



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 05:12 PM UTC

PDB ID : 4RY4 / pdb_00004ry4
Title : C-terminal mutant (Y448F) of HCV/J4 RNA polymerase
Authors : Jaeger, J.; Cherry, A.; Dennis, C.
Deposited on : 2014-12-13
Resolution : 2.59 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

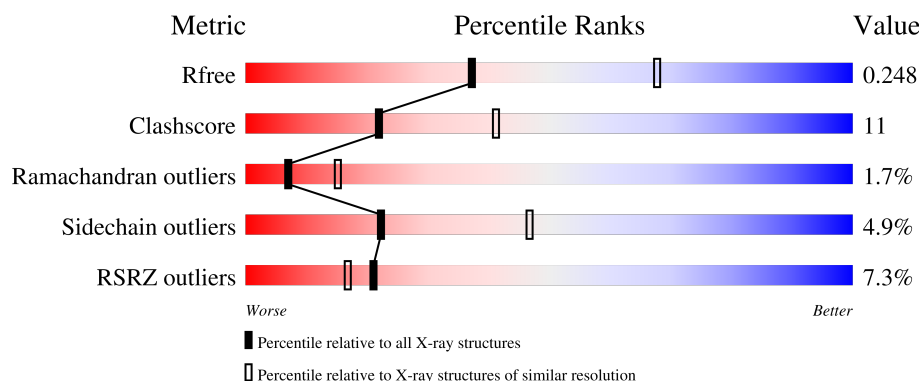
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.59 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	570	10% 73% 22% • •
1	B	570	4% 78% 18% • •

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9119 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 HCV J4 RNA polymerase (NS5B).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	566	Total	C	N	O	S	0	0	0
			4387	2763	777	815	32			
1	B	565	Total	C	N	O	S	0	0	0
			4382	2760	776	814	32			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	448	PHE	TYR	engineered mutation	UNP O92972
B	448	PHE	TYR	engineered mutation	UNP O92972

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	186	Total	O	0	0
			186	186		
2	B	164	Total	O	0	0
			164	164		

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	105.59Å 108.35Å 134.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.90 – 2.59 19.90 – 2.59	Depositor EDS
% Data completeness (in resolution range)	86.5 (19.90-2.59) 85.8 (19.90-2.59)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.43 (at 2.57Å)	Xtriage
Refinement program	PHENIX 1.8.4	Depositor
R, R_{free}	0.177 , 0.250 0.184 , 0.248	Depositor DCC
R_{free} test set	2841 reflections (6.50%)	wwPDB-VP
Wilson B-factor (Å ²)	13.0	Xtriage
Anisotropy	1.744	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 52.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.024 for k,h,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	9119	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.18% 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	0.58	1/4483 (0.0%)	0.97	10/6085 (0.2%)
1	B	0.58	0/4478	0.95	6/6078 (0.1%)
All	All	0.58	1/8961 (0.0%)	0.96	16/12163 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	6
1	B	0	2
All	All	0	8

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	331	GLU	CA-C	5.96	1.60	1.52

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	332	ASP	N-CA-C	-8.63	102.56	113.43
1	B	148	GLN	CA-C-N	7.80	129.59	119.84
1	B	148	GLN	C-N-CA	7.80	129.59	119.84
1	B	530	VAL	N-CA-C	6.41	117.82	108.53
1	A	563	SER	N-CA-C	-6.25	106.34	112.97
1	A	27	SER	N-CA-C	-6.17	104.67	111.82
1	A	30	LEU	N-CA-C	-6.03	104.05	111.40
1	A	333	ALA	N-CA-C	-5.45	104.56	111.11
1	A	331	GLU	CB-CG-CD	5.42	121.81	112.60
1	A	213	CYS	N-CA-C	-5.36	96.86	108.81
1	B	93	PRO	CA-C-N	5.32	125.64	119.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	93	PRO	C-N-CA	5.32	125.64	119.47
1	B	34	HIS	CB-CA-C	-5.13	100.21	110.42
1	A	547	LEU	N-CA-C	5.11	116.83	109.07
1	A	147	VAL	CA-C-N	5.05	127.40	120.39
1	A	147	VAL	C-N-CA	5.05	127.40	120.39

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	26	LEU	Peptide
1	A	27	SER	Peptide
1	A	29	SER	Peptide
1	A	330	GLN	Peptide
1	A	331	GLU	Peptide
1	A	437	GLU	Peptide
1	B	530	VAL	Peptide
1	B	531	ARG	Peptide

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	4387	0	4383	112	0
1	B	4382	0	4381	75	0
2	A	186	0	0	3	0
2	B	164	0	0	3	0
All	All	9119	0	8764	187	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 11.

All (187) 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:212:LYS:HG3	1:A:213:CYS:N	1.84	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:331:GLU:HG3	1:A:332:ASP:CG	2.01	0.86
1:A:26:LEU:HA	1:A:28:ASN:HB2	1.60	0.83
1:B:465:ARG:HD3	1:B:543:SER:HA	1.61	0.82
1:A:212:LYS:HG3	1:A:213:CYS:H	1.43	0.81
1:B:508:ARG:HH21	1:B:530:VAL:HG11	1.44	0.81
1:A:212:LYS:HG2	1:A:325:GLU:CD	2.07	0.79
1:A:219:TYR:HB3	1:A:320:LEU:HD23	1.70	0.73
1:A:329:THR:HA	1:A:331:GLU:OE2	1.90	0.72
1:A:433:LEU:HD22	1:A:438:GLN:HB2	1.71	0.70
1:B:260:LEU:O	1:B:277:ARG:NH2	2.23	0.70
1:A:375:ASP:OD1	1:A:376:ALA:N	2.24	0.70
1:A:200:ARG:NH1	2:A:677:HOH:O	2.22	0.70
1:A:328:GLY:N	1:A:331:GLU:OE1	2.21	0.69
1:A:132:THR:O	1:A:259:ARG:HD2	1.94	0.68
1:A:212:LYS:HE3	1:A:325:GLU:HG3	1.74	0.68
1:B:79:LYS:HG3	1:B:244:ASP:HB3	1.76	0.68
1:B:132:THR:O	1:B:259:ARG:HD2	1.95	0.67
1:A:547:LEU:HD12	1:A:548:SER:H	1.61	0.66
1:B:101:PHE:O	1:B:114:ARG:NH1	2.30	0.65
1:B:144:VAL:HG22	1:B:394:ARG:HG3	1.79	0.64
1:B:148:GLN:NE2	1:B:150:GLU:OE2	2.29	0.62
1:B:508:ARG:HH22	1:B:531:ARG:NH1	1.96	0.62
1:A:212:LYS:HZ2	1:A:213:CYS:HB3	1.64	0.62
1:A:82:LEU:HD13	1:A:249:ALA:HB2	1.81	0.62
1:A:52:VAL:HG22	1:A:226:SER:OG	2.01	0.61
1:B:82:LEU:HD13	1:B:249:ALA:HB2	1.82	0.61
1:B:530:VAL:HB	1:B:531:ARG:HB3	1.82	0.60
1:A:331:GLU:HG3	1:A:332:ASP:N	2.15	0.60
1:B:379:LYS:NZ	1:B:380:ARG:O	2.32	0.60
1:A:515:GLY:HA2	1:A:519:ALA:HB2	1.84	0.59
1:B:531:ARG:HG2	1:B:532:THR:N	2.17	0.59
1:A:347:SER:O	1:A:347:SER:OG	2.15	0.59
1:A:23:ILE:O	1:A:25:PRO:HD3	2.01	0.59
1:A:212:LYS:NZ	1:A:326:SER:OG	2.36	0.58
1:A:386:ARG:NH1	1:A:387:ASP:O	2.34	0.57
1:A:331:GLU:CG	1:A:332:ASP:N	2.67	0.57
1:B:200:ARG:NH2	1:B:316:ASN:OD1	2.37	0.56
1:B:397:TRP:CE2	1:B:401:ARG:HD2	2.41	0.56
1:A:26:LEU:CA	1:A:28:ASN:HB2	2.31	0.56
1:A:212:LYS:NZ	1:A:213:CYS:HB3	2.20	0.55
1:A:520:THR:OG1	1:A:523:ARG:NH2	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:230:GLU:HG2	1:B:262:ILE:HG12	1.88	0.55
1:B:440:GLU:HG3	1:B:457:LEU:HD12	1.87	0.55
1:A:336:LEU:HD22	1:A:356:PRO:HD3	1.89	0.55
1:B:34:HIS:N	1:B:34:HIS:ND1	2.54	0.55
1:B:508:ARG:NH2	1:B:530:VAL:HG11	2.18	0.55
1:B:519:ALA:O	1:B:523:ARG:HG3	2.07	0.55
1:A:337:ARG:O	1:A:341:GLU:HG3	2.06	0.54
1:B:531:ARG:CG	1:B:532:THR:N	2.70	0.54
1:A:22:PRO:O	1:A:24:ASN:N	2.38	0.54
1:B:74:LYS:O	1:B:77:THR:HB	2.08	0.54
1:A:191:TYR:O	1:A:194:GLN:HG2	2.07	0.54
1:A:212:LYS:H	1:A:325:GLU:CD	2.15	0.54
1:A:212:LYS:CG	1:A:213:CYS:H	2.17	0.54
1:A:505:ARG:HH21	1:A:531:ARG:CZ	2.21	0.54
1:A:22:PRO:HD3	1:A:401:ARG:CZ	2.39	0.53
1:B:313:MET:HE2	1:B:322:VAL:HG22	1.91	0.53
1:A:26:LEU:HA	1:A:28:ASN:CB	2.36	0.53
1:A:237:GLU:OE2	1:A:254:ARG:HD2	2.09	0.52
1:B:336:LEU:HD23	1:B:356:PRO:HD3	1.91	0.52
1:A:25:PRO:O	1:A:28:ASN:ND2	2.43	0.52
1:A:501:ARG:HD2	1:A:531:ARG:HH22	1.76	0.51
1:A:313:MET:HE2	1:A:322:VAL:HG22	1.93	0.51
1:B:508:ARG:HE	1:B:530:VAL:CG1	2.24	0.50
1:B:547:LEU:HD23	1:B:548:SER:N	2.27	0.50
1:B:187:MET:HE3	1:B:296:TYR:CD1	2.46	0.50
1:A:209:LYS:C	1:A:211:LYS:H	2.19	0.50
1:B:175:LEU:O	1:B:179:VAL:HB	2.12	0.50
1:B:331:GLU:H	1:B:331:GLU:CD	2.20	0.50
1:A:187:MET:HE1	1:A:292:THR:HG22	1.94	0.49
1:A:25:PRO:O	1:A:26:LEU:HD23	2.11	0.49
1:A:470:SER:O	1:A:474:LEU:HG	2.13	0.49
1:B:148:GLN:HE21	1:B:150:GLU:CD	2.18	0.49
1:A:485:VAL:O	1:A:489:LEU:HG	2.12	0.49
1:B:465:ARG:HD3	1:B:543:SER:CA	2.39	0.49
1:B:440:GLU:CG	1:B:457:LEU:HD12	2.42	0.49
1:B:26:LEU:HD22	1:B:432:ILE:HD13	1.94	0.49
1:A:160:ILE:HD12	1:A:282:SER:OG	2.13	0.49
1:A:495:PRO:HB2	1:A:499:THR:HG21	1.94	0.49
1:B:56:ARG:HD3	1:B:226:SER:O	2.12	0.49
1:B:439:LEU:HG	1:B:457:LEU:HD21	1.93	0.49
1:B:423:MET:HA	1:B:528:TRP:CZ2	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:327:ALA:O	1:B:331:GLU:HG3	2.12	0.48
1:B:148:GLN:HG3	1:B:149:PRO:HD2	1.95	0.48
1:B:446:GLN:C	1:B:447:ILE:HD12	2.38	0.48
1:B:313:MET:HB3	1:B:322:VAL:HG22	1.95	0.48
1:A:212:LYS:CG	1:A:213:CYS:N	2.64	0.48
1:A:21:LEU:HD12	1:A:401:ARG:NH2	2.29	0.48
1:A:105:ALA:O	1:A:109:ARG:HG3	2.14	0.48
1:A:233:ILE:HD13	1:A:262:ILE:HA	1.95	0.48
1:A:308:LEU:HB3	1:A:311:CYS:SG	2.54	0.48
1:A:398:GLU:HG2	1:A:403:THR:HG21	1.95	0.48
1:A:510:LYS:HE2	1:A:510:LYS:HB3	1.63	0.48
1:B:457:LEU:HB3	1:B:517:ARG:HE	1.79	0.47
1:A:22:PRO:HD3	1:A:401:ARG:NH2	2.28	0.47
1:A:328:GLY:N	1:A:331:GLU:HB3	2.29	0.47
1:A:547:LEU:HD12	1:A:548:SER:N	2.29	0.47
1:B:457:LEU:CB	1:B:517:ARG:HE	2.28	0.47
1:A:84:SER:OG	1:A:87:GLU:HG3	2.15	0.47
1:A:215:MET:HE2	1:A:332:ASP:HB3	1.97	0.47
1:B:151:LYS:HZ3	1:B:154:ARG:HH21	1.62	0.47
1:A:332:ASP:HA	1:A:335:ALA:HB3	1.97	0.47
1:B:531:ARG:HE	1:B:532:THR:HB	1.80	0.47
1:A:209:LYS:HA	1:A:209:LYS:HD2	1.67	0.47
1:A:21:LEU:HA	1:A:401:ARG:HH22	1.80	0.46
1:B:524:TYR:OH	1:B:537:THR:O	2.25	0.46
1:A:430:PHE:O	1:A:434:LEU:HB2	2.16	0.46
1:A:134:ILE:HG13	1:A:259:ARG:HB3	1.98	0.45
1:A:36:MET:HE2	1:A:491:LYS:HG3	1.98	0.45
1:B:147:VAL:HG21	1:B:151:LYS:HD3	1.97	0.45
1:A:439:LEU:O	1:A:456:PRO:HG2	2.16	0.45
1:B:508:ARG:NH1	1:B:512:LEU:HD11	2.31	0.45
1:A:28:ASN:HB3	1:A:29:SER:H	1.46	0.45
1:B:508:ARG:HE	1:B:530:VAL:HG11	1.81	0.45
1:A:308:LEU:CD1	1:A:335:ALA:HB1	2.47	0.45
1:A:328:GLY:C	1:A:331:GLU:HB3	2.42	0.45
1:B:455:GLU:OE2	1:B:517:ARG:NH2	2.43	0.45
1:A:511:LEU:HD21	1:A:521:CYS:HB2	1.99	0.44
1:B:518:ALA:O	1:B:521:CYS:HB2	2.17	0.44
1:A:25:PRO:C	1:A:28:ASN:HB2	2.42	0.44
1:A:150:GLU:O	1:A:151:LYS:HB2	2.18	0.44
1:A:331:GLU:HG3	1:A:332:ASP:CB	2.47	0.44
1:B:90:LYS:HA	1:B:90:LYS:HD2	1.55	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:100:LYS:NZ	2:B:692:HOH:O	2.51	0.44
1:B:184:GLN:NE2	1:B:194:GLN:OE1	2.50	0.44
1:B:47:LEU:O	1:B:51:LYS:HG3	2.18	0.44
1:A:442:ALA:HB2	1:A:455:GLU:HG3	2.00	0.44
1:B:150:GLU:H	1:B:150:GLU:HG3	1.41	0.44
1:A:219:TYR:HE2	1:A:221:THR:HG22	1.83	0.44
1:A:423:MET:HA	1:A:528:TRP:CZ2	2.52	0.44
1:A:270:LYS:HD2	1:A:272:GLN:NE2	2.32	0.44
1:A:472:PHE:CE2	1:A:525:LEU:HD23	2.53	0.44
1:B:48:ARG:HG2	1:B:159:LEU:HG	2.00	0.44
1:B:448:PHE:CE1	1:B:551:PHE:HD2	2.36	0.43
1:B:555:TYR:CD2	1:B:560:ILE:HG13	2.53	0.43
1:A:30:LEU:HD12	1:A:30:LEU:HA	1.83	0.43
1:A:59:VAL:HB	1:A:345:ARG:HG2	2.01	0.43
1:A:212:LYS:HG2	1:A:325:GLU:OE2	2.18	0.43
1:A:313:MET:HE2	1:A:313:MET:HB3	1.77	0.43
1:B:212:LYS:HB2	1:B:212:LYS:HE2	1.65	0.43
1:A:23:ILE:H	1:A:23:ILE:HG13	1.67	0.43
1:A:329:THR:C	1:A:331:GLU:HG2	2.43	0.43
1:A:458:ASP:OD2	1:A:517:ARG:NH1	2.52	0.43
1:B:524:TYR:CE2	1:B:536:LEU:HB3	2.53	0.43
1:B:478:SER:O	1:B:482:ILE:HG13	2.18	0.43
1:B:547:LEU:HD11	1:B:550:TRP:HB2	2.00	0.43
1:A:21:LEU:HD23	1:A:34:HIS:HB3	2.00	0.43
1:B:21:LEU:HD12	1:B:22:PRO:HD2	2.00	0.43
1:B:93:PRO:HA	1:B:94:PRO:HD3	1.92	0.43
1:A:58:GLN:HG3	1:A:347:SER:HB3	2.01	0.43
1:A:179:VAL:HG22	1:A:289:CYS:CB	2.48	0.43
1:A:386:ARG:NH2	2:A:675:HOH:O	2.51	0.42
1:B:184:GLN:HE21	1:B:194:GLN:CD	2.27	0.42
1:A:397:TRP:CD2	1:A:401:ARG:NH2	2.87	0.42
1:A:147:VAL:HB	1:A:152:GLY:HA2	2.02	0.42
1:A:148:GLN:CG	1:A:150:GLU:OE1	2.67	0.42
1:A:212:LYS:NZ	1:A:326:SER:O	2.48	0.42
1:B:264:GLY:HA3	2:B:628:HOH:O	2.19	0.42
1:A:310:ASP:N	1:A:310:ASP:OD1	2.52	0.42
1:A:489:LEU:HD22	1:A:494:VAL:HB	2.01	0.42
1:A:548:SER:C	1:A:550:TRP:H	2.27	0.42
1:A:505:ARG:O	1:A:508:ARG:HG2	2.20	0.42
1:A:74:LYS:O	1:A:77:THR:HB	2.20	0.42
1:B:18:GLU:HG2	1:B:401:ARG:NH2	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:23:ILE:HG13	2:A:754:HOH:O	2.20	0.41
1:A:227:THR:HB	1:A:347:SER:O	2.20	0.41
1:A:562:HIS:C	1:A:564:LEU:H	2.28	0.41
1:A:425:LEU:HA	1:A:425:LEU:HD12	1.71	0.41
1:A:509:ALA:C	1:A:511:LEU:H	2.28	0.41
1:B:547:LEU:HG	1:B:550:TRP:CD1	2.56	0.41
1:B:83:LEU:HB2	1:B:173:MET:HA	2.03	0.41
1:B:124:GLU:HG2	2:B:714:HOH:O	2.20	0.41
1:B:160:ILE:O	1:B:160:ILE:HG13	2.21	0.41
1:A:406:ASN:HD22	1:A:443:LEU:HD13	1.85	0.41
1:A:458:ASP:O	1:A:462:ILE:HG13	2.21	0.41
1:A:535:LYS:N	1:A:535:LYS:HD3	2.36	0.41
1:A:472:PHE:HE2	1:A:525:LEU:HD23	1.85	0.41
1:B:23:ILE:CD1	1:B:34:HIS:CD2	3.04	0.41
1:A:5:THR:O	1:A:275:GLY:HA3	2.21	0.40
1:B:84:SER:OG	1:B:87:GLU:HG3	2.21	0.40
1:A:527:ASN:O	1:A:530:VAL:HG22	2.21	0.40
1:B:23:ILE:HD13	1:B:34:HIS:CD2	2.56	0.40
1:A:236:GLU:OE1	1:A:280:ARG:NH2	2.39	0.40
1:A:345:ARG:C	1:A:347:SER:H	2.29	0.40
1:A:496:PRO:O	1:A:499:THR:HB	2.22	0.40
1:B:512:LEU:HD21	1:B:523:ARG:HG2	2.04	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	564/570 (99%)	515 (91%)	41 (7%)	8 (1%)	9	19
1	B	563/570 (99%)	522 (93%)	30 (5%)	11 (2%)	6	12
All	All	1127/1140 (99%)	1037 (92%)	71 (6%)	19 (2%)	7	15

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	329	THR
1	A	437	GLU
1	A	548	SER
1	B	103	TYR
1	B	548	SER
1	A	23	ILE
1	B	531	ARG
1	A	28	ASN
1	B	150	GLU
1	B	351	GLY
1	B	542	ALA
1	B	544	GLN
1	A	545	LEU
1	B	153	GLY
1	B	540	PRO
1	B	149	PRO
1	B	404	PRO
1	A	404	PRO
1	A	149	PRO

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	475/485 (98%)	460 (97%)	15 (3%)	34	62
1	B	475/485 (98%)	443 (93%)	32 (7%)	15	33
All	All	950/970 (98%)	903 (95%)	47 (5%)	22	47

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	VAL
1	A	77	THR
1	A	81	LYS
1	A	141	LYS

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Mol	Chain	Res	Type
1	A	179	VAL
1	A	209	LYS
1	A	313	MET
1	A	367	SER
1	A	379	LYS
1	A	384	LEU
1	A	425	LEU
1	A	436	GLN
1	A	461	GLN
1	A	499	THR
1	A	533	LYS
1	B	5	THR
1	B	18	GLU
1	B	34	HIS
1	B	47	LEU
1	B	49	GLN
1	B	52	VAL
1	B	77	THR
1	B	85	ILE
1	B	86	GLU
1	B	90	LYS
1	B	112	SER
1	B	144	VAL
1	B	150	GLU
1	B	179	VAL
1	B	181	THR
1	B	182	LEU
1	B	212	LYS
1	B	220	ASP
1	B	262	ILE
1	B	331	GLU
1	B	352	ASP
1	B	355	GLN
1	B	372	VAL
1	B	431	SER
1	B	432	ILE
1	B	433	LEU
1	B	439	LEU
1	B	454	ILE
1	B	517	ARG
1	B	531	ARG
1	B	534	LEU

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Mol	Chain	Res	Type
1	B	535	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	A	33	HIS
1	A	206	ASN
1	A	273	ASN
1	A	402	HIS
1	A	411	ASN
1	A	428	HIS
1	A	483	ASN
1	B	184	GLN
1	B	406	ASN
1	B	483	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](#)

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 ⓘ

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	566/570 (99%)	0.40	59 (10%) 11 9	8, 38, 75, 88	0
1	B	565/570 (99%)	-0.17	23 (4%) 41 36	8, 23, 49, 70	0
All	All	1131/1140 (99%)	0.11	82 (7%) 21 17	8, 29, 70, 88	0

All (82) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	544	GLN	7.6
1	B	558	GLY	5.9
1	A	566	ARG	5.6
1	A	26	LEU	5.4
1	B	565	SER	4.9
1	A	565	SER	4.8
1	B	152	GLY	4.7
1	A	331	GLU	4.7
1	A	24	ASN	4.6
1	B	545	LEU	4.6
1	A	326	SER	4.4
1	B	547	LEU	4.3
1	A	23	ILE	4.3
1	A	152	GLY	4.1
1	B	564	LEU	4.0
1	A	149	PRO	4.0
1	A	327	ALA	3.7
1	B	563	SER	3.6
1	A	28	ASN	3.5
1	A	151	LYS	3.5
1	A	22	PRO	3.5
1	B	153	GLY	3.5
1	A	27	SER	3.4
1	A	212	LYS	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	544	GLN	3.4
1	B	543	SER	3.4
1	A	548	SER	3.3
1	A	332	ASP	3.2
1	A	148	GLN	3.1
1	A	564	LEU	3.0
1	A	25	PRO	3.0
1	A	405	ILE	3.0
1	A	29	SER	3.0
1	A	563	SER	2.9
1	A	532	THR	2.9
1	B	151	LYS	2.9
1	A	543	SER	2.9
1	A	545	LEU	2.9
1	A	150	GLU	2.9
1	A	34	HIS	2.8
1	A	35	ASN	2.7
1	A	541	ALA	2.7
1	A	16	ALA	2.7
1	B	402	HIS	2.7
1	A	15	ALA	2.6
1	B	86	GLU	2.6
1	A	375	ASP	2.5
1	A	436	GLN	2.5
1	B	548	SER	2.5
1	A	476	SER	2.4
1	A	153	GLY	2.4
1	A	213	CYS	2.4
1	A	325	GLU	2.4
1	A	403	THR	2.3
1	A	14	CYS	2.3
1	A	209	LYS	2.3
1	A	519	ALA	2.3
1	A	404	PRO	2.3
1	A	547	LEU	2.3
1	B	559	ASP	2.3
1	A	502	HIS	2.3
1	B	149	PRO	2.3
1	A	475	HIS	2.3
1	A	530	VAL	2.3
1	B	532	THR	2.2
1	A	21	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	546	ASP	2.2
1	A	206	ASN	2.2
1	A	30	LEU	2.2
1	A	489	LEU	2.2
1	B	365	SER	2.2
1	A	509	ALA	2.1
1	A	542	ALA	2.1
1	B	541	ALA	2.1
1	B	405	ILE	2.1
1	A	401	ARG	2.1
1	A	448	PHE	2.1
1	A	525	LEU	2.1
1	B	148	GLN	2.1
1	B	542	ALA	2.1
1	A	537	THR	2.0
1	A	210	SER	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.