



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 05:04 pm GMT

PDB ID : 4RY4  
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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

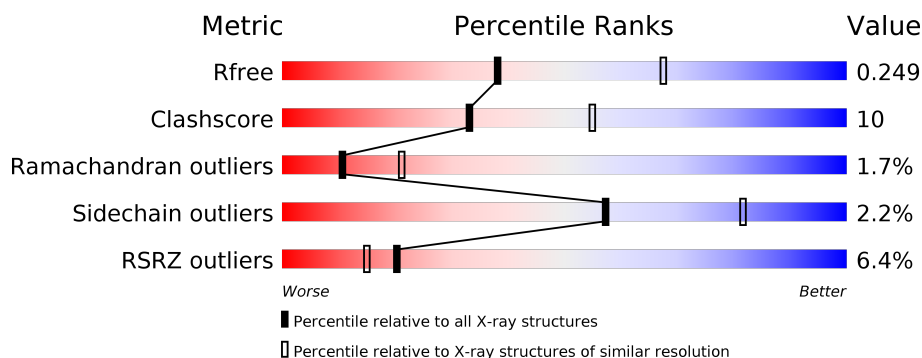
# 1 Overall quality at a glance

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))
$R_{free}$	100719	2542 (2.60-2.60)
Clashscore	112137	2895 (2.60-2.60)
Ramachandran outliers	110173	2848 (2.60-2.60)
Sidechain outliers	110143	2848 (2.60-2.60)
RSRZ outliers	101464	2550 (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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	<div> <div>9%</div> <div>76%</div> <div>20%</div> <div>• •</div> </div>
1	B	570	<div> <div>4%</div> <div>80%</div> <div>18%</div> <div>• • •</div> </div>

## 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

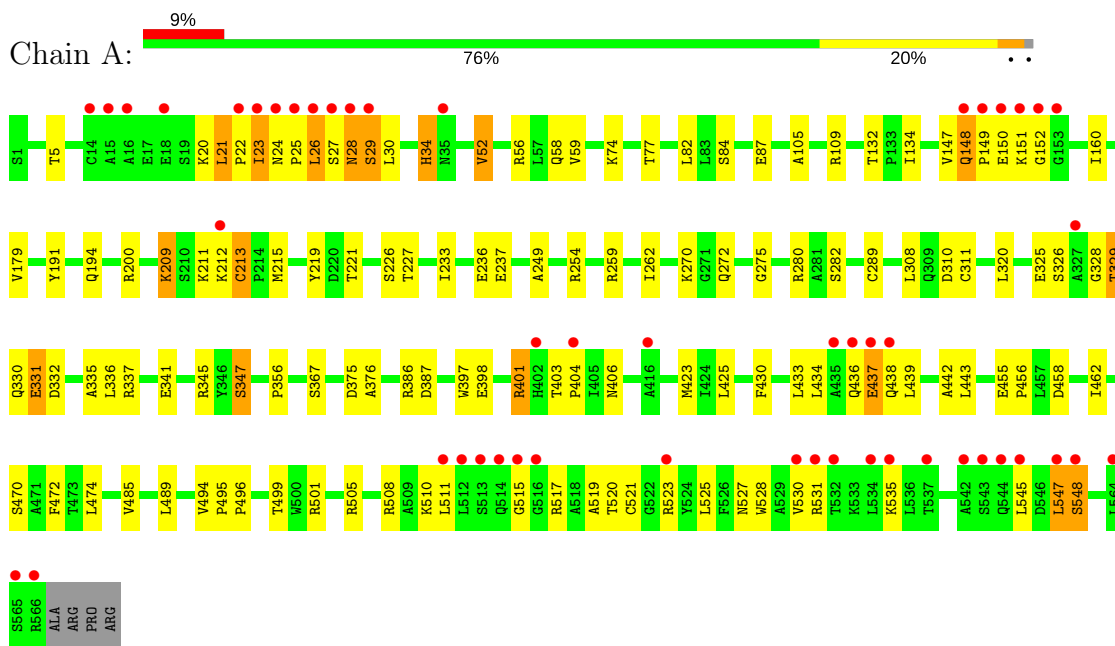
- Molecule 2 is water.

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

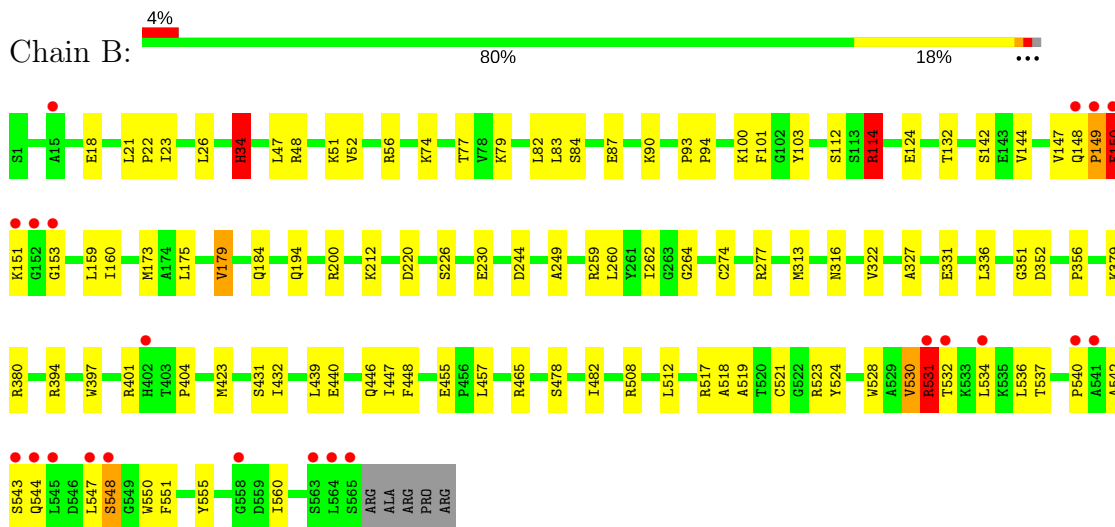
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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: HCV J4 RNA polymerase (NS5B)



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## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	105.59Å 108.35Å 134.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.90 – 2.59 29.96 – 2.59	Depositor EDS
% Data completeness (in resolution range)	86.5 (19.90-2.59) 86.0 (29.96-2.59)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	6.43 (at 2.57Å)	Xtriage
Refinement program	PHENIX 1.8.4	Depositor
R, $R_{free}$	0.177 , 0.250 0.179 , 0.249	Depositor DCC
$R_{free}$ test set	2723 reflections (6.48%)	DCC
Wilson B-factor (Å <sup>2</sup> )	13.0	Xtriage
Anisotropy	1.744	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 48.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	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 <sup>2</sup> )	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.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>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 [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	0.46	0/4483	0.68	4/6085 (0.1%)
1	B	0.47	1/4478 (0.0%)	0.66	3/6078 (0.0%)
All	All	0.46	1/8961 (0.0%)	0.67	7/12163 (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	B	274	CYS	CB-SG	-6.08	1.72	1.82

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	547	LEU	CA-CB-CG	6.98	131.35	115.30
1	A	21	LEU	CA-CB-CG	6.87	131.11	115.30
1	B	114	ARG	NE-CZ-NH1	6.63	123.61	120.30
1	A	213	CYS	N-CA-C	-5.24	96.86	111.00
1	B	34	HIS	CB-CA-C	-5.09	100.21	110.40
1	A	401	ARG	NE-CZ-NH2	-5.08	117.76	120.30
1	B	114	ARG	NH1-CZ-NH2	-5.08	113.81	119.40

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 ⓘ

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	101	0
1	B	4382	0	4381	71	0
2	A	186	0	0	3	0
2	B	164	0	0	3	0
All	All	9119	0	8764	172	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 10.

All (172) 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
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:331:GLU:HG3	1:A:332:ASP:CG	2.01	0.81
1:A:212:LYS:HG2	1:A:325:GLU:CD	2.07	0.75
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:331:GLU:HG3	1:A:332:ASP:N	2.15	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: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
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:ND1	1:B:34:HIS:N	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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: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:175:LEU:O	1:B:179:VAL:HB	2.12	0.50
1:A:25:PRO:O	1:A:26:LEU:HD23	2.11	0.49
1:A:212:LYS:H	1:A:325:GLU:CD	2.15	0.49
1:A:470:SER:O	1:A:474:LEU:HG	2.13	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:439:LEU:HG	1:B:457:LEU:HD21	1.93	0.49
1:B:56:ARG:HD3	1:B:226:SER:O	2.12	0.49
1:B:423:MET:HA	1:B:528:TRP:CZ2	2.48	0.48
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: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:105:ALA:O	1:A:109:ARG:HG3	2.14	0.48
1:A:21:LEU:HD12	1:A:401:ARG:NH2	2.29	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:209:LYS:C	1:A:211:LYS:H	2.19	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:331:GLU:CD	1:B:331:GLU:H	2.20	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:B:148:GLN:HE21	1:B:150:GLU:CD	2.18	0.45
1:A:215:MET:HE2	1:A:332:ASP:HB3	1.99	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: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: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:90:LYS:HD2	1:B:90:LYS:HA	1.55	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:446:GLN:C	1:B:447:ILE:HD12	2.38	0.43
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: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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:179:VAL:HG22	1:A:289:CYS:CB	2.48	0.43
1:A:58:GLN:HG3	1:A:347:SER:HB3	2.01	0.43
1:A:386:ARG:NH2	2:A:675:HOH:O	2.51	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: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
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:425:LEU:HA	1:A:425:LEU:HD12	1.71	0.41
1:B:547:LEU:HG	1:B:550:TRP:CD1	2.56	0.41
1:B:124:GLU:HG2	2:B:714:HOH:O	2.20	0.41
1:B:160:ILE:HG13	1:B:160:ILE:O	2.21	0.41
1:B:83:LEU:HB2	1:B:173:MET:HA	2.03	0.41
1:A:406:ASN:HD22	1:A:443:LEU:HD13	1.85	0.41
1:A:535:LYS:HD3	1:A:535:LYS:N	2.36	0.41
1:A:458:ASP:O	1:A:462:ILE:HG13	2.21	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: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

### 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	564/570 (99%)	515 (91%)	41 (7%)	8 (1%)	13	26
1	B	563/570 (99%)	522 (93%)	30 (5%)	11 (2%)	9	17
All	All	1127/1140 (99%)	1037 (92%)	71 (6%)	19 (2%)	11	21

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%)	466 (98%)	9 (2%)	62	84
1	B	475/485 (98%)	463 (98%)	12 (2%)	53	79
All	All	950/970 (98%)	929 (98%)	21 (2%)	57	81

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	LYS
1	A	34	HIS
1	A	52	VAL
1	A	56	ARG
1	A	148	GLN
1	A	209	LYS
1	A	347	SER
1	A	367	SER
1	A	436	GLN
1	B	34	HIS
1	B	52	VAL
1	B	112	SER
1	B	114	ARG
1	B	142	SER
1	B	150	GLU
1	B	179	VAL
1	B	220	ASP
1	B	352	ASP
1	B	431	SER
1	B	531	ARG
1	B	534	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	49	GLN
1	A	206	ASN
1	A	411	ASN
1	A	428	HIS
1	B	184	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 carbohydrates 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	566/570 (99%)	0.30	50 (8%) 11 7	8, 38, 75, 88	0
1	B	565/570 (99%)	-0.15	22 (3%) 40 32	8, 23, 49, 70	0
All	All	1131/1140 (99%)	0.07	72 (6%) 20 15	8, 29, 70, 88	0

All (72) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	566	ARG	8.1
1	A	149	PRO	6.6
1	A	25	PRO	6.6
1	A	24	ASN	6.4
1	A	151	LYS	6.3
1	B	565	SER	6.3
1	A	152	GLY	6.0
1	B	545	LEU	5.7
1	A	544	GLN	5.6
1	B	151	LYS	5.4
1	B	152	GLY	5.2
1	A	535	LYS	5.1
1	B	543	SER	5.0
1	A	436	GLN	5.0
1	A	26	LEU	4.9
1	A	565	SER	4.9
1	B	564	LEU	4.8
1	A	28	ASN	4.7
1	B	153	GLY	4.5
1	B	149	PRO	4.5
1	A	548	SER	4.3
1	A	16	ALA	4.2
1	A	564	LEU	4.1
1	A	15	ALA	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	153	GLY	4.1
1	A	545	LEU	4.0
1	B	532	THR	3.8
1	A	27	SER	3.8
1	A	23	ILE	3.7
1	B	544	GLN	3.7
1	A	435	ALA	3.6
1	A	148	GLN	3.4
1	A	437	GLU	3.3
1	A	402	HIS	3.3
1	A	547	LEU	3.3
1	A	438	GLN	3.2
1	A	22	PRO	3.2
1	A	404	PRO	3.0
1	A	513	SER	3.0
1	B	547	LEU	3.0
1	B	541	ALA	3.0
1	A	212	LYS	3.0
1	B	402	HIS	2.9
1	A	511	LEU	2.9
1	A	543	SER	2.9
1	A	532	THR	2.8
1	A	150	GLU	2.8
1	A	14	CYS	2.8
1	A	515	GLY	2.7
1	A	514	GLN	2.7
1	B	540	PRO	2.7
1	A	512	LEU	2.7
1	B	531	ARG	2.7
1	A	29	SER	2.6
1	B	148	GLN	2.6
1	B	563	SER	2.6
1	A	537	THR	2.6
1	A	534	LEU	2.6
1	A	18	GLU	2.5
1	A	530	VAL	2.5
1	B	15	ALA	2.4
1	B	150	GLU	2.4
1	B	558	GLY	2.3
1	B	534	LEU	2.2
1	A	327	ALA	2.2
1	A	516	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	531	ARG	2.2
1	A	542	ALA	2.2
1	A	416	ALA	2.0
1	A	35	ASN	2.0
1	B	548	SER	2.0
1	A	523	ARG	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 carbohydrates 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.