



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 10:10 AM UTC

PDB ID : 9L7N / pdb_00009l7n
Title : PEDV 3CLpro mutant (C144A) in complex with nsp12/13 peptide substrate
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Deposited on : 2024-12-26
Resolution : 2.23 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
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

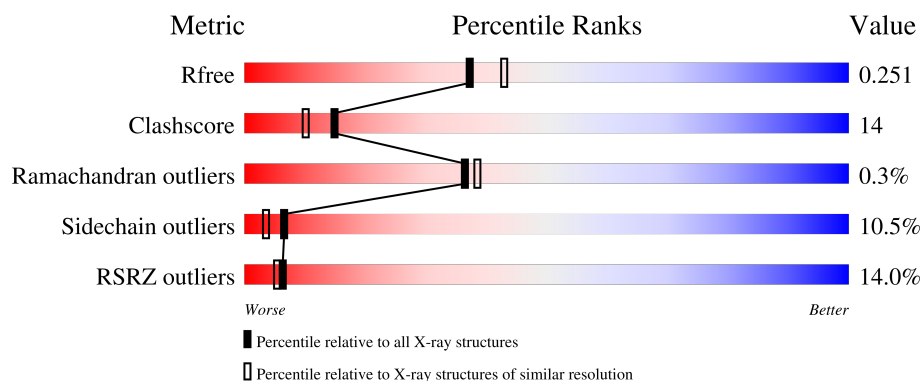
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.23 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	3416 (2.26-2.22)
Clashscore	190562	3556 (2.26-2.22)
Ramachandran outliers	187476	3500 (2.26-2.22)
Sidechain outliers	187428	3501 (2.26-2.22)
RSRZ outliers	180081	3415 (2.26-2.22)

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	308	12% 71% 23% • •
1	B	308	15% 68% 27% • •
2	C	6	17% 83%
2	D	6	33% 17% 67% 17%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4730 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 ORF1ab polyprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	298	Total	C	N	O	S	0	0	0
			2266	1432	389	430	15			
1	B	298	Total	C	N	O	S	0	0	0
			2265	1433	389	428	15			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP A0A023J7B5
A	144	ALA	CYS	engineered mutation	UNP A0A023J7B5
A	300	HIS	-	expression tag	UNP A0A023J7B5
A	301	HIS	-	expression tag	UNP A0A023J7B5
A	302	HIS	-	expression tag	UNP A0A023J7B5
A	303	HIS	-	expression tag	UNP A0A023J7B5
A	304	HIS	-	expression tag	UNP A0A023J7B5
A	305	HIS	-	expression tag	UNP A0A023J7B5
A	306	HIS	-	expression tag	UNP A0A023J7B5
A	307	HIS	-	expression tag	UNP A0A023J7B5
B	0	MET	-	initiating methionine	UNP A0A023J7B5
B	144	ALA	CYS	engineered mutation	UNP A0A023J7B5
B	300	HIS	-	expression tag	UNP A0A023J7B5
B	301	HIS	-	expression tag	UNP A0A023J7B5
B	302	HIS	-	expression tag	UNP A0A023J7B5
B	303	HIS	-	expression tag	UNP A0A023J7B5
B	304	HIS	-	expression tag	UNP A0A023J7B5
B	305	HIS	-	expression tag	UNP A0A023J7B5
B	306	HIS	-	expression tag	UNP A0A023J7B5
B	307	HIS	-	expression tag	UNP A0A023J7B5

- Molecule 2 is a protein called Replicase polyprotein 1ab.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	6	Total 44	C 28	N 8	O 8	0	0	0
2	D	6	Total 44	C 28	N 8	O 8	0	0	0

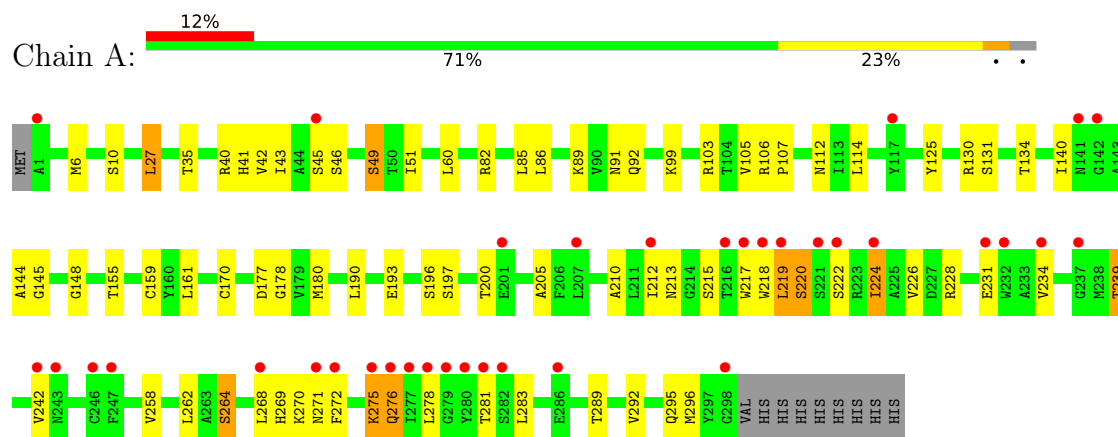
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	70	Total 70	O 70	0	0
3	B	40	Total 40	O 40	0	0
3	C	1	Total 1	O 1	0	0

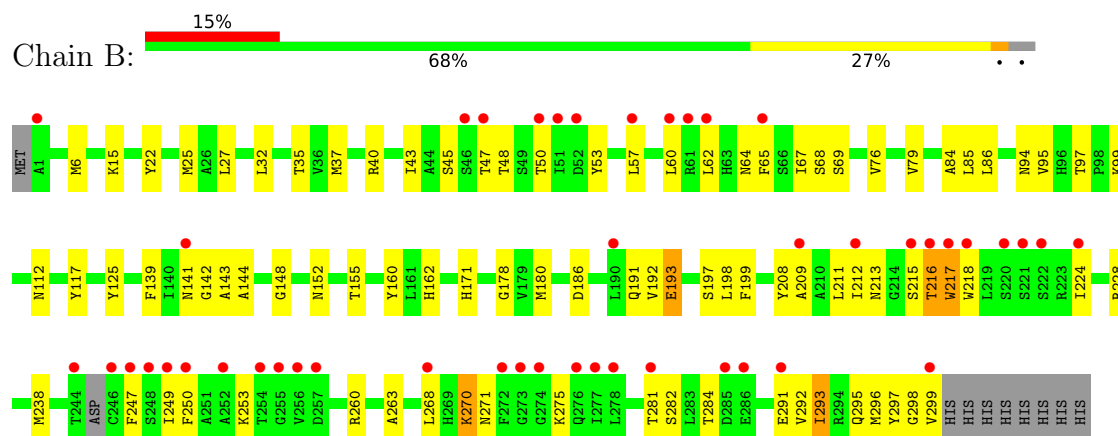
3 Residue-property plots [i](#)

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: ORF1ab polypeptide



• Molecule 1: ORF1ab polypeptide



• Molecule 2: Replicase polypeptide 1ab



• Molecule 2: Replicase polypeptide 1ab



4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	172.05Å 172.05Å 58.95Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	33.84 – 2.23 33.84 – 2.23	Depositor EDS
% Data completeness (in resolution range)	99.7 (33.84-2.23) 99.7 (33.84-2.23)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.62 (at 2.22Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, R_{free}	0.218 , 0.256 0.223 , 0.251	Depositor DCC
R_{free} test set	1987 reflections (6.26%)	wwPDB-VP
Wilson B-factor (Å ²)	40.7	Xtriage
Anisotropy	0.229	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 33.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.005 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4730	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.38% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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 [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.58	0/2313	0.86	0/3142
1	B	0.55	0/2311	0.84	1/3138 (0.0%)
2	C	1.06	0/43	1.09	0/56
2	D	0.89	0/43	1.44	0/56
All	All	0.57	0/4710	0.86	1/6392 (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	B	216	THR	CB-CA-C	6.75	123.86	110.42

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	2266	0	2210	48	0
1	B	2265	0	2214	74	0
2	C	44	0	50	7	0
2	D	44	0	50	22	0
3	A	70	0	0	4	0
3	B	40	0	0	3	0
3	C	1	0	0	4	0
All	All	4730	0	4524	126	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 14.

All (126) 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:276:GLN:HB3	1:A:281:THR:HG22	1.44	0.96
1:B:144:ALA:H	2:D:149:GLN:CG	1.97	0.77
1:A:130:ARG:NH2	1:A:170:CYS:SG	2.56	0.77
1:B:47:THR:HG21	2:D:148:LEU:HG	1.68	0.75
2:C:144:LYS:HE2	3:C:201:HOH:O	1.88	0.74
1:B:144:ALA:HB2	2:D:149:GLN:HG3	1.70	0.73
1:A:103:ARG:HB3	3:A:428:HOH:O	1.89	0.73
1:B:144:ALA:H	2:D:149:GLN:HG3	1.54	0.72
1:A:40:ARG:HA	1:A:86:LEU:HG	1.74	0.69
1:A:200:THR:H	1:A:239:THR:HG22	1.57	0.69
2:C:148:LEU:O	2:C:149:GLN:C	2.39	0.66
1:A:105:VAL:HG13	1:A:159:CYS:HB2	1.78	0.65
1:A:46:SER:HB3	1:A:51:ILE:HD11	1.79	0.65
1:A:6:MET:HE2	1:B:125:TYR:CE1	2.33	0.64
1:B:144:ALA:CB	2:D:149:GLN:HG3	2.27	0.64
1:A:125:TYR:CE1	1:B:6:MET:HE2	2.34	0.62
1:B:212:ILE:HB	1:B:296:MET:HE3	1.82	0.62
1:B:217:TRP:CZ3	1:B:218:TRP:HD1	2.17	0.61
1:B:144:ALA:H	2:D:149:GLN:HG2	1.66	0.60
1:A:35:THR:HG22	1:A:89:LYS:CD	2.34	0.58
1:B:141:ASN:HA	2:D:149:GLN:HB2	1.86	0.58
1:B:152:ASN:O	1:B:155:THR:HG22	2.04	0.57
1:A:210:ALA:HB1	1:A:215:SER:HB3	1.86	0.57
1:B:67:ILE:HD12	1:B:76:VAL:HG22	1.88	0.56
1:B:292:VAL:O	1:B:296:MET:HG2	2.05	0.56
1:B:143:ALA:N	2:D:149:GLN:HG2	2.20	0.56
1:B:95:VAL:HG22	3:B:417:HOH:O	2.06	0.56
1:A:276:GLN:HA	1:A:281:THR:HA	1.88	0.56
1:B:141:ASN:OD1	2:D:148:LEU:HB3	2.05	0.55
2:C:144:LYS:CE	3:C:201:HOH:O	2.52	0.55
1:A:43:ILE:HG21	1:A:60:LEU:HD12	1.90	0.54
1:A:112:ASN:O	1:A:148:GLY:HA2	2.08	0.54
1:B:22:TYR:CE2	1:B:64:ASN:HB2	2.43	0.54
2:C:144:LYS:CD	3:C:201:HOH:O	2.55	0.54
1:B:142:GLY:H	2:D:149:GLN:CD	2.16	0.54
1:B:144:ALA:CB	2:D:149:GLN:HE21	2.21	0.54
1:A:107:PRO:HB3	1:A:131:SER:HA	1.88	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:144:ALA:N	2:D:149:GLN:HG3	2.22	0.53
1:A:10:SER:HB2	1:A:114:LEU:HD13	1.91	0.52
1:B:47:THR:CG2	2:D:148:LEU:HG	2.37	0.52
1:B:15:LYS:NZ	3:B:407:HOH:O	2.42	0.51
1:A:281:THR:HG21	1:B:281:THR:HG21	1.92	0.51
1:B:35:THR:HG23	1:B:37:MET:HE1	1.93	0.51
1:B:218:TRP:HB2	1:B:268:LEU:HD11	1.91	0.51
1:B:209:ALA:HA	1:B:296:MET:HE2	1.92	0.49
1:B:216:THR:O	1:B:218:TRP:N	2.45	0.49
1:B:247:PHE:HA	1:B:250:PHE:HD2	1.78	0.49
1:A:218:TRP:CD1	1:A:218:TRP:H	2.29	0.49
1:A:106:ARG:NH1	3:A:407:HOH:O	2.46	0.49
1:B:142:GLY:H	2:D:149:GLN:CG	2.25	0.49
1:A:35:THR:HG22	1:A:89:LYS:HD3	1.95	0.48
1:B:213:ASN:ND2	1:B:296:MET:HE1	2.28	0.48
1:A:205:ALA:HB2	1:A:289:THR:HG22	1.96	0.48
1:B:85:LEU:HG	1:B:178:GLY:HA2	1.95	0.48
1:B:117:TYR:CE1	1:B:143:ALA:HB2	2.48	0.48
1:A:281:THR:CG2	1:B:281:THR:HG21	2.43	0.48
1:A:292:VAL:O	1:A:296:MET:HG2	2.14	0.48
1:A:85:LEU:HG	1:A:178:GLY:HA2	1.95	0.47
1:B:211:LEU:HD23	1:B:215:SER:O	2.15	0.47
1:A:91:ASN:OD1	1:A:92:GLN:HG3	2.14	0.47
1:B:37:MET:HE2	1:B:37:MET:HB2	1.75	0.47
1:B:212:ILE:HD12	1:B:297:TYR:OH	2.14	0.47
1:B:216:THR:O	1:B:217:TRP:C	2.58	0.47
2:D:148:LEU:CD2	2:D:149:GLN:HE22	2.28	0.47
1:A:144:ALA:HB2	2:C:149:GLN:C	2.39	0.47
1:A:27:LEU:HD11	1:A:42:VAL:HB	1.96	0.46
1:A:82:ARG:NH2	1:A:177:ASP:HB3	2.30	0.46
1:A:103:ARG:HD2	3:A:428:HOH:O	2.16	0.46
2:D:148:LEU:HD22	2:D:149:GLN:HE22	1.80	0.46
1:A:99:LYS:HE2	1:A:155:THR:OG1	2.15	0.46
1:A:41:HIS:CE1	2:C:148:LEU:O	2.69	0.46
1:B:270:LYS:HB3	1:B:270:LYS:HE2	1.51	0.46
1:B:186:ASP:OD1	1:B:186:ASP:N	2.40	0.45
1:B:94:ASN:HB3	1:B:97:THR:OG1	2.17	0.45
1:B:142:GLY:H	2:D:149:GLN:HG2	1.82	0.45
1:B:160:TYR:OH	1:B:162:HIS:HD2	2.00	0.45
1:B:40:ARG:HG3	1:B:53:TYR:CD1	2.52	0.45
2:C:144:LYS:HD2	3:C:201:HOH:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:213:ASN:HB2	1:A:278:LEU:HD21	1.99	0.45
1:A:224:ILE:HD13	1:A:224:ILE:HA	1.80	0.44
1:B:139:PHE:HD1	1:B:143:ALA:HB1	1.83	0.44
1:B:238:MET:HE2	1:B:238:MET:HB3	1.94	0.44
1:B:84:ALA:HB1	1:B:180:MET:HE2	1.99	0.44
1:A:145:GLY:HA2	1:A:161:LEU:HG	1.99	0.44
1:B:99:LYS:HG2	1:B:155:THR:OG1	2.18	0.44
2:D:147:VAL:O	2:D:149:GLN:N	2.49	0.44
1:B:142:GLY:N	2:D:149:GLN:HG2	2.32	0.43
1:B:25:MET:HE3	1:B:47:THR:HG23	2.00	0.43
1:A:258:VAL:O	1:A:262:LEU:HG	2.19	0.43
1:A:220:SER:HB3	1:A:264:SER:CA	2.49	0.43
1:B:47:THR:HB	2:D:147:VAL:HG13	2.01	0.43
2:D:148:LEU:HD23	2:D:148:LEU:HA	1.77	0.43
1:B:297:TYR:C	1:B:299:VAL:H	2.27	0.42
1:A:106:ARG:HA	1:A:106:ARG:HD3	1.77	0.42
1:B:180:MET:CE	1:B:186:ASP:HB3	2.49	0.42
1:A:276:GLN:HE21	1:A:276:GLN:HB2	1.62	0.42
1:B:148:GLY:HA3	1:B:160:TYR:HB3	2.01	0.42
1:B:65:PHE:CE2	1:B:79:VAL:HG21	2.55	0.42
1:A:46:SER:OG	1:A:49:SER:O	2.31	0.42
1:B:297:TYR:O	1:B:299:VAL:N	2.52	0.42
1:B:293:ILE:HD13	1:B:293:ILE:HA	1.79	0.42
1:A:268:LEU:O	1:A:269:HIS:C	2.62	0.42
1:A:272:PHE:HE2	1:A:283:LEU:HG	1.85	0.42
1:B:40:ARG:O	1:B:43:ILE:HG12	2.20	0.42
1:B:112:ASN:O	1:B:148:GLY:HA2	2.20	0.42
1:B:208:TYR:O	1:B:212:ILE:HG12	2.20	0.42
1:A:219:LEU:HD23	1:A:219:LEU:HA	1.82	0.41
1:B:32:LEU:O	1:B:35:THR:HG22	2.19	0.41
1:B:217:TRP:CD2	1:B:218:TRP:N	2.88	0.41
1:B:193:GLU:H	1:B:193:GLU:HG3	1.60	0.41
1:A:217:TRP:CZ2	1:A:275:LYS:HB2	2.56	0.41
1:A:134:THR:HB	1:A:170:CYS:HB3	2.02	0.40
1:A:289:THR:HG23	3:A:406:HOH:O	2.21	0.40
1:B:139:PHE:HD2	1:B:171:HIS:CG	2.39	0.40
1:B:144:ALA:HB3	2:D:149:GLN:HE21	1.85	0.40
1:A:89:LYS:HD2	1:A:89:LYS:HA	1.81	0.40
1:B:84:ALA:CB	1:B:180:MET:HE2	2.52	0.40
1:B:198:LEU:HB2	1:B:238:MET:HE3	2.04	0.40
1:A:6:MET:HE2	1:B:125:TYR:HE1	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:40:ARG:HA	1:B:86:LEU:HG	2.04	0.40
1:B:199:PHE:HB2	3:B:413:HOH:O	2.22	0.40
1:B:224:ILE:HG22	1:B:263:ALA:HB2	2.04	0.40
1:A:180:MET:HE2	1:A:180:MET:HB2	1.66	0.40
1:B:60:LEU:HD12	1:B:60:LEU:HA	1.89	0.40
1:B:62:LEU:HD23	1:B:62:LEU:HA	1.86	0.40
1:B:224:ILE:HG13	1:B:228:ARG:HG2	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 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	296/308 (96%)	280 (95%)	15 (5%)	1 (0%)	36	38
1	B	294/308 (96%)	282 (96%)	11 (4%)	1 (0%)	36	38
2	C	4/6 (67%)	4 (100%)	0	0	100	100
2	D	4/6 (67%)	3 (75%)	1 (25%)	0	100	100
All	All	598/628 (95%)	569 (95%)	27 (4%)	2 (0%)	36	38

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	234	VAL
1	B	298	GLY

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	243/254 (96%)	219 (90%)	24 (10%)	7	4
1	B	243/254 (96%)	220 (90%)	23 (10%)	8	5
2	C	5/5 (100%)	3 (60%)	2 (40%)	0	0
2	D	5/5 (100%)	2 (40%)	3 (60%)	0	0
All	All	496/518 (96%)	444 (90%)	52 (10%)	6	3

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	LEU
1	A	45	SER
1	A	49	SER
1	A	140	ILE
1	A	190	LEU
1	A	193	GLU
1	A	196	SER
1	A	197	SER
1	A	212	ILE
1	A	219	LEU
1	A	220	SER
1	A	222	SER
1	A	224	ILE
1	A	226	VAL
1	A	228	ARG
1	A	231	GLU
1	A	239	THR
1	A	242	VAL
1	A	264	SER
1	A	270	LYS
1	A	271	ASN
1	A	275	LYS
1	A	276	GLN
1	A	295	GLN
1	B	27	LEU
1	B	45	SER
1	B	48	THR
1	B	50	THR
1	B	57	LEU
1	B	68	SER

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Mol	Chain	Res	Type
1	B	69	SER
1	B	191	GLN
1	B	192	VAL
1	B	193	GLU
1	B	197	SER
1	B	217	TRP
1	B	249	ILE
1	B	253	LYS
1	B	260	ARG
1	B	270	LYS
1	B	271	ASN
1	B	275	LYS
1	B	282	SER
1	B	284	THR
1	B	291	GLU
1	B	293	ILE
1	B	295	GLN
2	C	145	SER
2	C	147	VAL
2	D	144	LYS
2	D	145	SER
2	D	148	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	96	HIS
1	A	243	ASN
1	A	266	GLN
1	A	276	GLN
1	B	152	ASN
1	B	162	HIS
1	B	243	ASN
1	B	266	GLN
2	C	149	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	298/308 (96%)	0.71	36 (12%) 8 8	23, 41, 80, 94	0
1	B	298/308 (96%)	0.98	46 (15%) 5 4	30, 50, 76, 90	0
2	C	6/6 (100%)	1.43	1 (16%) 4 3	29, 30, 30, 30	0
2	D	6/6 (100%)	2.02	2 (33%) 1 0	30, 30, 30, 33	0
All	All	608/628 (96%)	0.86	85 (13%) 6 5	23, 46, 78, 94	0

All (85) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	273	GLY	4.7
1	B	250	PHE	4.4
1	A	281	THR	4.3
1	A	1	ALA	4.2
1	A	298	GLY	4.1
2	D	148	LEU	4.0
1	A	272	PHE	4.0
1	B	216	THR	3.9
1	B	277	ILE	3.8
1	B	244	THR	3.8
1	B	249	ILE	3.7
1	A	212	ILE	3.7
1	B	47	THR	3.6
1	A	280	TYR	3.5
1	B	190	LEU	3.5
1	A	141	ASN	3.5
1	B	299	VAL	3.5
1	B	278	LEU	3.4
1	B	217	TRP	3.4
1	B	268	LEU	3.4
1	B	212	ILE	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	224	ILE	3.3
1	A	278	LEU	3.2
1	B	286	GLU	3.1
1	B	254	THR	3.1
1	A	277	ILE	3.1
1	B	46	SER	3.1
1	B	256	VAL	3.0
1	B	52	ASP	3.0
1	A	246	CYS	3.0
1	B	246	CYS	2.9
1	A	217	TRP	2.9
1	A	275	LYS	2.8
1	A	243	ASN	2.7
1	A	234	VAL	2.7
1	B	1	ALA	2.7
1	B	220	SER	2.6
1	B	65	PHE	2.6
1	B	247	PHE	2.6
1	A	286	GLU	2.5
1	B	272	PHE	2.5
1	A	271	ASN	2.5
1	B	215	SER	2.5
1	B	57	LEU	2.5
1	B	141	ASN	2.4
1	B	218	TRP	2.4
1	A	279	GLY	2.4
1	A	242	VAL	2.4
1	B	285	ASP	2.4
1	B	281	THR	2.4
1	A	45	SER	2.3
1	A	276	GLN	2.3
1	B	60	LEU	2.3
1	A	232	TRP	2.3
1	A	247	PHE	2.3
1	A	117	TYR	2.3
1	A	237	GLY	2.3
1	A	216	THR	2.3
1	B	50	THR	2.3
1	B	221	SER	2.3
1	A	201	GLU	2.2
1	B	224	ILE	2.2
2	C	148	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	252	ALA	2.2
1	A	282	SER	2.2
1	B	257	ASP	2.2
1	B	209	ALA	2.2
1	A	221	SER	2.2
1	A	222	SER	2.2
1	B	222	SER	2.2
1	B	274	GLY	2.2
1	B	276	GLN	2.2
2	D	147	VAL	2.1
1	B	291	GLU	2.1
1	B	255	GLY	2.1
1	B	61	ARG	2.1
1	A	207	LEU	2.1
1	A	268	LEU	2.1
1	B	51	ILE	2.1
1	B	248	SER	2.1
1	A	219	LEU	2.1
1	B	62	LEU	2.1
1	A	142	GLY	2.0
1	A	218	TRP	2.0
1	A	231	GLU	2.0

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.