



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 02:57 PM GMT

PDB ID : 2D3U
Title : X-ray crystal structure of hepatitis C virus RNA dependent RNA polymerase in complex with non-nucleoside analogue inhibitor
Authors : Biswal, B.K.; Wang, M.; Cherney, M.M.; Chan, L.; Yannopoulos, C.G.; Bilimoria, D.; Bedard, J.; James, M.N.G.
Deposited on : 2005-10-02
Resolution : 2.00 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

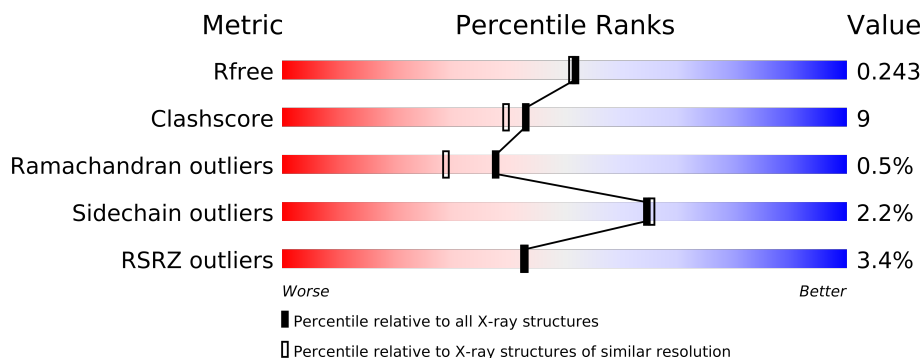
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.00 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}	66092	4888 (2.00-2.00)
Clashscore	79885	6188 (2.00-2.00)
Ramachandran outliers	78287	6102 (2.00-2.00)
Sidechain outliers	78261	6100 (2.00-2.00)
RSRZ outliers	66119	4890 (2.00-2.00)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	570	
1	B	570	

2 Entry composition i

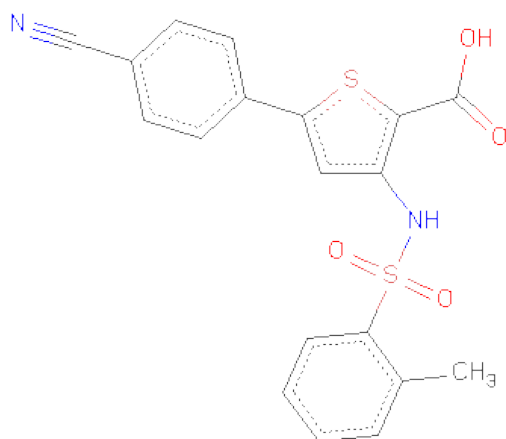
There are 3 unique types of molecules in this entry. The entry contains 9496 atoms, of which 0 are hydrogen and 0 are deuterium.

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 polyprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	558	Total	C	N	O	S	0	0	0
			4340	2738	765	806	31			
1	B	559	Total	C	N	O	S	0	0	0
			4348	2744	766	807	31			

- Molecule 2 is 5-(4-CYANOPHENYL)-3-[(2-METHYLPHENYL)SULFONYL]AMINO}THIOPHENE-2-CARBOXYLICACID (three-letter code: CCT) (formula: C₁₉H₁₄N₂O₄S₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			27	19	2	4	2		
2	B	1	Total	C	N	O	S	0	0
			27	19	2	4	2		

- Molecule 3 is water.

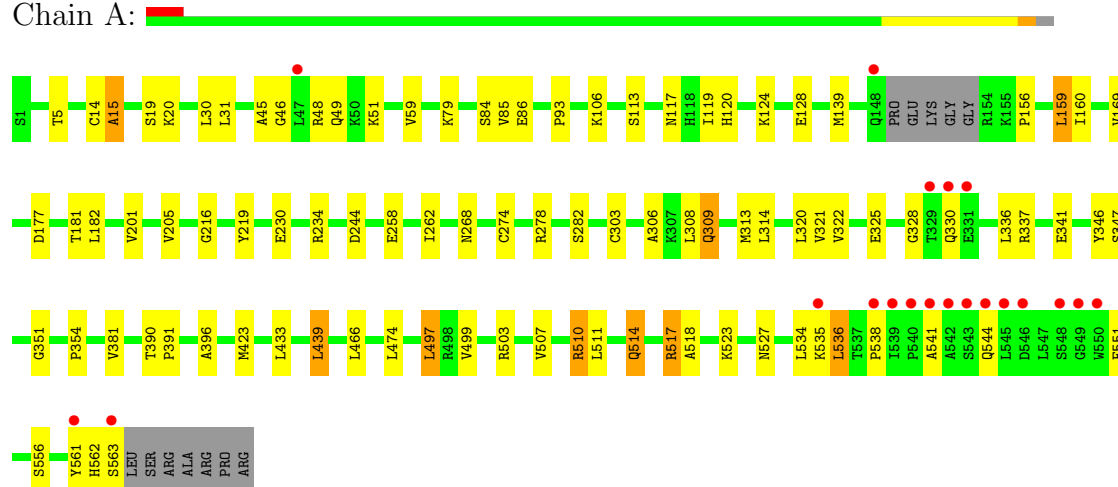
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	365	Total 365	O 365	0	0
3	B	389	Total 389	O 389	0	0

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 errors 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 ($\text{RSRZ} > 2$). 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.

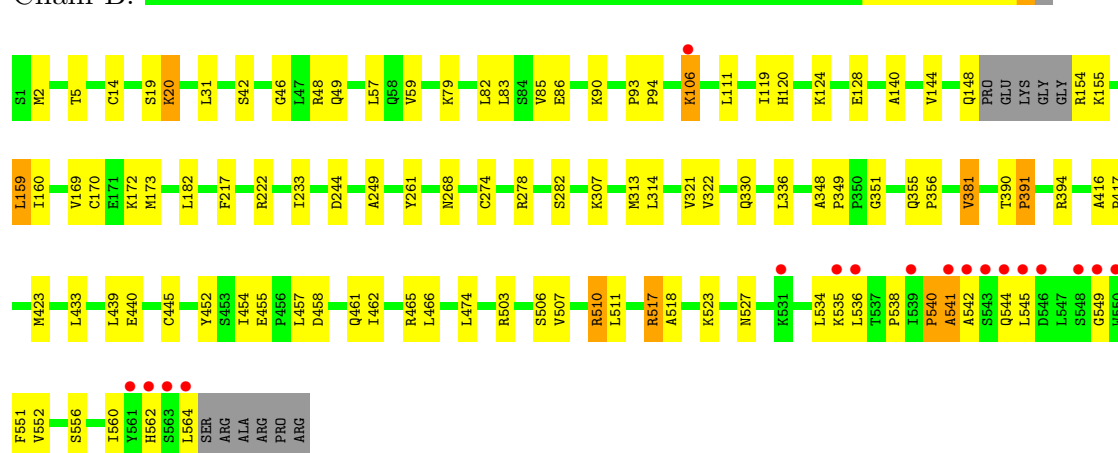
- Molecule 1: polypeptide

Chain A:



- Molecule 1: polypeptide

Chain B:



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	84.92Å 104.31Å 127.01Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.57 – 2.00 37.57 – 2.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (37.57-2.00) 98.9 (37.57-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.78 (at 2.00Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.208 , 0.245 0.208 , 0.243	Depositor DCC
R_{free} test set	3863 reflections (5.08%)	DCC
Wilson B-factor (Å ²)	22.7	Xtriage
Anisotropy	0.802	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 44.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	4 of 76206 reflections (0.005%)	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9496	wwPDB-VP
Average B, all atoms (Å ²)	29.0	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 50.36 % 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 6.5373e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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

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	0.40	0/4434	0.63	1/6017 (0.0%)
1	B	0.41	0/4442	0.64	1/6028 (0.0%)
All	All	0.40	0/8876	0.64	2/12045 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	351	GLY	N-CA-C	-5.34	99.75	113.10
1	A	351	GLY	N-CA-C	-5.07	100.44	113.10

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4340	0	4357	70	0
1	B	4348	0	4368	85	0
2	A	27	0	13	1	0
2	B	27	0	13	1	0
3	A	365	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	389	0	0	11	0
All	All	9496	0	8751	154	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 9.

All (154) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:5:THR:HG23	1:B:278:ARG:HH22	1.16	1.03
1:A:5:THR:HG23	1:A:278:ARG:HH22	1.39	0.88
1:A:336:LEU:HD21	1:A:354:PRO:HG2	1.56	0.88
1:B:5:THR:CG2	1:B:278:ARG:HH22	1.88	0.85
1:B:5:THR:HG23	1:B:278:ARG:NH2	1.91	0.84
1:A:5:THR:HG21	1:A:278:ARG:HH12	1.41	0.83
1:B:106:LYS:NZ	1:B:106:LYS:HA	1.93	0.82
1:B:462:ILE:HG13	3:B:2234:HOH:O	1.79	0.82
1:B:527:ASN:HD21	1:B:534:LEU:H	1.27	0.82
1:B:458:ASP:HB3	3:B:2234:HOH:O	1.80	0.80
1:A:527:ASN:HD21	1:A:534:LEU:H	1.27	0.79
1:B:222:ARG:HD3	3:B:2384:HOH:O	1.83	0.77
1:A:313:MET:HG2	1:A:322:VAL:HG22	1.67	0.76
1:B:313:MET:HG2	1:B:322:VAL:HG22	1.67	0.76
1:A:48:ARG:HG2	1:A:159:LEU:HD13	1.69	0.75
1:B:148:GLN:HG3	3:B:2287:HOH:O	1.88	0.73
1:B:106:LYS:HZ3	1:B:106:LYS:HA	1.53	0.72
1:A:5:THR:CG2	1:A:278:ARG:HH12	2.01	0.72
1:B:541:ALA:O	1:B:544:GLN:HG2	1.91	0.70
1:A:314:LEU:HB3	1:A:321:VAL:CG1	2.22	0.70
1:A:337:ARG:O	1:A:341:GLU:HG3	1.90	0.70
1:B:433:LEU:HB3	1:B:439:LEU:HD12	1.72	0.70
1:A:510:ARG:HH11	1:A:510:ARG:HG2	1.57	0.68
1:B:455:GLU:HB3	3:B:2218:HOH:O	1.94	0.67
1:A:119:ILE:HD13	1:A:169:VAL:HG11	1.78	0.65
1:B:523:LYS:HE2	1:B:534:LEU:HD23	1.79	0.65
1:B:182:LEU:HD23	1:B:182:LEU:C	2.18	0.65
1:B:2:MET:HB2	1:B:278:ARG:HH21	1.62	0.64
1:B:86:GLU:O	1:B:90:LYS:HG2	1.97	0.64
1:A:336:LEU:CD2	1:A:354:PRO:HG2	2.28	0.64
1:B:154:ARG:N	3:B:2284:HOH:O	2.31	0.63
1:B:510:ARG:HH21	1:B:510:ARG:HG2	1.64	0.63
1:B:314:LEU:HB3	1:B:321:VAL:CG1	2.28	0.63
1:A:182:LEU:HD23	1:A:182:LEU:C	2.20	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:452:TYR:HA	1:B:562:HIS:O	1.99	0.62
1:B:172:LYS:HE3	1:B:560:ILE:HD13	1.80	0.62
1:B:170:CYS:HA	1:B:173:MET:CE	2.31	0.61
1:B:170:CYS:HA	1:B:173:MET:HE3	1.81	0.61
1:B:461:GLN:HG3	3:B:2217:HOH:O	2.00	0.60
1:B:381:VAL:HG11	1:B:474:LEU:CD2	2.32	0.59
1:A:423:MET:HB2	2:A:1001:CCT:H22	1.86	0.58
1:A:381:VAL:HG11	1:A:474:LEU:CD2	2.34	0.58
1:A:309:GLN:HB3	1:A:325:GLU:HB3	1.86	0.57
1:A:5:THR:HG23	1:A:278:ARG:NH2	2.15	0.57
1:A:510:ARG:NH1	1:A:510:ARG:HG2	2.20	0.57
1:B:48:ARG:HG2	1:B:159:LEU:HD13	1.85	0.57
1:A:19:SER:OG	1:A:20:LYS:HD2	2.06	0.56
1:B:314:LEU:HB3	1:B:321:VAL:HG12	1.87	0.55
1:B:564:LEU:HD23	3:B:2219:HOH:O	2.06	0.55
1:B:79:LYS:HA	1:B:244:ASP:HB3	1.89	0.55
1:A:556:SER:HB3	3:A:1349:HOH:O	2.06	0.54
1:B:510:ARG:NH2	1:B:510:ARG:HG2	2.22	0.54
1:B:527:ASN:ND2	1:B:534:LEU:H	2.01	0.54
1:B:124:LYS:O	1:B:128:GLU:HG3	2.07	0.54
1:B:461:GLN:HE21	1:B:541:ALA:C	2.10	0.54
1:B:119:ILE:HD13	1:B:169:VAL:HG11	1.89	0.54
1:B:511:LEU:HB3	1:B:518:ALA:O	2.09	0.53
1:A:14:CYS:HB2	1:A:139:MET:CE	2.38	0.53
1:B:86:GLU:HG2	1:B:111:LEU:HD13	1.89	0.53
1:B:423:MET:HB2	2:B:2001:CCT:H22	1.91	0.53
1:B:390:THR:HB	1:B:391:PRO:HD3	1.91	0.53
1:A:177:ASP:O	1:A:181:THR:HG23	2.10	0.52
1:A:314:LEU:HB3	1:A:321:VAL:HG12	1.89	0.52
1:A:541:ALA:O	1:A:544:GLN:HB2	2.11	0.51
1:B:556:SER:HB3	3:B:2341:HOH:O	2.10	0.51
1:B:83:LEU:HB2	1:B:173:MET:HA	1.92	0.51
1:B:445:CYS:SG	1:B:454:ILE:HD12	2.50	0.51
1:A:390:THR:HB	1:A:391:PRO:HD3	1.93	0.51
1:B:461:GLN:HB3	1:B:545:LEU:HD11	1.93	0.51
1:A:20:LYS:N	1:A:20:LYS:HD2	2.26	0.50
1:B:506:SER:O	1:B:510:ARG:HD3	2.11	0.50
1:B:517:ARG:HH11	1:B:517:ARG:HG2	1.77	0.50
1:B:466:LEU:HD22	1:B:551:PHE:HE2	1.77	0.50
1:B:268:ASN:HB3	1:B:274:CYS:SG	2.52	0.50
1:B:457:LEU:HB2	3:B:2218:HOH:O	2.11	0.50
1:A:46:GLY:HA2	1:A:49:GLN:HE21	1.77	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:160:ILE:HA	1:A:282:SER:OG	2.12	0.49
1:A:328:GLY:HA2	3:A:1286:HOH:O	2.12	0.49
1:A:433:LEU:HB3	1:A:439:LEU:HD12	1.95	0.49
1:A:51:LYS:HE3	1:A:156:PRO:HG3	1.95	0.48
1:B:540:PRO:O	1:B:542:ALA:N	2.46	0.48
1:A:14:CYS:HB2	1:A:139:MET:HE2	1.96	0.48
1:B:144:VAL:HB	1:B:394:ARG:HG2	1.95	0.48
1:A:433:LEU:HB3	1:A:439:LEU:CD1	2.44	0.48
1:A:113:SER:O	1:A:117:ASN:ND2	2.47	0.48
1:B:106:LYS:HZ2	1:B:106:LYS:HA	1.76	0.47
1:A:497:LEU:O	1:A:497:LEU:HD22	2.15	0.47
1:B:527:ASN:HD21	1:B:534:LEU:N	2.04	0.47
1:A:84:SER:OG	1:A:86:GLU:HG2	2.14	0.47
1:B:2:MET:HB2	1:B:278:ARG:NH2	2.29	0.47
1:A:14:CYS:O	1:A:15:ALA:HB2	2.14	0.47
1:A:268:ASN:HB3	1:A:274:CYS:SG	2.54	0.47
1:B:313:MET:CE	3:B:2347:HOH:O	2.62	0.46
1:B:182:LEU:HD23	1:B:182:LEU:O	2.15	0.46
1:B:82:LEU:HD13	1:B:249:ALA:HB2	1.97	0.46
1:B:336:LEU:HD12	1:B:356:PRO:HD3	1.97	0.46
1:A:31:LEU:C	1:A:31:LEU:HD12	2.36	0.46
1:A:30:LEU:HD23	1:A:396:ALA:HA	1.97	0.46
1:A:527:ASN:ND2	1:A:534:LEU:H	2.04	0.46
1:A:46:GLY:HA2	1:A:49:GLN:NE2	2.31	0.45
1:A:466:LEU:HD22	1:A:551:PHE:HE2	1.82	0.45
1:B:86:GLU:HG3	1:B:111:LEU:HD22	1.98	0.45
1:A:511:LEU:HB3	1:A:518:ALA:O	2.16	0.45
1:A:499:VAL:O	1:A:503:ARG:HG3	2.16	0.45
1:A:79:LYS:HA	1:A:244:ASP:HB3	1.99	0.44
1:A:346:TYR:O	1:A:347:SER:HB3	2.17	0.44
1:B:19:SER:H	1:B:20:LYS:NZ	2.15	0.44
1:B:523:LYS:HG3	1:B:534:LEU:HD22	1.99	0.44
1:A:201:VAL:O	1:A:205:VAL:HG23	2.18	0.44
1:A:336:LEU:C	1:A:336:LEU:HD23	2.38	0.44
1:A:45:ALA:O	1:A:49:GLN:HG3	2.17	0.44
1:B:217:PHE:CE2	1:B:336:LEU:HD21	2.53	0.44
1:B:336:LEU:HA	1:B:336:LEU:HD23	1.86	0.44
1:A:503:ARG:O	1:A:507:VAL:HG23	2.18	0.43
1:B:93:PRO:HA	1:B:94:PRO:HD3	1.85	0.43
1:A:5:THR:HG21	1:A:278:ARG:NH1	2.22	0.43
1:B:416:ALA:HB3	1:B:417:PRO:HD3	2.01	0.43
1:A:514:GLN:HB3	1:A:518:ALA:HB3	2.00	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:124:LYS:HE2	1:A:128:GLU:OE1	2.18	0.43
1:B:523:LYS:HG3	1:B:534:LEU:CD2	2.49	0.43
1:A:381:VAL:HG11	1:A:474:LEU:HD22	2.00	0.43
1:B:155:LYS:HE2	1:B:155:LYS:HB3	1.88	0.43
1:A:219:TYR:HB3	1:A:320:LEU:HD23	2.01	0.42
1:A:535:LYS:O	1:A:536:LEU:HB2	2.17	0.42
1:A:85:VAL:HG21	1:A:120:HIS:NE2	2.35	0.42
1:B:348:ALA:N	1:B:349:PRO:CD	2.82	0.42
1:B:517:ARG:NH1	1:B:517:ARG:HG2	2.34	0.42
1:B:503:ARG:O	1:B:507:VAL:HG23	2.19	0.42
1:A:59:VAL:CG1	1:B:59:VAL:HG13	2.49	0.42
1:B:160:ILE:HA	1:B:282:SER:OG	2.19	0.42
1:A:93:PRO:HG3	1:A:561:TYR:HB2	2.00	0.42
1:A:234:ARG:NH1	1:A:258:GLU:OE2	2.39	0.42
1:A:523:LYS:HE2	1:A:534:LEU:HD23	2.00	0.42
1:B:42:SER:HA	1:B:140:ALA:CB	2.50	0.42
1:B:535:LYS:HG3	1:B:536:LEU:N	2.35	0.42
1:B:46:GLY:HA2	1:B:49:GLN:HE21	1.84	0.42
1:B:85:VAL:HG21	1:B:120:HIS:CE1	2.54	0.42
1:B:355:GLN:O	1:B:355:GLN:HG3	2.19	0.41
1:A:230:GLU:HG3	1:A:262:ILE:HG23	2.01	0.41
1:B:465:ARG:HG3	1:B:465:ARG:HH11	1.85	0.41
1:A:313:MET:HE2	1:A:313:MET:HB2	1.80	0.41
1:B:461:GLN:CB	1:B:545:LEU:HD11	2.51	0.41
1:B:170:CYS:HA	1:B:173:MET:HE2	2.03	0.41
1:B:307:LYS:HB2	1:B:307:LYS:HE3	1.89	0.41
1:B:233:ILE:HD13	1:B:261:TYR:O	2.20	0.41
1:A:517:ARG:HH11	1:A:517:ARG:HG2	1.84	0.41
1:A:216:GLY:HA2	1:A:322:VAL:O	2.20	0.41
1:A:535:LYS:HG3	1:A:536:LEU:H	1.86	0.41
1:B:182:LEU:CD2	1:B:182:LEU:C	2.89	0.40
1:A:306:ALA:HB3	1:A:308:LEU:HD13	2.03	0.40
1:A:330:GLN:HA	1:A:330:GLN:OE1	2.21	0.40
1:B:549:GLY:HA2	1:B:552:VAL:CG2	2.52	0.40
1:B:535:LYS:CG	1:B:536:LEU:N	2.85	0.40
1:A:562:HIS:O	1:A:563:SER:C	2.59	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	554/570 (97%)	540 (98%)	11 (2%)	3 (0%)	38	29
1	B	555/570 (97%)	542 (98%)	10 (2%)	3 (0%)	38	29
All	All	1109/1140 (97%)	1082 (98%)	21 (2%)	6 (0%)	38	29

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	540	PRO
1	B	541	ALA
1	A	538	PRO
1	A	15	ALA
1	B	538	PRO
1	A	536	LEU

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	476/485 (98%)	467 (98%)	9 (2%)	69	71
1	B	477/485 (98%)	465 (98%)	12 (2%)	60	59
All	All	953/970 (98%)	932 (98%)	21 (2%)	64	65

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

Mol	Chain	Res	Type
1	A	106	LYS
1	A	159	LEU
1	A	303	CYS

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Mol	Chain	Res	Type
1	A	309	GLN
1	A	439	LEU
1	A	497	LEU
1	A	510	ARG
1	A	514	GLN
1	A	517	ARG
1	B	14	CYS
1	B	20	LYS
1	B	31	LEU
1	B	57	LEU
1	B	106	LYS
1	B	159	LEU
1	B	330	GLN
1	B	381	VAL
1	B	391	PRO
1	B	440	GLU
1	B	510	ARG
1	B	517	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	HIS
1	A	49	GLN
1	A	273	ASN
1	A	374	HIS
1	A	514	GLN
1	A	527	ASN
1	A	544	GLN
1	B	49	GLN
1	B	120	HIS
1	B	273	ASN
1	B	330	GLN
1	B	461	GLN
1	B	527	ASN
1	B	544	GLN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

2 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	CCT	A	1001	-	29,29,29	2.03	5 (17%)	40,42,42	1.69	4 (10%)
2	CCT	B	2001	-	29,29,29	2.16	9 (31%)	40,42,42	1.77	4 (10%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	CCT	A	1001	-	-	0/16/21/21	0/3/3/3
2	CCT	B	2001	-	-	0/16/21/21	0/3/3/3

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2001	CCT	C9-C8	5.99	1.44	1.39
2	A	1001	CCT	C9-C8	5.94	1.44	1.39
2	B	2001	CCT	C21-C20	4.39	1.43	1.39
2	B	2001	CCT	S18-N17	4.02	1.70	1.63
2	A	1001	CCT	C21-C20	3.83	1.43	1.39
2	A	1001	CCT	S18-N17	3.72	1.69	1.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2001	CCT	C19-C20	2.77	1.44	1.40
2	A	1001	CCT	O26-S18	2.35	1.46	1.43
2	A	1001	CCT	C19-C20	2.25	1.43	1.40
2	B	2001	CCT	O27-S18	2.20	1.45	1.43
2	B	2001	CCT	C6-C5	2.14	1.43	1.39
2	B	2001	CCT	C6-C1	2.06	1.42	1.38
2	B	2001	CCT	O26-S18	2.04	1.45	1.43
2	B	2001	CCT	C4-C5	2.01	1.43	1.39

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2001	CCT	C20-S18-N17	7.26	114.75	107.10
2	A	1001	CCT	C20-S18-N17	6.71	114.18	107.10
2	B	2001	CCT	O27-S18-O26	-5.32	112.39	119.55
2	A	1001	CCT	O27-S18-O26	-5.20	112.56	119.55
2	A	1001	CCT	C14-C7-S11	3.40	124.26	116.73
2	B	2001	CCT	C14-C7-S11	3.12	123.63	116.73
2	A	1001	CCT	O16-C14-C7	-2.15	119.17	123.11
2	B	2001	CCT	O16-C14-C7	-2.12	119.21	123.11

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

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	558/570 (97%)	-0.03	20 (3%)	41 40	14, 27, 50, 81	0
1	B	559/570 (98%)	-0.09	18 (3%)	45 45	12, 25, 50, 79	0
All	All	1117/1140 (97%)	-0.06	38 (3%)	43 43	12, 26, 50, 81	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	564	LEU	8.4
1	A	563	SER	7.6
1	B	563	SER	6.3
1	B	542	ALA	6.3
1	A	541	ALA	5.7
1	A	542	ALA	5.2
1	A	544	GLN	5.2
1	B	544	GLN	4.9
1	A	543	SER	4.7
1	B	549	GLY	4.5
1	A	545	LEU	4.2
1	B	543	SER	4.1
1	B	541	ALA	3.9
1	B	562	HIS	3.8
1	A	535	LYS	3.5
1	B	546	ASP	3.5
1	A	329	THR	3.4
1	A	539	ILE	3.4
1	B	545	LEU	3.3
1	B	539	ILE	3.3
1	B	535	LYS	3.0
1	A	549	GLY	3.0
1	B	548	SER	2.8
1	A	550	TRP	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	531	LYS	2.5
1	B	561	TYR	2.4
1	A	540	PRO	2.4
1	A	546	ASP	2.4
1	A	548	SER	2.3
1	B	550	TRP	2.3
1	A	148	GLN	2.2
1	A	330	GLN	2.2
1	A	538	PRO	2.2
1	A	561	TYR	2.1
1	B	536	LEU	2.1
1	B	106	LYS	2.1
1	A	47	LEU	2.0
1	A	331	GLU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	CCT	A	1001	27/27	0.11	0.99	26,31,35,36	0
2	CCT	B	2001	27/27	0.12	0.25	21,27,30,32	0

6.5 Other polymers ⓘ

There are no such residues in this entry.