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

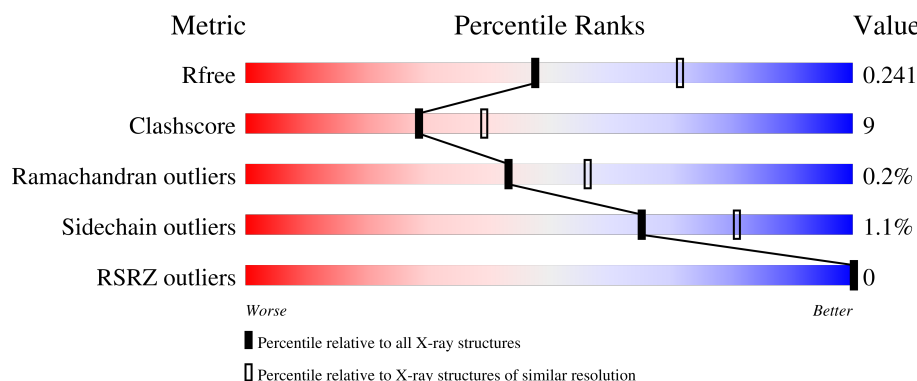
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.38 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	7164 (2.40-2.36)
Clashscore	190562	7722 (2.40-2.36)
Ramachandran outliers	187476	7626 (2.40-2.36)
Sidechain outliers	187428	7627 (2.40-2.36)
RSRZ outliers	180081	7170 (2.40-2.36)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	135	
1	B	135	
1	C	135	
1	D	135	
1	E	135	

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Mol	Chain	Length	Quality of chain
1	F	135	
1	G	135	
1	H	135	
1	I	135	
1	J	135	
1	K	135	
1	L	135	
1	M	135	
1	N	135	
1	O	135	
1	P	135	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 14103 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Gag polyprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	111	Total	C	N	O	S	0	0	0
			879	556	161	159	3			
1	B	111	Total	C	N	O	S	0	0	0
			879	556	161	159	3			
1	C	109	Total	C	N	O	S	0	0	0
			868	550	159	156	3			
1	D	107	Total	C	N	O	S	0	0	0
			854	542	157	152	3			
1	E	111	Total	C	N	O	S	0	0	0
			879	556	161	159	3			
1	F	111	Total	C	N	O	S	0	0	0
			879	556	161	159	3			
1	G	106	Total	C	N	O	S	0	0	0
			842	535	152	152	3			
1	H	107	Total	C	N	O	S	0	0	0
			849	540	153	153	3			
1	I	105	Total	C	N	O	S	0	0	0
			838	534	151	150	3			
1	J	102	Total	C	N	O	S	0	0	0
			817	521	148	145	3			
1	K	108	Total	C	N	O	S	0	0	0
			859	545	155	156	3			
1	L	106	Total	C	N	O	S	0	0	0
			845	538	152	152	3			
1	M	103	Total	C	N	O	S	0	0	0
			823	524	149	147	3			
1	N	105	Total	C	N	O	S	0	0	0
			838	534	151	150	3			
1	O	108	Total	C	N	O	S	0	0	0
			864	548	158	155	3			
1	P	107	Total	C	N	O	S	0	0	0
			854	542	157	152	3			

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	G	1	Total	O	S	0	0
			5	4	1		
2	H	1	Total	O	S	0	0
			5	4	1		
2	I	1	Total	O	S	0	0
			5	4	1		
2	I	1	Total	O	S	0	0
			5	4	1		
2	J	1	Total	O	S	0	0
			5	4	1		
2	J	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	K	1	Total	O	S	0	0
			5	4	1		
2	K	1	Total	O	S	0	0
			5	4	1		
2	L	1	Total	O	S	0	0
			5	4	1		
2	L	1	Total	O	S	0	0
			5	4	1		
2	L	1	Total	O	S	0	0
			5	4	1		
2	N	1	Total	O	S	0	0
			5	4	1		
2	P	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	17	Total	O	0	0
			17	17		
3	B	29	Total	O	0	0
			29	29		
3	C	10	Total	O	0	0
			10	10		
3	D	17	Total	O	0	0
			17	17		
3	E	24	Total	O	0	0
			24	24		
3	F	28	Total	O	0	0
			28	28		
3	G	22	Total	O	0	0
			22	22		
3	H	28	Total	O	0	0
			28	28		
3	I	25	Total	O	0	0
			25	25		
3	J	19	Total	O	0	0
			19	19		
3	K	25	Total	O	0	0
			25	25		
3	L	17	Total	O	0	0
			17	17		

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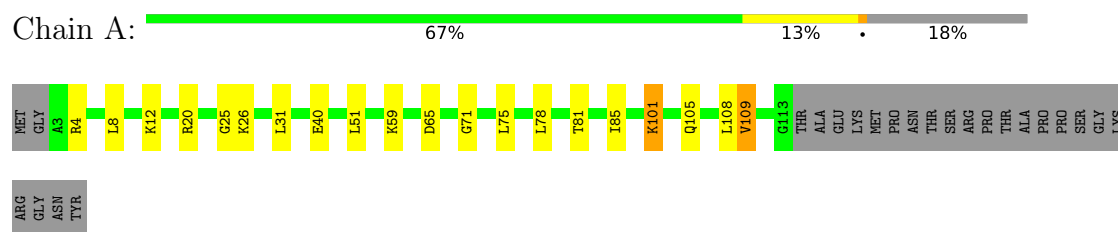
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	M	14	Total 14	O 14	0	0
3	N	27	Total 27	O 27	0	0
3	O	21	Total 21	O 21	0	0
3	P	13	Total 13	O 13	0	0

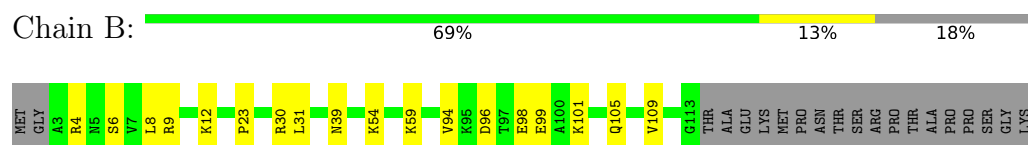
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). 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.

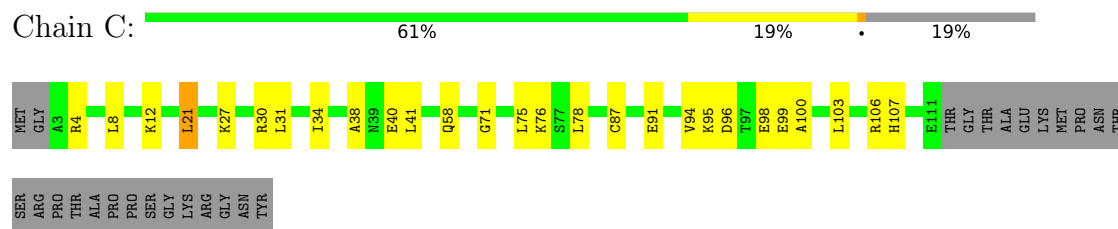
- Molecule 1: Gag polypeptide



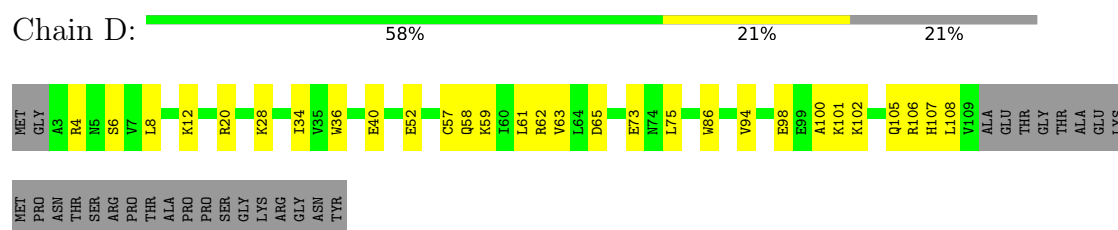
- Molecule 1: Gag polypeptide



- Molecule 1: Gag polypeptide

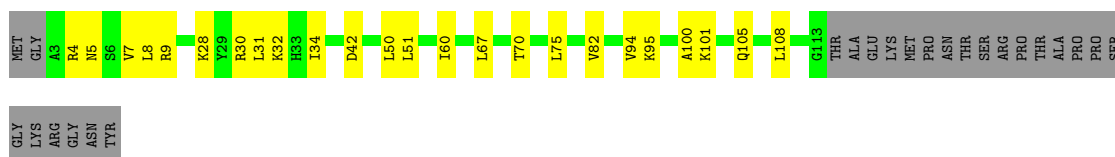


- Molecule 1: Gag polypeptide



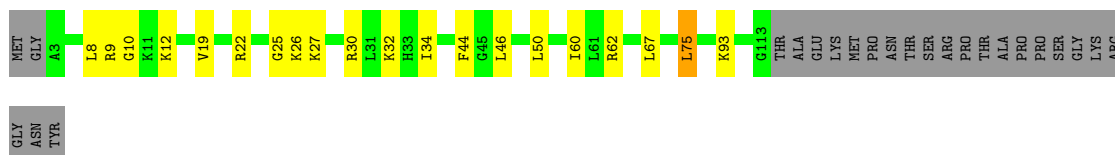
- Molecule 1: Gag polypeptide





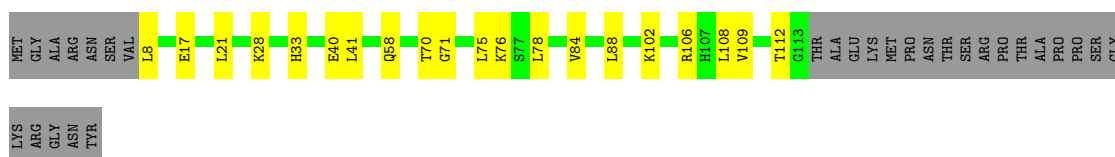
- Molecule 1: Gag polyprotein

Chain F: 67% 14% 18%



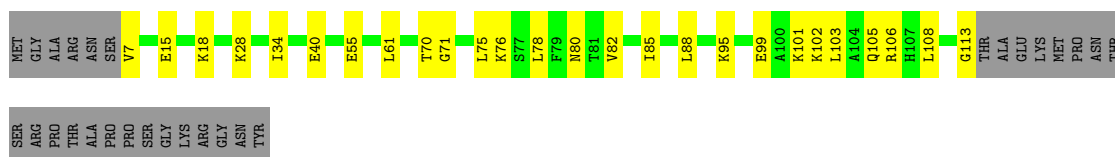
- Molecule 1: Gag polyprotein

Chain G: 64% 15% 21%



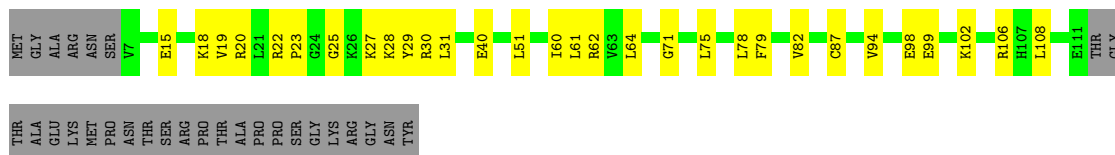
- Molecule 1: Gag polyprotein

Chain H: 60% 19% 21%



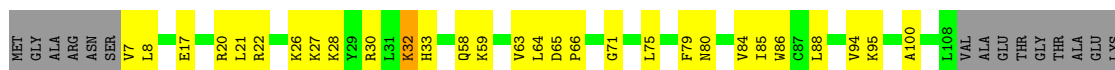
- Molecule 1: Gag polyprotein

Chain I: 56% 22% 22%



- Molecule 1: Gag polyprotein

Chain J: 54% 21% 24%



MET
PRO
ASN
THR
ARG
SER
ARG
PRO
THR
ALA
PRO
PRO
SER
GLY
LYS
ARG
GLY
ASN
TYR

- Molecule 1: Gag polypeptide

Chain K:  67% 13% 20%

MET GLY ALA ARG N5 S6 V7 L8 L21 K27 K28 L31 I34 E40 G71 L75 L78 I85 V94 A100 Q105 V109 T112 GLY THR ALA GLU LYS MET PRO ASN THR SER ARG PRO THR ALA PRO PRO PRO MET SER GLY LYS ARG GLY ASN TYR

- Molecule 1: Gag polypeptide

Chain L:  61% 17% 21%

MET GLY ALA ARG ASN SER V7 L8 R9 L16 L17 K18 L21 R22 P23 K27 R30 L31 K32 H33 I34 Q58 G71 L75 N80 V84 I85 W86 C87 L88 T97 E98 K101 L108 T112 GLY THR ALA GLU LYS MET SER PRO MET ASN THR SER ARG PRO

THR
ALA
PRO
PRO
GLY
LYS
GLY
TYR

- Molecule 1: Gag polypeptide

Chain M:  56% 19% 24%

MET GLY ALA ARG ASN S6 V7 L8 R20 R21 R22 P23 G24 G25 K26 E40 L50 S53 G56 I60 V63 L64 T70 E73 N74 L75 K76 K77 L78 F79 N80 I85 L88 V94 E98 E99 A100 K101 K102 R106 H107 L108 VAL ALA GLU THR

GLY
THR
ALA
GLU
LYS
MET
PRO
ASN
THR
SER
PRO
THR
ALA
PRO
SER
GLY
LYS
ARG
ASN
TYR

- Molecule 1: Gag polypeptide

Chain N:  61% 17% 22%

MET GLY ALA ARG ASN SER V7 L8 L16 R20 R21 K27 K28 H33 W36 K54 E55 K59 I60 L61 R62 T70 S77 N80 I85 L88 V94 A100 K101 Q105 L108 E111 THR GLY THR ALA GLU LYS MET PRO ASN THR SER

ARG
PRO
THR
ALA
PRO
PRO
SER
GLY
LYS
ARG
ASN
TYR

- Molecule 1: Gag polypeptide

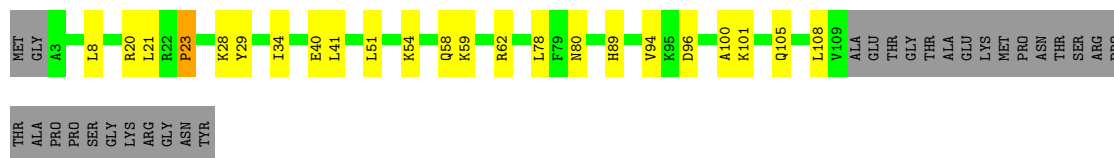
Chain O:  57% 21% 20%

MET GLY A3 R4 V7 L8 R9 G10 K12 P23 GLY G25 K26 K27 K28 E40 L50 L51 K54 Q58 K59 I60 L61 R62 G71 L75 L78 F79 W86 H89 E92 K93 V94 K95 D96 A100 L103 R106 H107 L108 E111 GLY

THR
ALA
GLU
LYS
MET
PRO
PRO
THR
THR
ARG
PRO
THR
ALA
PRO
SER
SER
GLY
LYS
ARG
GLY
ASN
TYR

- Molecule 1: Gag polypeptide

Chain P:



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	123.78Å 123.78Å 108.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.19 – 2.38 46.19 – 2.38	Depositor EDS
% Data completeness (in resolution range)	99.8 (46.19-2.38) 99.8 (46.19-2.38)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.47 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487, PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.210 , 0.248 0.209 , 0.241	Depositor DCC
R_{free} test set	3371 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	38.5	Xtriage
Anisotropy	0.551	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 42.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.487 for k,h,-l	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	14103	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 75.96 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.1429e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	0.09	0/891	0.23	0/1194
1	B	0.11	0/891	0.26	0/1194
1	C	0.12	0/880	0.32	0/1179
1	D	0.10	0/866	0.27	0/1160
1	E	0.09	0/891	0.28	0/1194
1	F	0.09	0/891	0.24	0/1194
1	G	0.13	0/854	0.28	0/1144
1	H	0.10	0/861	0.28	0/1154
1	I	0.10	0/850	0.29	0/1139
1	J	0.16	0/829	0.31	0/1110
1	K	0.08	0/871	0.22	0/1168
1	L	0.10	0/857	0.27	0/1149
1	M	0.12	0/835	0.34	1/1118 (0.1%)
1	N	0.13	0/850	0.32	0/1139
1	O	0.12	0/875	0.29	0/1171
1	P	0.11	0/866	0.31	0/1160
All	All	0.11	0/13858	0.28	1/18567 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	74	ASN	N-CA-C	-6.13	104.52	111.14

There are no chirality outliers.

There are no planarity outliers.

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	879	0	926	13	0
1	B	879	0	926	14	0
1	C	868	0	916	16	0
1	D	854	0	905	19	0
1	E	879	0	926	20	0
1	F	879	0	926	14	0
1	G	842	0	888	16	0
1	H	849	0	897	20	0
1	I	838	0	887	20	0
1	J	817	0	867	21	0
1	K	859	0	905	11	0
1	L	845	0	894	16	0
1	M	823	0	872	15	0
1	N	838	0	887	15	0
1	O	864	0	912	24	0
1	P	854	0	905	12	0
2	A	10	0	0	0	0
2	B	10	0	0	0	0
2	C	5	0	0	0	0
2	E	10	0	0	0	0
2	G	5	0	0	0	0
2	H	5	0	0	0	0
2	I	10	0	0	1	0
2	J	10	0	0	0	0
2	K	10	0	0	0	0
2	L	15	0	0	1	0
2	N	5	0	0	0	0
2	P	5	0	0	0	0
3	A	17	0	0	1	0
3	B	29	0	0	2	0
3	C	10	0	0	0	0
3	D	17	0	0	1	0
3	E	24	0	0	3	0
3	F	28	0	0	2	0
3	G	22	0	0	0	0
3	H	28	0	0	3	0
3	I	25	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	J	19	0	0	0	0
3	K	25	0	0	1	0
3	L	17	0	0	4	0
3	M	14	0	0	1	0
3	N	27	0	0	0	0
3	O	21	0	0	2	0
3	P	13	0	0	0	0
All	All	14103	0	14439	247	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 9.

All (247) 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:O:103:LEU:HA	1:O:106:ARG:HD3	1.60	0.82
1:I:62:ARG:HG3	1:I:108:LEU:HD11	1.61	0.80
1:D:8:LEU:HD12	1:D:34:ILE:HD11	1.67	0.77
1:C:103:LEU:HG	1:C:106:ARG:HH12	1.49	0.76
1:C:71:GLY:HA3	1:C:75:LEU:HD23	1.69	0.74
1:M:22:ARG:HE	1:M:25:GLY:HA3	1.52	0.74
1:E:75:LEU:HD13	1:G:70:THR:HB	1.69	0.73
1:C:8:LEU:HD22	1:C:12:LYS:HB3	1.69	0.73
1:K:7:VAL:HG12	1:K:8:LEU:HD22	1.72	0.72
1:J:75:LEU:HD22	1:N:70:THR:HB	1.71	0.71
1:H:15:GLU:HA	1:H:18:LYS:HD2	1.74	0.69
1:E:30:ARG:HG2	1:E:32:LYS:H	1.57	0.69
1:N:21:LEU:HD12	1:N:27:LYS:HB3	1.73	0.68
1:J:71:GLY:HA3	1:J:75:LEU:HD23	1.76	0.67
1:D:102:LYS:HE3	1:D:106:ARG:HH21	1.58	0.67
1:I:87:CYS:SG	3:I:323:HOH:O	2.52	0.67
1:H:71:GLY:HA3	1:H:75:LEU:HD23	1.75	0.67
1:N:94:VAL:HG11	1:N:100:ALA:HB2	1.76	0.67
1:M:73:GLU:HA	1:M:76:LYS:HB2	1.77	0.66
1:B:8:LEU:HD22	1:B:12:LYS:HB3	1.79	0.64
1:C:94:VAL:HG21	1:C:100:ALA:HB2	1.79	0.64
1:N:61:LEU:HB3	1:N:108:LEU:HD11	1.80	0.64
1:F:67:LEU:HD13	1:H:70:THR:HG21	1.78	0.64
1:H:61:LEU:HB3	1:H:108:LEU:HD11	1.79	0.63
1:E:51:LEU:HD21	1:E:82:VAL:HG22	1.80	0.63
1:B:4:ARG:HD3	1:B:31:LEU:HD22	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:94:VAL:HG21	1:D:100:ALA:HB2	1.81	0.63
1:D:98:GLU:HA	1:D:101:LYS:HD3	1.80	0.62
1:F:22:ARG:HH12	1:F:27:LYS:HD3	1.66	0.61
1:J:94:VAL:HG21	1:J:100:ALA:HB2	1.81	0.61
1:L:7:VAL:N	3:L:302:HOH:O	2.34	0.60
1:E:28:LYS:NZ	3:E:304:HOH:O	2.33	0.60
1:I:27:LYS:NZ	3:I:304:HOH:O	2.34	0.60
1:E:7:VAL:HG12	1:E:8:LEU:HG	1.83	0.60
1:L:30:ARG:NH2	3:L:303:HOH:O	2.35	0.60
1:F:44:PHE:HB2	1:F:46:LEU:HG	1.84	0.59
1:N:8:LEU:HD21	1:N:88:LEU:HD13	1.85	0.59
1:K:94:VAL:HG21	1:K:100:ALA:HB2	1.83	0.59
1:I:20:ARG:HA	1:I:28:LYS:HA	1.84	0.59
1:D:8:LEU:HD22	1:D:12:LYS:HB3	1.84	0.58
1:B:101:LYS:NZ	1:H:113:GLY:O	2.35	0.58
1:N:85:ILE:HA	1:N:88:LEU:HD12	1.85	0.58
1:L:7:VAL:N	3:L:305:HOH:O	2.36	0.58
1:E:70:THR:HB	1:G:75:LEU:HD13	1.85	0.57
1:E:101:LYS:NZ	3:E:306:HOH:O	2.38	0.57
1:O:9:ARG:NH1	1:O:10:GLY:H	2.02	0.56
1:J:64:LEU:HB2	1:J:79:PHE:HD2	1.71	0.56
1:O:62:ARG:HG3	1:O:108:LEU:HD11	1.87	0.56
1:L:32:LYS:NZ	3:L:306:HOH:O	2.37	0.56
1:A:59:LYS:NZ	1:E:42:ASP:O	2.31	0.56
1:F:22:ARG:HE	1:F:25:GLY:HA3	1.71	0.56
1:I:71:GLY:HA3	1:I:75:LEU:HD22	1.88	0.55
1:F:93:LYS:NZ	3:F:205:HOH:O	2.36	0.55
1:A:26:LYS:NZ	3:A:303:HOH:O	2.40	0.55
1:O:4:ARG:HH12	1:O:9:ARG:HH11	1.53	0.55
1:H:102:LYS:O	1:H:106:ARG:HB2	2.05	0.55
1:C:4:ARG:HD3	1:C:31:LEU:HD22	1.89	0.55
1:C:8:LEU:HD12	1:C:34:ILE:HD11	1.88	0.55
1:H:95:LYS:N	1:H:99:GLU:OE1	2.28	0.55
1:M:8:LEU:HD21	1:M:88:LEU:HD13	1.88	0.55
1:A:51:LEU:HD22	1:A:85:ILE:HD12	1.90	0.54
1:N:21:LEU:HD21	1:N:33:HIS:CE1	2.42	0.54
1:J:17:GLU:HG3	1:K:31:LEU:HD12	1.90	0.54
1:O:54:LYS:HB3	1:O:89:HIS:HB3	1.90	0.54
1:M:53:SER:HG	1:M:56:GLY:H	1.51	0.54
1:E:5:ASN:O	1:E:9:ARG:HG2	2.08	0.54
1:O:12:LYS:NZ	3:O:203:HOH:O	2.40	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:75:LEU:HD13	1:H:70:THR:HB	1.89	0.53
1:H:40:GLU:HB3	1:H:78:LEU:HD22	1.90	0.53
1:D:4:ARG:NH1	1:D:8:LEU:O	2.42	0.53
1:M:20:ARG:NH2	3:M:205:HOH:O	2.42	0.53
1:C:21:LEU:HD12	1:C:27:LYS:HB3	1.91	0.52
1:C:71:GLY:O	1:C:76:LYS:NZ	2.42	0.52
1:J:27:LYS:H	1:J:27:LYS:HD3	1.74	0.52
1:J:27:LYS:H	1:J:27:LYS:CD	2.23	0.52
1:G:41:LEU:HD23	1:G:78:LEU:HD21	1.91	0.51
1:O:71:GLY:HA3	1:O:75:LEU:HD12	1.92	0.51
1:J:32:LYS:H	1:J:32:LYS:HZ3	1.57	0.51
1:N:54:LYS:HG3	1:N:55:GLU:N	2.26	0.51
1:K:105:GLN:O	1:K:109:VAL:HG23	2.10	0.51
1:A:71:GLY:HA3	1:A:75:LEU:HD12	1.93	0.50
1:D:73:GLU:H	1:D:73:GLU:CD	2.19	0.50
1:M:94:VAL:HG21	1:M:100:ALA:HB2	1.92	0.50
1:G:58:GLN:HE22	1:G:108:LEU:HD23	1.76	0.50
1:O:94:VAL:HG21	1:O:100:ALA:N	2.27	0.50
1:A:8:LEU:HD22	1:A:12:LYS:HB3	1.93	0.50
1:H:28:LYS:NZ	3:H:305:HOH:O	2.40	0.49
1:E:8:LEU:HD12	1:E:34:ILE:HG13	1.94	0.49
1:O:59:LYS:HG3	1:O:62:ARG:HH12	1.76	0.49
1:F:22:ARG:HH21	1:F:26:LYS:H	1.60	0.49
1:O:4:ARG:HH12	1:O:9:ARG:NH1	2.10	0.49
1:F:8:LEU:HD12	1:F:34:ILE:HG13	1.94	0.49
1:O:40:GLU:HB3	1:O:78:LEU:HD22	1.94	0.49
1:A:20:ARG:HD3	1:A:25:GLY:O	2.13	0.49
1:N:59:LYS:HG3	1:N:62:ARG:HH12	1.78	0.49
1:A:108:LEU:HD23	1:G:109:VAL:HG13	1.95	0.49
1:J:22:ARG:HH21	1:J:27:LYS:HB2	1.78	0.49
1:E:50:LEU:HB2	1:E:60:ILE:HD11	1.94	0.48
1:I:23:PRO:HG3	1:I:98:GLU:HG3	1.95	0.48
1:P:40:GLU:HB3	1:P:78:LEU:HD22	1.94	0.48
1:B:6:SER:HA	1:B:9:ARG:HH21	1.79	0.48
1:A:109:VAL:HG23	1:G:109:VAL:HG12	1.95	0.48
1:F:62:ARG:NH1	3:F:206:HOH:O	2.37	0.48
1:P:105:GLN:HA	1:P:108:LEU:HB2	1.94	0.48
1:K:71:GLY:HA3	1:K:75:LEU:HD22	1.96	0.48
1:A:109:VAL:HG13	1:G:106:ARG:HG3	1.96	0.48
1:J:65:ASP:HB3	1:J:66:PRO:HD3	1.95	0.48
1:C:58:GLN:OE1	1:C:107:HIS:ND1	2.39	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:8:LEU:HD22	1:F:12:LYS:HB3	1.95	0.48
1:F:25:GLY:C	1:F:26:LYS:HD3	2.39	0.48
1:G:71:GLY:O	1:G:76:LYS:NZ	2.47	0.47
1:N:36:TRP:CH2	1:N:77:SER:HB3	2.48	0.47
1:E:5:ASN:HA	1:E:9:ARG:HD3	1.95	0.47
1:G:21:LEU:HD21	1:G:33:HIS:CE1	2.49	0.47
1:B:39:ASN:ND2	3:B:306:HOH:O	2.48	0.47
1:J:20:ARG:HG3	1:J:95:LYS:O	2.13	0.47
1:B:109:VAL:HG13	1:H:106:ARG:HG3	1.95	0.47
1:I:15:GLU:HA	1:I:18:LYS:HE3	1.96	0.47
1:L:23:PRO:HG3	1:L:98:GLU:HB2	1.96	0.47
1:O:62:ARG:NH2	3:O:202:HOH:O	2.45	0.47
1:J:30:ARG:NH2	1:K:28:LYS:HB2	2.30	0.47
1:N:105:GLN:HA	1:N:108:LEU:HB2	1.96	0.47
1:P:8:LEU:HD12	1:P:34:ILE:HD11	1.97	0.47
1:D:98:GLU:OE1	1:D:101:LYS:NZ	2.44	0.47
1:M:22:ARG:HH21	1:M:26:LYS:H	1.61	0.47
1:K:34:ILE:HD12	1:K:85:ILE:HD11	1.96	0.47
1:B:94:VAL:HB	1:B:99:GLU:HB3	1.95	0.47
1:C:94:VAL:HG23	1:C:99:GLU:HB3	1.97	0.46
1:M:85:ILE:HA	1:M:88:LEU:HD12	1.97	0.46
1:C:40:GLU:HB3	1:C:78:LEU:HD22	1.96	0.46
1:J:7:VAL:HG12	1:J:8:LEU:HG	1.97	0.46
1:P:20:ARG:HA	1:P:28:LYS:HG2	1.97	0.46
1:O:7:VAL:HG13	1:O:51:LEU:HB3	1.98	0.46
1:H:76:LYS:HE3	1:H:76:LYS:HB2	1.75	0.46
1:J:58:GLN:HG3	1:J:86:TRP:CD1	2.51	0.46
1:B:30:ARG:CZ	1:C:30:ARG:HE	2.28	0.45
1:L:21:LEU:HD12	1:L:27:LYS:HB3	1.97	0.45
1:I:31:LEU:HD12	1:L:17:GLU:HG3	1.98	0.45
1:C:38:ALA:HA	1:C:41:LEU:HD12	1.98	0.45
1:D:102:LYS:O	1:D:106:ARG:HB2	2.16	0.45
1:O:93:LYS:HD2	1:O:93:LYS:HA	1.71	0.45
1:O:50:LEU:HD22	1:O:59:LYS:HD2	1.99	0.45
1:G:109:VAL:O	1:G:112:THR:HG22	2.16	0.45
1:N:36:TRP:HH2	1:N:77:SER:HB3	1.82	0.45
1:F:30:ARG:HD2	1:F:32:LYS:HZ2	1.82	0.45
1:L:9:ARG:HB3	2:L:203:SO4:O3	2.17	0.45
1:L:80:ASN:HB3	1:L:97:THR:CG2	2.47	0.45
1:E:67:LEU:HD13	1:G:70:THR:HG21	1.99	0.45
1:F:9:ARG:HG2	1:F:10:GLY:N	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:21:LEU:HD12	1:K:27:LYS:HB3	1.99	0.45
1:O:92:GLU:HG2	1:O:103:LEU:HD22	1.99	0.45
1:J:63:VAL:HG12	1:J:64:LEU:HD23	1.99	0.44
1:B:54:LYS:NZ	3:B:305:HOH:O	2.48	0.44
1:C:96:ASP:OD1	1:C:98:GLU:N	2.51	0.44
1:G:102:LYS:O	1:G:106:ARG:HB2	2.17	0.44
1:H:18:LYS:HA	1:H:28:LYS:HD3	1.98	0.44
1:J:59:LYS:HD2	1:J:59:LYS:HA	1.70	0.44
1:I:94:VAL:HG12	1:I:99:GLU:HG2	2.00	0.44
1:O:23:PRO:HA	1:O:96:ASP:CG	2.43	0.44
1:O:58:GLN:HE21	1:O:86:TRP:CD1	2.35	0.44
1:D:62:ARG:NH2	3:D:206:HOH:O	2.49	0.44
1:J:26:LYS:O	1:J:28:LYS:HG3	2.17	0.44
1:P:80:ASN:OD1	1:P:101:LYS:HD2	2.17	0.44
1:J:85:ILE:HA	1:J:88:LEU:HD12	1.99	0.44
1:P:54:LYS:HB3	1:P:89:HIS:HB3	2.00	0.44
1:A:4:ARG:HD3	1:A:31:LEU:HD22	1.98	0.43
1:B:23:PRO:HA	1:B:96:ASP:CG	2.43	0.43
1:O:26:LYS:O	1:O:28:LYS:NZ	2.49	0.43
1:B:23:PRO:HG3	1:B:98:GLU:HB2	2.00	0.43
1:G:40:GLU:HB3	1:G:78:LEU:HD22	1.99	0.43
1:I:40:GLU:HB3	1:I:78:LEU:HD22	2.01	0.43
1:E:30:ARG:HH11	1:E:30:ARG:HB2	1.83	0.43
1:I:61:LEU:HB3	1:I:108:LEU:HD22	2.01	0.43
1:M:40:GLU:HB3	1:M:78:LEU:HD22	2.01	0.43
1:B:6:SER:OG	1:E:42:ASP:OD2	2.30	0.43
1:I:22:ARG:HB2	1:I:25:GLY:HA3	2.01	0.43
1:B:30:ARG:NE	1:C:30:ARG:HE	2.17	0.43
1:I:61:LEU:HD22	1:I:79:PHE:CE2	2.53	0.43
1:A:101:LYS:O	1:A:105:GLN:HB2	2.18	0.43
1:O:58:GLN:HE21	1:O:86:TRP:NE1	2.16	0.43
1:P:23:PRO:HA	1:P:96:ASP:OD2	2.19	0.43
1:P:41:LEU:HD11	1:P:51:LEU:HG	2.01	0.43
1:L:58:GLN:HE21	1:L:86:TRP:NE1	2.17	0.43
1:A:40:GLU:HB3	1:A:78:LEU:HD22	2.00	0.42
1:L:16:LEU:C	1:L:18:LYS:H	2.27	0.42
1:O:95:LYS:HG3	1:O:96:ASP:OD1	2.19	0.42
1:L:71:GLY:HA3	1:L:75:LEU:HD22	2.01	0.42
1:N:20:ARG:HA	1:N:28:LYS:HA	2.01	0.42
1:D:58:GLN:NE2	1:D:107:HIS:HB3	2.34	0.42
1:J:80:ASN:O	1:J:84:VAL:HG23	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:102:LYS:O	1:M:106:ARG:HG3	2.19	0.42
1:I:30:ARG:NH2	2:I:201:SO4:S	2.93	0.42
1:B:105:GLN:NE2	3:H:302:HOH:O	2.52	0.42
1:K:40:GLU:HB2	1:K:78:LEU:HD13	2.01	0.42
1:N:80:ASN:OD1	1:N:101:LYS:HD2	2.20	0.42
1:O:61:LEU:HD22	1:O:79:PHE:CE1	2.55	0.42
1:E:9:ARG:HA	1:E:9:ARG:HD2	1.60	0.42
1:J:22:ARG:HH21	1:J:27:LYS:HE3	1.85	0.42
1:I:75:LEU:HD13	1:M:70:THR:HB	2.02	0.42
1:L:84:VAL:O	1:L:88:LEU:HG	2.19	0.42
1:O:4:ARG:HE	1:O:4:ARG:HB3	1.70	0.42
1:D:6:SER:HB3	1:D:52:GLU:OE1	2.20	0.42
1:E:95:LYS:NZ	3:E:311:HOH:O	2.47	0.42
1:H:7:VAL:N	3:H:311:HOH:O	2.53	0.42
1:L:80:ASN:CG	1:L:101:LYS:HD2	2.45	0.41
1:M:50:LEU:HB2	1:M:60:ILE:HD11	2.02	0.41
1:P:21:LEU:HD23	1:P:29:TYR:CE1	2.55	0.41
1:D:65:ASP:OD1	1:D:105:GLN:NE2	2.53	0.41
1:F:50:LEU:HB2	1:F:60:ILE:HD11	2.00	0.41
1:G:84:VAL:O	1:G:88:LEU:HG	2.19	0.41
1:I:19:VAL:HG12	1:I:29:TYR:HD2	1.85	0.41
1:K:40:GLU:HG2	3:K:301:HOH:O	2.19	0.41
1:D:59:LYS:O	1:D:63:VAL:HG23	2.20	0.41
1:I:60:ILE:HG23	1:I:64:LEU:HD23	2.02	0.41
1:J:21:LEU:HD21	1:J:33:HIS:CE1	2.56	0.41
1:K:94:VAL:HG11	1:K:100:ALA:HA	2.03	0.41
1:M:23:PRO:HG3	1:M:98:GLU:HB2	2.02	0.41
1:O:9:ARG:HD2	1:O:9:ARG:HA	1.74	0.41
1:G:71:GLY:HA3	1:G:75:LEU:HD22	2.02	0.41
1:H:55:GLU:OE1	1:H:55:GLU:N	2.49	0.41
1:H:85:ILE:HA	1:H:88:LEU:HD12	2.03	0.41
1:H:80:ASN:OD1	1:H:101:LYS:HD2	2.20	0.41
1:M:80:ASN:OD1	1:M:101:LYS:HD2	2.20	0.41
1:A:81:THR:O	1:A:85:ILE:HG13	2.20	0.41
1:G:17:GLU:O	1:G:28:LYS:HD3	2.21	0.41
1:N:101:LYS:HE3	1:N:101:LYS:HB3	1.78	0.41
1:D:36:TRP:O	1:D:40:GLU:HG2	2.21	0.41
1:D:57:CYS:O	1:D:61:LEU:HG	2.21	0.41
1:H:78:LEU:O	1:H:82:VAL:HG23	2.21	0.41
1:I:51:LEU:HD21	1:I:82:VAL:HG22	2.03	0.41
1:I:102:LYS:O	1:I:106:ARG:HG2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:94:VAL:HG21	1:P:100:ALA:HB2	2.02	0.41
1:D:102:LYS:HE3	1:D:106:ARG:NH2	2.29	0.41
1:H:34:ILE:HD12	1:H:85:ILE:HD11	2.03	0.41
1:H:105:GLN:HA	1:H:108:LEU:HB2	2.03	0.41
1:M:63:VAL:HG12	1:M:64:LEU:HD23	2.03	0.41
1:C:87:CYS:O	1:C:91:GLU:N	2.54	0.40
1:E:94:VAL:HG11	1:E:100:ALA:HA	2.02	0.40
1:E:105:GLN:HA	1:E:108:LEU:HB3	2.02	0.40
1:L:34:ILE:HD12	1:L:85:ILE:HD11	2.03	0.40
1:P:58:GLN:OE1	1:P:58:GLN:HA	2.21	0.40
1:I:60:ILE:HG21	1:I:82:VAL:HG21	2.04	0.40
1:P:59:LYS:HG3	1:P:62:ARG:NH2	2.37	0.40
1:D:58:GLN:HG2	1:D:86:TRP:NE1	2.37	0.40
1:L:108:LEU:HD12	1:L:108:LEU:HA	1.92	0.40
1:D:20:ARG:HA	1:D:28:LYS:HA	2.04	0.40
1:E:4:ARG:HD3	1:E:31:LEU:HD22	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	109/135 (81%)	108 (99%)	1 (1%)	0	100	100
1	B	109/135 (81%)	107 (98%)	2 (2%)	0	100	100
1	C	107/135 (79%)	106 (99%)	0	1 (1%)	14	20
1	D	105/135 (78%)	102 (97%)	3 (3%)	0	100	100
1	E	109/135 (81%)	107 (98%)	2 (2%)	0	100	100
1	F	109/135 (81%)	107 (98%)	2 (2%)	0	100	100
1	G	104/135 (77%)	102 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	H	105/135 (78%)	104 (99%)	1 (1%)	0	100	100
1	I	103/135 (76%)	98 (95%)	5 (5%)	0	100	100
1	J	100/135 (74%)	99 (99%)	1 (1%)	0	100	100
1	K	106/135 (78%)	105 (99%)	1 (1%)	0	100	100
1	L	104/135 (77%)	100 (96%)	4 (4%)	0	100	100
1	M	101/135 (75%)	99 (98%)	2 (2%)	0	100	100
1	N	103/135 (76%)	102 (99%)	1 (1%)	0	100	100
1	O	104/135 (77%)	101 (97%)	2 (2%)	1 (1%)	12	17
1	P	105/135 (78%)	103 (98%)	1 (1%)	1 (1%)	12	17
All	All	1683/2160 (78%)	1650 (98%)	30 (2%)	3 (0%)	43	56

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	21	LEU
1	P	23	PRO
1	O	7	VAL

5.3.2 Protein sidechains ⓘ

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

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	95/114 (83%)	92 (97%)	3 (3%)	34	53
1	B	95/114 (83%)	94 (99%)	1 (1%)	65	81
1	C	94/114 (82%)	93 (99%)	1 (1%)	65	81
1	D	93/114 (82%)	91 (98%)	2 (2%)	45	65
1	E	95/114 (83%)	95 (100%)	0	100	100
1	F	95/114 (83%)	93 (98%)	2 (2%)	47	67
1	G	91/114 (80%)	90 (99%)	1 (1%)	65	81
1	H	92/114 (81%)	91 (99%)	1 (1%)	65	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	I	91/114 (80%)	91 (100%)	0	100	100
1	J	89/114 (78%)	88 (99%)	1 (1%)	65	81
1	K	94/114 (82%)	93 (99%)	1 (1%)	65	81
1	L	92/114 (81%)	92 (100%)	0	100	100
1	M	90/114 (79%)	89 (99%)	1 (1%)	65	81
1	N	91/114 (80%)	90 (99%)	1 (1%)	65	81
1	O	94/114 (82%)	93 (99%)	1 (1%)	65	81
1	P	93/114 (82%)	93 (100%)	0	100	100
All	All	1484/1824 (81%)	1468 (99%)	16 (1%)	65	81

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	65	ASP
1	A	101	LYS
1	A	109	VAL
1	B	59	LYS
1	C	95	LYS
1	D	75	LEU
1	D	108	LEU
1	F	19	VAL
1	F	75	LEU
1	G	8	LEU
1	H	103	LEU
1	J	32	LYS
1	K	6	SER
1	M	53	SER
1	N	16	LEU
1	O	12	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	39	ASN
1	G	58	GLN
1	I	58	GLN
1	I	107	HIS
1	J	80	ASN

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Mol	Chain	Res	Type
1	N	58	GLN
1	N	105	GLN
1	O	5	ASN
1	O	58	GLN
1	P	5	ASN

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](#)

20 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	SO4	K	201	-	4,4,4	0.23	0	6,6,6	0.07	0
2	SO4	N	201	-	4,4,4	0.24	0	6,6,6	0.08	0
2	SO4	E	202	-	4,4,4	0.23	0	6,6,6	0.07	0
2	SO4	L	201	-	4,4,4	0.24	0	6,6,6	0.07	0
2	SO4	E	201	-	4,4,4	0.23	0	6,6,6	0.07	0
2	SO4	L	203	-	4,4,4	0.24	0	6,6,6	0.07	0
2	SO4	L	202	-	4,4,4	0.24	0	6,6,6	0.08	0
2	SO4	C	201	-	4,4,4	0.23	0	6,6,6	0.07	0
2	SO4	B	202	-	4,4,4	0.23	0	6,6,6	0.08	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	SO4	I	201	-	4,4,4	0.24	0	6,6,6	0.09	0
2	SO4	B	201	-	4,4,4	0.23	0	6,6,6	0.08	0
2	SO4	I	202	-	4,4,4	0.23	0	6,6,6	0.07	0
2	SO4	A	202	-	4,4,4	0.23	0	6,6,6	0.09	0
2	SO4	H	201	-	4,4,4	0.24	0	6,6,6	0.06	0
2	SO4	P	201	-	4,4,4	0.23	0	6,6,6	0.08	0
2	SO4	G	201	-	4,4,4	0.23	0	6,6,6	0.07	0
2	SO4	K	202	-	4,4,4	0.23	0	6,6,6	0.07	0
2	SO4	A	201	-	4,4,4	0.24	0	6,6,6	0.08	0
2	SO4	J	202	-	4,4,4	0.23	0	6,6,6	0.07	0
2	SO4	J	201	-	4,4,4	0.23	0	6,6,6	0.07	0

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.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	L	203	SO4	1	0
2	I	201	SO4	1	0

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 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	111/135 (82%)	-1.52	0 100 100	20, 40, 56, 62	0
1	B	111/135 (82%)	-1.54	0 100 100	22, 39, 57, 63	0
1	C	109/135 (80%)	-1.28	0 100 100	32, 50, 67, 84	0
1	D	107/135 (79%)	-1.32	0 100 100	28, 48, 70, 86	0
1	E	111/135 (82%)	-1.48	0 100 100	24, 39, 60, 77	0
1	F	111/135 (82%)	-1.52	0 100 100	24, 38, 58, 75	0
1	G	106/135 (78%)	-1.47	0 100 100	25, 38, 61, 99	0
1	H	107/135 (79%)	-1.48	0 100 100	26, 39, 60, 98	0
1	I	105/135 (77%)	-1.35	0 100 100	30, 49, 66, 84	0
1	J	102/135 (75%)	-1.30	0 100 100	30, 48, 73, 87	0
1	K	108/135 (80%)	-1.44	0 100 100	26, 40, 60, 75	0
1	L	106/135 (78%)	-1.46	0 100 100	24, 42, 61, 86	0
1	M	103/135 (76%)	-1.33	0 100 100	27, 48, 69, 96	0
1	N	105/135 (77%)	-1.34	0 100 100	25, 46, 70, 90	0
1	O	108/135 (80%)	-1.26	0 100 100	30, 52, 74, 88	0
1	P	107/135 (79%)	-1.26	0 100 100	31, 51, 72, 83	0
All	All	1717/2160 (79%)	-1.40	0 100 100	20, 44, 66, 99	0

There are no RSRZ outliers to report.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	SO4	P	201	5/5	0.97	0.05	76,89,102,105	0
2	SO4	I	202	5/5	0.98	0.03	43,61,71,90	0
2	SO4	L	203	5/5	0.98	0.03	77,91,103,108	0
2	SO4	C	201	5/5	0.98	0.05	67,70,91,130	0
2	SO4	J	201	5/5	0.99	0.02	38,42,57,79	0
2	SO4	K	201	5/5	0.99	0.02	39,39,55,60	0
2	SO4	L	201	5/5	0.99	0.02	30,37,58,82	0
2	SO4	I	201	5/5	0.99	0.03	45,50,56,70	0
2	SO4	N	201	5/5	0.99	0.06	40,47,54,71	0
2	SO4	E	202	5/5	0.99	0.04	73,85,97,98	0
2	SO4	B	202	5/5	1.00	0.02	18,43,58,69	0
2	SO4	A	201	5/5	1.00	0.03	35,50,76,76	0
2	SO4	J	202	5/5	1.00	0.02	35,38,46,49	0
2	SO4	E	201	5/5	1.00	0.03	34,48,58,69	0
2	SO4	K	202	5/5	1.00	0.02	16,33,57,66	0
2	SO4	A	202	5/5	1.00	0.02	21,28,57,62	0
2	SO4	L	202	5/5	1.00	0.03	27,39,55,61	0
2	SO4	G	201	5/5	1.00	0.02	38,44,55,64	0
2	SO4	H	201	5/5	1.00	0.02	39,42,64,76	0
2	SO4	B	201	5/5	1.00	0.02	20,42,54,74	0

6.5 Other polymers [i](#)

There are no such residues in this entry.