



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:32 PM UTC

PDB ID : 2P5P / pdb_00002p5p
Title : Crystal Structure Analysis of the West Nile virus envelope (E) protein domain III
Authors : Gao, F.; Yuan, F.; Gao, G.F.
Deposited on : 2007-03-16
Resolution : 2.80 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

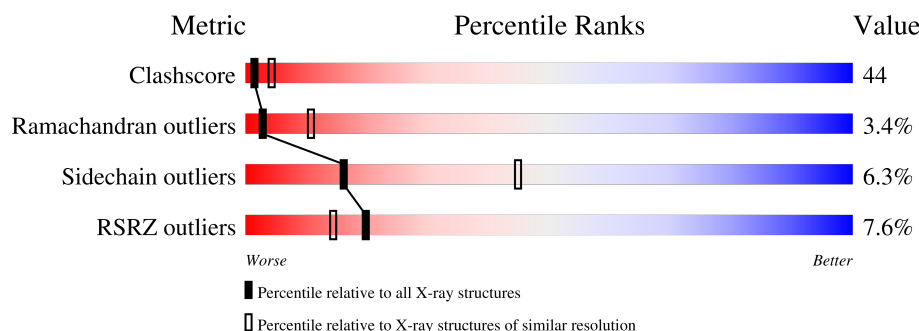
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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))
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	117	5% 36% 43% 8% 14%
1	B	117	3% 35% 45% 5% 14%
1	C	117	11% 25% 51% 9% 14%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 2457 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 Genome polyprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	101	Total	C	N	O	S	0	0	0
			758	484	128	144	2			
1	B	101	Total	C	N	O	S	0	0	0
			758	484	128	144	2			
1	C	101	Total	C	N	O	S	0	0	0
			758	484	128	144	2			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	312	LEU	ALA	conflict	UNP P06935
A	313	GLY	ARG	conflict	UNP P06935
A	369	ALA	SER	conflict	UNP P06935
A	413	LYS	ARG	conflict	UNP P06935
B	312	LEU	ALA	conflict	UNP P06935
B	313	GLY	ARG	conflict	UNP P06935
B	369	ALA	SER	conflict	UNP P06935
B	413	LYS	ARG	conflict	UNP P06935
C	312	LEU	ALA	conflict	UNP P06935
C	313	GLY	ARG	conflict	UNP P06935
C	369	ALA	SER	conflict	UNP P06935
C	413	LYS	ARG	conflict	UNP P06935

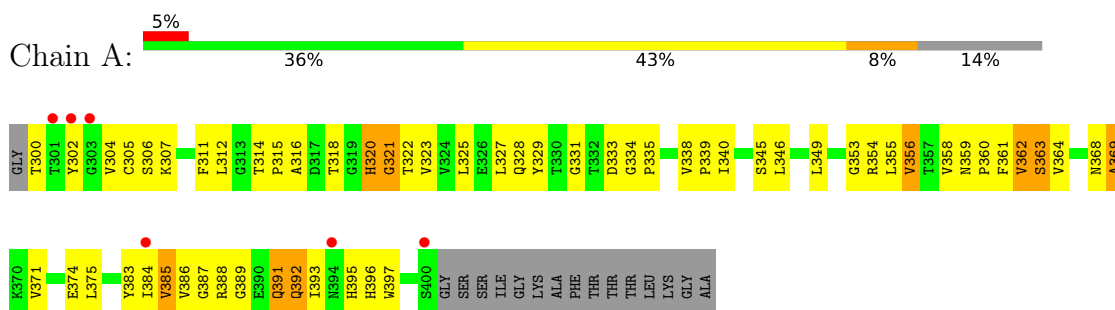
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	64	Total	O	0	0
			64	64		
2	B	60	Total	O	0	0
			60	60		
2	C	59	Total	O	0	0
			59	59		

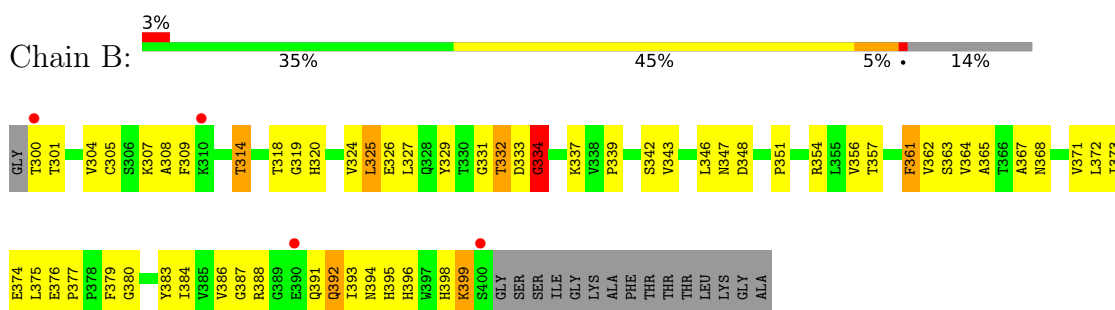
3 Residue-property plots [i](#)

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.

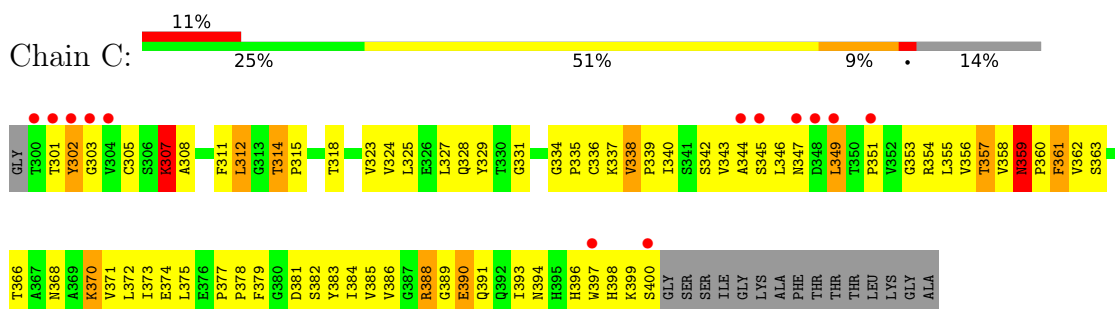
• Molecule 1: Genome polyprotein



• Molecule 1: Genome polyprotein



• Molecule 1: Genome polyprotein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	52.56Å 59.69Å 95.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.80 30.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	(Not available) (30.00-2.80) 84.7 (30.00-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.45 (at 2.51Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.244 , 0.276 0.258 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	33.9	Xtriage
Anisotropy	0.348	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 80.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	2457	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.13% 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

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 >5	RMSZ	# Z >5
1	A	0.57	0/777	1.11	5/1063 (0.5%)
1	B	0.50	0/777	1.09	6/1063 (0.6%)
1	C	0.56	0/777	1.18	8/1063 (0.8%)
All	All	0.54	0/2331	1.13	19/3189 (0.6%)

There are no bond length outliers.

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	356	VAL	N-CA-C	-12.72	100.87	111.81
1	C	362	VAL	N-CA-C	-10.17	92.67	108.23
1	C	356	VAL	N-CA-C	-8.91	103.16	111.45
1	B	362	VAL	N-CA-C	-8.86	94.68	108.23
1	C	359	ASN	CA-C-N	8.06	129.91	119.84
1	C	359	ASN	C-N-CA	8.06	129.91	119.84
1	A	353	GLY	N-CA-C	-6.72	101.88	111.42
1	A	362	VAL	N-CA-C	-6.55	97.55	106.85
1	A	363	SER	N-CA-C	6.17	120.50	113.15
1	C	361	PHE	N-CA-C	6.04	119.32	109.24
1	B	319	GLY	N-CA-C	-5.65	107.19	115.72
1	A	358	VAL	N-CA-C	5.37	116.94	109.80
1	B	392	GLN	N-CA-C	5.31	118.02	110.10
1	C	390	GLU	N-CA-C	-5.28	107.02	112.93
1	C	338	VAL	N-CA-C	5.26	113.07	107.76
1	B	334	GLY	CA-C-N	5.17	124.93	119.76
1	B	334	GLY	C-N-CA	5.17	124.93	119.76
1	C	312	LEU	N-CA-C	-5.06	101.50	109.25
1	B	332	THR	N-CA-C	-5.05	107.06	114.39

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	758	0	750	62	0
1	B	758	0	750	52	0
1	C	758	0	750	94	0
2	A	64	0	0	7	0
2	B	60	0	0	4	0
2	C	59	0	0	4	0
All	All	2457	0	2250	199	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 44.

All (199) 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:364:VAL:HG13	1:C:358:VAL:HG13	1.16	1.15
1:C:386:VAL:HB	1:C:393:ILE:HD11	1.27	1.10
1:C:388:ARG:NE	1:C:389:GLY:H	1.50	1.08
1:C:311:PHE:HE2	1:C:393:ILE:HD13	1.12	1.05
1:C:301:THR:HG22	1:C:302:TYR:H	1.24	1.01
1:C:393:ILE:HD12	1:C:393:ILE:O	1.61	1.00
1:C:342:SER:HB3	1:C:353:GLY:HA3	1.46	0.97
1:C:311:PHE:CE2	1:C:393:ILE:HD13	2.04	0.89
1:C:388:ARG:HE	1:C:389:GLY:H	1.18	0.89
1:C:301:THR:HG22	1:C:302:TYR:N	1.88	0.89
1:C:349:LEU:HD12	1:C:349:LEU:H	1.38	0.89
1:C:386:VAL:CB	1:C:393:ILE:HD11	2.03	0.88
1:C:386:VAL:HB	1:C:393:ILE:CD1	2.05	0.87
1:A:355:LEU:HD23	1:A:375:LEU:HD13	1.56	0.86
1:C:378:PRO:HG2	1:C:382:SER:HB3	1.61	0.82
1:C:338:VAL:HB	1:C:360:PRO:HB2	1.62	0.82
1:A:364:VAL:HG13	1:C:358:VAL:CG1	2.04	0.82
1:A:388:ARG:HA	1:A:392:GLN:HB2	1.63	0.81
1:A:364:VAL:CG1	1:C:358:VAL:HG13	2.08	0.76
1:C:311:PHE:HE2	1:C:393:ILE:CD1	1.96	0.76
1:C:388:ARG:NE	1:C:389:GLY:N	2.32	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:314:THR:HG22	1:C:315:PRO:HD2	1.67	0.75
1:A:363:SER:HB2	1:C:358:VAL:HG12	1.70	0.74
1:C:388:ARG:HE	1:C:389:GLY:N	1.85	0.73
1:B:308:ALA:HB2	1:B:391:GLN:HB3	1.70	0.72
1:C:388:ARG:CD	1:C:389:GLY:H	2.02	0.72
1:B:332:THR:HG22	1:B:367:ALA:HB2	1.72	0.71
1:B:326:GLU:C	1:B:327:LEU:HD12	2.15	0.71
1:B:307:LYS:HG3	1:B:331:GLY:HA2	1.71	0.71
1:C:327:LEU:HB2	1:C:371:VAL:HG22	1.73	0.70
1:B:354:ARG:HG2	1:B:376:GLU:HB3	1.72	0.70
1:C:301:THR:HG23	1:C:335:PRO:HB2	1.74	0.69
1:C:301:THR:CG2	1:C:302:TYR:H	1.96	0.69
1:A:305:CYS:HB3	1:A:329:TYR:CZ	2.27	0.69
1:A:318:THR:HG21	2:A:472:HOH:O	1.92	0.69
1:B:309:PHE:O	1:B:393:ILE:HD13	1.92	0.69
1:A:383:TYR:CE1	1:A:396:HIS:HB2	2.27	0.69
1:B:334:GLY:HA2	1:B:365:ALA:HA	1.74	0.68
1:A:312:LEU:HD11	1:A:328:GLN:HB2	1.76	0.68
1:A:335:PRO:HA	1:A:362:VAL:O	1.95	0.67
1:A:383:TYR:HE1	1:A:396:HIS:HB2	1.58	0.67
1:B:314:THR:HG22	1:B:395:HIS:NE2	2.10	0.67
1:C:311:PHE:HE1	1:C:325:LEU:HD22	1.59	0.66
1:C:393:ILE:HD12	1:C:393:ILE:C	2.20	0.66
1:B:327:LEU:HD13	1:B:371:VAL:HG23	1.78	0.65
1:C:337:LYS:NZ	1:C:359:ASN:HB2	2.12	0.65
1:C:327:LEU:HB2	1:C:371:VAL:CG2	2.28	0.64
1:A:388:ARG:CA	1:A:392:GLN:HB2	2.27	0.64
1:C:301:THR:HG23	1:C:335:PRO:CB	2.28	0.64
1:C:377:PRO:HG2	1:C:399:LYS:HD2	1.81	0.63
1:B:356:VAL:HB	1:B:374:GLU:O	1.97	0.63
1:B:342:SER:HB2	2:B:465:HOH:O	1.99	0.63
1:A:334:GLY:HA2	1:A:335:PRO:C	2.24	0.62
1:C:344:ALA:O	1:C:382:SER:HA	1.99	0.62
1:B:329:TYR:CE2	1:B:331:GLY:HA3	2.34	0.62
1:C:312:LEU:HD21	1:C:328:GLN:HB2	1.80	0.62
1:A:338:VAL:HB	1:A:360:PRO:HB2	1.81	0.61
1:A:374:GLU:OE1	1:C:370:LYS:HE3	2.00	0.61
1:C:301:THR:CG2	1:C:302:TYR:N	2.59	0.61
1:C:308:ALA:HB2	1:C:391:GLN:HB3	1.82	0.61
1:B:383:TYR:CE1	1:B:396:HIS:HB2	2.36	0.60
1:B:327:LEU:HB2	1:B:371:VAL:HG22	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:337:LYS:HB2	1:B:361:PHE:CE1	2.36	0.60
1:B:339:PRO:HA	2:B:450:HOH:O	2.01	0.59
1:C:334:GLY:HA2	1:C:335:PRO:C	2.26	0.59
1:A:316:ALA:O	1:A:323:VAL:HA	2.03	0.58
1:C:386:VAL:CG2	1:C:393:ILE:HD11	2.33	0.58
1:C:302:TYR:HB2	1:C:335:PRO:O	2.04	0.57
1:A:356:VAL:HB	1:A:374:GLU:HG2	1.86	0.57
1:C:351:PRO:HG3	2:C:425:HOH:O	2.05	0.57
1:A:389:GLY:C	1:A:391:GLN:H	2.13	0.57
1:C:340:ILE:HA	1:C:385:VAL:O	2.05	0.57
1:B:374:GLU:C	1:B:375:LEU:HD12	2.29	0.57
1:A:345:SER:HA	1:A:383:TYR:HD2	1.69	0.56
1:A:363:SER:HB2	1:C:358:VAL:CG1	2.34	0.56
1:C:307:LYS:HG2	1:C:331:GLY:HA2	1.88	0.56
1:C:358:VAL:O	1:C:359:ASN:C	2.48	0.56
1:C:381:ASP:CG	1:C:398:HIS:HD1	2.14	0.56
1:B:304:VAL:HG22	1:B:305:CYS:N	2.20	0.55
1:B:327:LEU:HD12	1:B:327:LEU:N	2.21	0.55
1:B:377:PRO:HG2	1:B:399:LYS:HG3	1.89	0.55
1:C:371:VAL:C	1:C:372:LEU:HD22	2.31	0.55
1:C:372:LEU:HD22	1:C:372:LEU:N	2.21	0.55
1:C:337:LYS:HE2	1:C:359:ASN:HB2	1.89	0.55
1:A:328:GLN:HG3	2:A:424:HOH:O	2.07	0.54
1:C:343:VAL:O	1:C:383:TYR:HB2	2.08	0.54
1:C:391:GLN:CD	1:C:391:GLN:N	2.65	0.54
2:A:456:HOH:O	1:C:357:THR:HG23	2.07	0.54
1:C:311:PHE:CE1	1:C:325:LEU:HD22	2.42	0.53
1:C:337:LYS:CE	1:C:359:ASN:HB2	2.38	0.53
1:B:384:ILE:O	1:B:394:ASN:HA	2.09	0.53
1:A:340:ILE:HA	1:A:385:VAL:O	2.09	0.52
1:C:329:TYR:O	1:C:368:ASN:HA	2.11	0.51
1:C:377:PRO:HG3	1:C:397:TRP:CD1	2.46	0.51
1:A:386:VAL:HB	1:A:393:ILE:CG1	2.41	0.51
1:C:301:THR:CG2	1:C:335:PRO:HB2	2.39	0.51
1:B:325:LEU:HD12	1:B:327:LEU:HD11	1.93	0.51
1:A:307:LYS:HG2	1:A:333:ASP:OD2	2.11	0.50
1:B:332:THR:O	1:B:334:GLY:N	2.44	0.50
1:A:391:GLN:H	1:A:391:GLN:HE21	1.58	0.50
1:B:379:PHE:CZ	1:B:399:LYS:HE2	2.46	0.50
1:C:338:VAL:HB	1:C:360:PRO:CB	2.37	0.50
1:C:354:ARG:HB2	2:C:436:HOH:O	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:315:PRO:HG3	1:C:325:LEU:CD2	2.42	0.49
1:A:322:THR:HB	1:A:375:LEU:O	2.12	0.49
1:A:368:ASN:O	1:A:369:ALA:O	2.30	0.49
1:A:391:GLN:NE2	1:A:391:GLN:N	2.60	0.49
1:C:323:VAL:HG12	1:C:377:PRO:HD3	1.95	0.49
1:B:339:PRO:HG2	1:B:387:GLY:HA2	1.94	0.49
1:C:305:CYS:N	1:C:336:CYS:HB2	2.27	0.49
1:C:340:ILE:HG13	1:C:385:VAL:O	2.11	0.48
1:A:340:ILE:HG13	1:A:385:VAL:O	2.12	0.48
1:C:388:ARG:O	1:C:391:GLN:HG2	2.13	0.48
1:A:361:PHE:HB2	2:A:431:HOH:O	2.13	0.48
1:A:374:GLU:OE1	1:C:370:LYS:CE	2.61	0.48
1:A:388:ARG:N	1:A:392:GLN:HB2	2.29	0.48
1:A:311:PHE:CZ	1:A:395:HIS:HB2	2.48	0.48
1:B:308:ALA:CB	1:B:391:GLN:HB3	2.41	0.48
1:B:327:LEU:HB2	1:B:371:VAL:CG2	2.43	0.48
1:C:386:VAL:HB	1:C:393:ILE:CG1	2.44	0.48
1:C:390:GLU:H	1:C:391:GLN:NE2	2.11	0.47
1:A:361:PHE:N	2:A:431:HOH:O	2.48	0.47
1:B:327:LEU:HD13	1:B:371:VAL:CG2	2.44	0.47
1:B:372:LEU:C	1:B:373:ILE:HG13	2.39	0.47
1:A:327:LEU:HB2	1:A:371:VAL:CG2	2.44	0.47
1:B:304:VAL:CG2	1:B:339:PRO:HG3	2.44	0.47
1:C:307:LYS:HB2	1:C:329:TYR:CZ	2.48	0.47
1:B:339:PRO:O	1:B:386:VAL:HA	2.15	0.47
1:C:388:ARG:HE	1:C:389:GLY:CA	2.27	0.47
1:B:342:SER:O	1:B:351:PRO:HA	2.14	0.47
1:A:361:PHE:CZ	1:C:363:SER:HB2	2.50	0.46
1:B:373:ILE:HG22	1:B:375:LEU:CD1	2.45	0.46
1:C:325:LEU:HB2	1:C:373:ILE:HB	1.97	0.46
1:C:345:SER:O	1:C:346:LEU:C	2.57	0.46
1:B:356:VAL:H	1:B:375:LEU:HA	1.80	0.46
1:C:323:VAL:O	1:C:374:GLU:HA	2.16	0.46
1:B:380:GLY:O	1:B:398:HIS:HA	2.15	0.46
1:C:325:LEU:HD11	1:C:384:ILE:HG21	1.97	0.45
1:C:343:VAL:O	1:C:383:TYR:N	2.50	0.45
1:A:329:TYR:CE2	1:A:331:GLY:HA3	2.51	0.45
1:A:339:PRO:HG2	1:A:387:GLY:HA2	1.99	0.45
1:C:339:PRO:O	1:C:386:VAL:HA	2.17	0.45
1:B:300:THR:HG22	1:B:301:THR:N	2.32	0.45
1:B:308:ALA:HB2	1:B:391:GLN:CB	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:301:THR:HG21	1:C:361:PHE:CE2	2.52	0.45
1:A:386:VAL:HB	1:A:393:ILE:HD11	1.98	0.44
1:B:379:PHE:HA	1:B:399:LYS:HB3	1.99	0.44
1:A:307:LYS:O	1:A:329:TYR:HE1	2.00	0.44
1:C:355:LEU:HD23	1:C:375:LEU:HG	2.00	0.44
1:C:368:ASN:ND2	2:C:421:HOH:O	2.50	0.44
1:A:320:HIS:HB2	1:A:321:GLY:H	1.46	0.44
1:A:385:VAL:HG12	1:B:347:ASN:ND2	2.33	0.44
1:A:323:VAL:HG11	1:A:397:TRP:CE2	2.52	0.44
1:A:391:GLN:HE21	1:A:391:GLN:N	2.15	0.44
1:B:334:GLY:HA2	1:B:365:ALA:CA	2.47	0.44
1:C:311:PHE:CE2	1:C:393:ILE:CD1	2.83	0.44
1:A:304:VAL:HG12	1:A:305:CYS:N	2.33	0.44
1:A:359:ASN:N	1:A:360:PRO:HD3	2.33	0.44
1:C:342:SER:CB	1:C:353:GLY:HA3	2.34	0.44
1:C:379:PHE:HD1	1:C:400:SER:O	2.01	0.43
1:A:375:LEU:HG	2:A:470:HOH:O	2.17	0.43
1:B:329:TYR:CZ	1:B:331:GLY:HA3	2.53	0.43
1:C:357:THR:HB	2:C:454:HOH:O	2.17	0.43
1:A:314:THR:O	1:A:315:PRO:C	2.62	0.43
1:C:323:VAL:CG1	1:C:375:LEU:HB2	2.49	0.43
1:C:327:LEU:O	1:C:370:LYS:HA	2.18	0.43
1:B:386:VAL:HB	1:B:393:ILE:CG1	2.49	0.42
1:A:311:PHE:CE2	1:A:395:HIS:HB2	2.53	0.42
1:B:363:SER:C	1:B:364:VAL:HG13	2.44	0.42
1:A:305:CYS:HB3	1:A:329:TYR:OH	2.19	0.42
1:A:349:LEU:HD22	1:A:349:LEU:N	2.34	0.42
1:B:388:ARG:HA	1:B:392:GLN:HG2	2.01	0.42
1:A:391:GLN:H	1:A:391:GLN:NE2	2.17	0.42
1:B:373:ILE:CG2	1:B:375:LEU:HD11	2.49	0.42
1:C:338:VAL:HA	1:C:339:PRO:HD3	1.77	0.42
1:C:383:TYR:CZ	1:C:396:HIS:HB2	2.54	0.42
1:C:301:THR:HG23	1:C:335:PRO:HB3	2.02	0.42
1:C:346:LEU:O	1:C:347:ASN:C	2.62	0.42
1:A:325:LEU:HD11	1:A:384:ILE:HG21	2.01	0.42
1:B:343:VAL:CG2	1:B:383:TYR:HB2	2.50	0.42
1:C:329:TYR:CE2	1:C:331:GLY:HA3	2.55	0.42
1:B:318:THR:HG21	1:B:324:VAL:HG23	2.01	0.42
1:C:314:THR:HG22	1:C:315:PRO:CD	2.43	0.42
1:A:306:SER:C	1:A:307:LYS:HD3	2.45	0.41
1:A:389:GLY:C	1:A:391:GLN:N	2.74	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:300:THR:HB	2:A:466:HOH:O	2.20	0.41
1:B:346:LEU:HG	2:B:462:HOH:O	2.20	0.41
1:C:318:THR:CG2	1:C:324:VAL:HG13	2.50	0.41
1:B:320:HIS:CE1	2:B:428:HOH:O	2.73	0.41
1:A:368:ASN:C	1:A:369:ALA:O	2.64	0.41
1:A:307:LYS:HB2	1:A:329:TYR:CE1	2.55	0.41
1:B:357:THR:HB	1:B:373:ILE:HG23	2.02	0.41
1:A:327:LEU:HB2	1:A:371:VAL:HG23	2.02	0.41
1:B:367:ALA:O	1:B:368:ASN:HB2	2.20	0.41
1:B:373:ILE:HG22	1:B:375:LEU:HD12	2.03	0.40
1:A:323:VAL:HG12	1:A:397:TRP:CZ2	2.56	0.40
1:C:307:LYS:HB2	1:C:329:TYR:CE1	2.56	0.40
1:A:354:ARG:O	1:A:375:LEU:HD12	2.21	0.40
1:C:302:TYR:HB3	1:C:303:GLY:H	1.55	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	99/117 (85%)	86 (87%)	8 (8%)	5 (5%)	1	5
1	B	99/117 (85%)	87 (88%)	10 (10%)	2 (2%)	6	21
1	C	99/117 (85%)	84 (85%)	12 (12%)	3 (3%)	3	12
All	All	297/351 (85%)	257 (86%)	30 (10%)	10 (3%)	3	11

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	369	ALA
1	A	302	TYR
1	A	320	HIS

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Mol	Chain	Res	Type
1	C	302	TYR
1	B	333	ASP
1	B	334	GLY
1	A	346	LEU
1	C	307	LYS
1	C	359	ASN
1	A	321	GLY

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	85/95 (90%)	82 (96%)	3 (4%)	32	67
1	B	85/95 (90%)	80 (94%)	5 (6%)	18	48
1	C	85/95 (90%)	77 (91%)	8 (9%)	8	27
All	All	255/285 (90%)	239 (94%)	16 (6%)	16	45

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

Mol	Chain	Res	Type
1	A	385	VAL
1	A	391	GLN
1	A	392	GLN
1	B	314	THR
1	B	325	LEU
1	B	348	ASP
1	B	361	PHE
1	B	399	LYS
1	C	307	LYS
1	C	314	THR
1	C	349	LEU
1	C	357	THR
1	C	366	THR
1	C	370	LYS
1	C	388	ARG

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Mol	Chain	Res	Type
1	C	394	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	320	HIS
1	A	391	GLN
1	B	328	GLN
1	B	394	ASN
1	C	320	HIS
1	C	359	ASN
1	C	368	ASN
1	C	391	GLN

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](#)

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 [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	101/117 (86%)	0.40	6 (5%)	28	21	9, 26, 45, 64	0
1	B	101/117 (86%)	0.63	4 (3%)	42	33	16, 36, 48, 70	0
1	C	101/117 (86%)	0.81	13 (12%)	7	6	19, 36, 71, 80	0
All	All	303/351 (86%)	0.61	23 (7%)	20	14	9, 34, 61, 80	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	400	SER	3.4
1	C	302	TYR	3.3
1	A	400	SER	3.2
1	C	303	GLY	3.2
1	A	301	THR	3.1
1	C	300	THR	3.0
1	B	300	THR	2.6
1	C	397	TRP	2.5
1	C	348	ASP	2.4
1	C	344	ALA	2.4
1	C	349	LEU	2.4
1	C	400	SER	2.4
1	C	347	ASN	2.3
1	C	351	PRO	2.3
1	B	310	LYS	2.3
1	A	303	GLY	2.3
1	C	345	SER	2.2
1	A	394	ASN	2.2
1	A	384	ILE	2.2
1	C	301	THR	2.2
1	B	390	GLU	2.2
1	A	302	TYR	2.2
1	C	304	VAL	2.1

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.