WORLDWIDE PDB
PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2014 – 05:20 PM GMT

PDB ID	:	4MTP
Title	:	RdRp from Japanesese Encephalitis Virus
Authors	:	Surana, P.; Nair, D.T.
Deposited on	:	2013-09-20
Resolution	:	3.65 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org
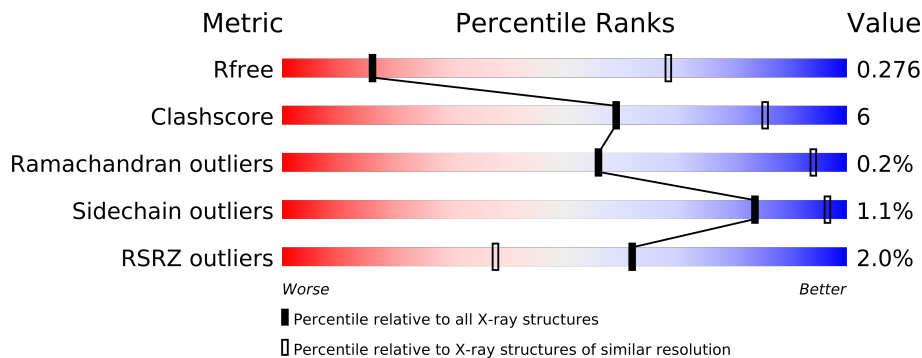
A user guide is available at http://wwpdb.org/ValidationPDFNotes.html

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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
Mogul	:	1.16 November 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	trunk22714
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)	:	trunk22714

1 Overall quality at a glance ⓘ

The reported resolution of this entry is 3.65 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	Percentile Ranks	Value
Rfree		0.276
Clashscore		6
Ramachandran outliers		0.2%
Sidechain outliers		1.1%
RSRZ outliers		2.0%

Worse   Better

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	1021 (3.94-3.38)
Clashscore	79885	1025 (3.90-3.42)
Ramachandran outliers	78287	1195 (3.92-3.40)
Sidechain outliers	78261	1193 (3.92-3.40)
RSRZ outliers	66119	1021 (3.94-3.38)

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	634	
1	B	634	
1	C	634	
1	D	634	

2 Entry composition ⓘ

There are 2 unique types of molecules in this entry. The entry contains 18722 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 RNA dependent RNA polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	591	Total	C	N	O	S	0	0	0
			4781	3021	862	868	30			
1	B	591	Total	C	N	O	S	0	0	0
			4781	3021	862	868	30			
1	C	585	Total	C	N	O	S	0	0	0
			4728	2986	854	858	30			
1	D	546	Total	C	N	O	S	0	0	0
			4424	2801	795	804	24			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	373	ARG	LYS	CONFLICT	UNP G3LHD9
A	429	ASN	ASP	CONFLICT	UNP G3LHD9
A	836	ALA	THR	CONFLICT	UNP G3LHD9
B	373	ARG	LYS	CONFLICT	UNP G3LHD9
B	429	ASN	ASP	CONFLICT	UNP G3LHD9
B	836	ALA	THR	CONFLICT	UNP G3LHD9
C	373	ARG	LYS	CONFLICT	UNP G3LHD9
C	429	ASN	ASP	CONFLICT	UNP G3LHD9
C	836	ALA	THR	CONFLICT	UNP G3LHD9
D	373	ARG	LYS	CONFLICT	UNP G3LHD9
D	429	ASN	ASP	CONFLICT	UNP G3LHD9
D	836	ALA	THR	CONFLICT	UNP G3LHD9

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	2	Total	Zn	0	0
			2	2		
2	A	2	Total	Zn	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	2	Total 2	Zn 2	0	0
2	C	2	Total 2	Zn 2	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 (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.
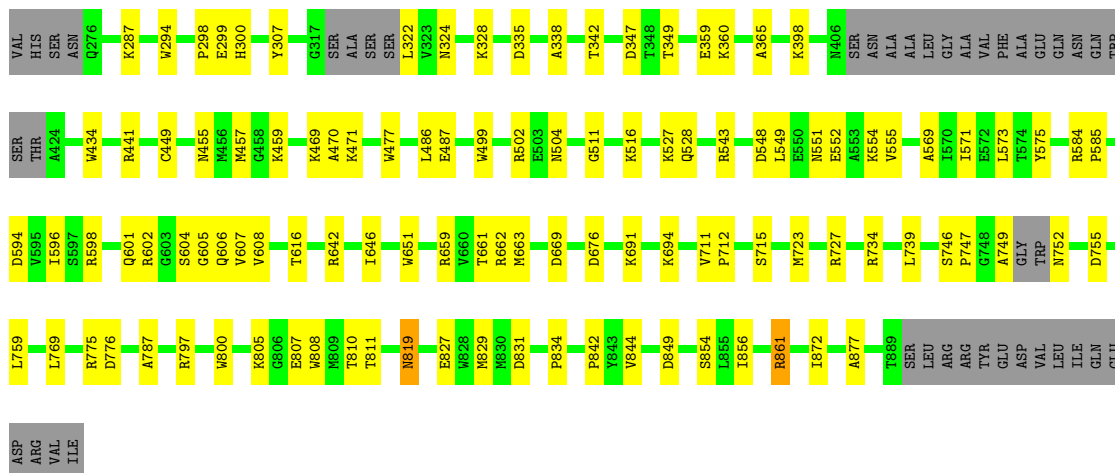
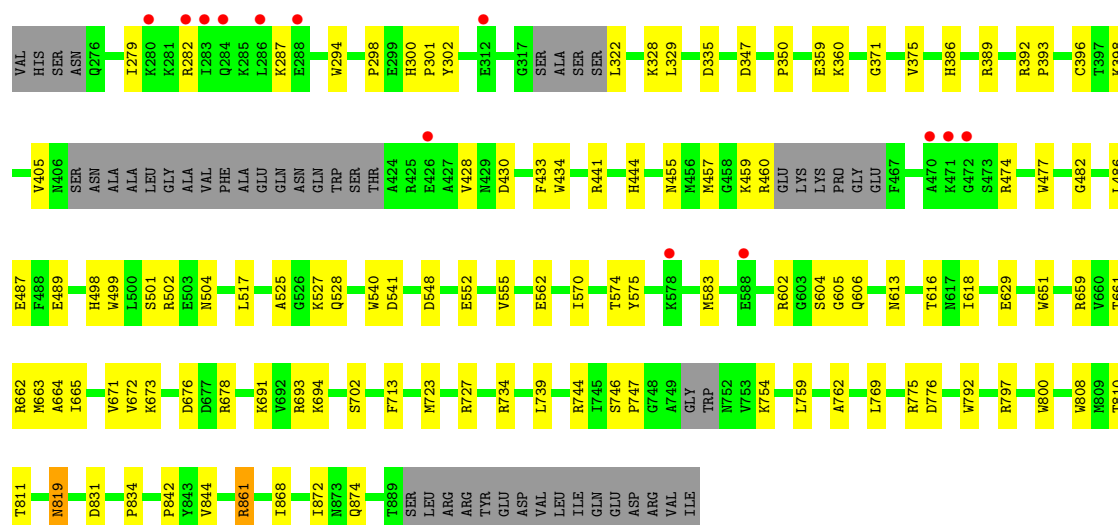• Molecule 1: RNA dependent RNA polymerase

Chain A:

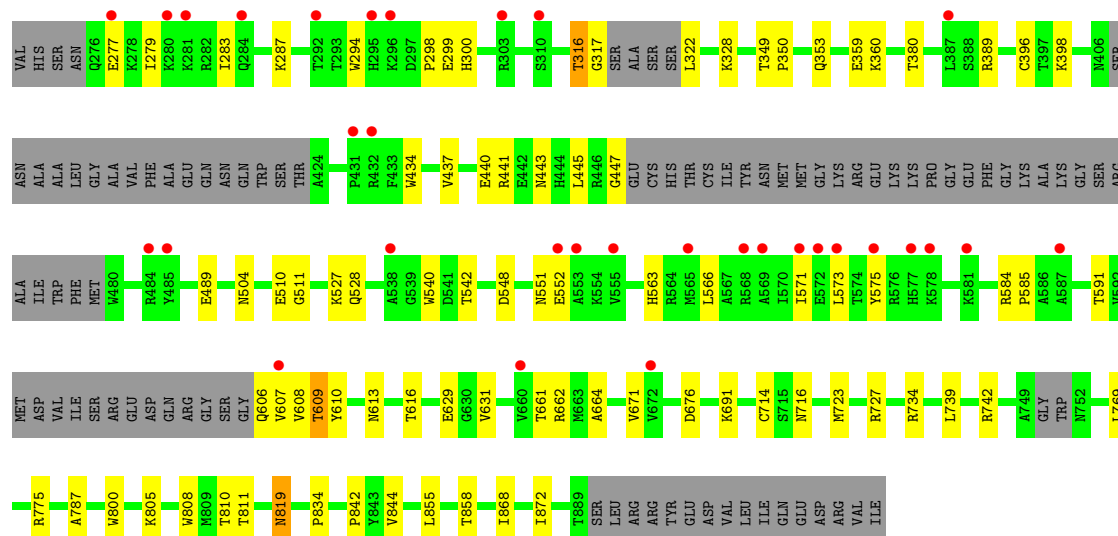• Molecule 1: RNA dependent RNA polymerase

Chain B:

• Molecule 1: RNA dependent RNA polymerase

Chain C:

• Molecule 1: RNA dependent RNA polymerase

Chain D:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	119.47Å 174.01Å 182.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	56.78 – 3.65 58.00 – 3.65	Depositor EDS
% Data completeness (in resolution range)	99.1 (56.78-3.65) 99.5 (58.00-3.65)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.61 (at 3.67Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, R_{free}	0.226 , 0.273 0.225 , 0.276	Depositor DCC
R_{free} test set	2153 reflections (5.03%)	DCC
Wilson B-factor (Å^2)	86.6	Xtriage
Anisotropy	0.222	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , -10.0	EDS
Estimated twinning fraction	0.026 for -h,l,k	Xtriage
L-test for twinning	$< |L| > = 0.44$, $< L^2 > = 0.27$	Xtriage
Outliers	1 of 42866 reflections (0.002%)	Xtriage
F_o,F_c correlation	0.89	EDS
Total number of atoms	18722	wwPDB-VP
Average B, all atoms (Å^2)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.41% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities 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: ZN

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	0.23	0/4894	0.42	0/6618
1	B	0.22	0/4894	0.41	0/6618
1	C	0.22	0/4838	0.41	0/6543
1	D	0.21	0/4528	0.42	0/6131
All	All	0.22	0/19154	0.42	0/25910

There are no bond length outliers.

There are no bond angle outliers.

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	4781	0	4702	60	0
1	B	4781	0	4702	60	0
1	C	4728	0	4646	66	0
1	D	4424	0	4350	43	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	18722	0	18400	227	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 6.

All (227) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:528:GLN:O	1:A:662:ARG:NH2	2.20	0.75
1:B:749:ALA:O	1:B:752:ASN:N	2.22	0.73
1:A:460:ARG:HB2	1:A:476:ILE:HD11	1.70	0.73
1:B:502:ARG:NH2	1:B:663:MET:O	2.21	0.72
1:A:527:LYS:NZ	1:A:661:THR:OG1	2.23	0.71
1:B:775:ARG:NH2	1:B:844:VAL:O	2.25	0.70
1:A:298:PRO:O	1:A:300:HIS:N	2.23	0.69
1:A:775:ARG:NH2	1:A:844:VAL:O	2.25	0.69
1:A:749:ALA:O	1:A:752:ASN:N	2.27	0.68
1:C:775:ARG:NH2	1:C:844:VAL:O	2.27	0.68
1:B:359:GLU:HG3	1:B:360:LYS:HG2	1.75	0.68
1:B:819:ASN:HD21	1:B:834:PRO:HA	1.58	0.67
1:A:819:ASN:HD21	1:A:834:PRO:HA	1.60	0.67
1:D:298:PRO:O	1:D:300:HIS:N	2.26	0.67
1:A:307:TYR:HH	1:A:310:SER:HG	1.42	0.67
1:C:776:ASP:OD1	1:C:861:ARG:NH1	2.28	0.66
1:B:455:ASN:ND2	1:B:457:MET:SD	2.68	0.66
1:C:676:ASP:OD1	1:C:678:ARG:NE	2.27	0.66
1:C:528:GLN:O	1:C:662:ARG:NH2	2.29	0.65
1:B:477:TRP:HB2	1:B:605:GLY:HA3	1.79	0.65
1:D:527:LYS:NZ	1:D:661:THR:OG1	2.29	0.65
1:B:527:LYS:NZ	1:B:661:THR:OG1	2.30	0.65
1:C:663:MET:HG2	1:C:672:VAL:HG12	1.77	0.65
1:D:528:GLN:O	1:D:662:ARG:NH2	2.28	0.65
1:C:477:TRP:HB2	1:C:605:GLY:HA3	1.79	0.64
1:B:602:ARG:O	1:B:606:GLN:NE2	2.30	0.64
1:D:664:ALA:HB3	1:D:671:VAL:HB	1.79	0.64
1:D:775:ARG:NH2	1:D:844:VAL:O	2.31	0.64
1:C:527:LYS:NZ	1:C:661:THR:OG1	2.31	0.64
1:A:776:ASP:OD1	1:A:861:ARG:NH1	2.31	0.63
1:C:602:ARG:O	1:C:606:GLN:NE2	2.31	0.63
1:C:396:CYS:HB2	1:C:489:GLU:HA	1.82	0.62
1:A:469:LYS:HE2	1:A:471:LYS:HE2	1.82	0.62
1:D:317:GLY:HA2	1:D:349:THR:HG22	1.80	0.62
1:A:455:ASN:ND2	1:A:457:MET:SD	2.73	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:298:PRO:O	1:B:300:HIS:N	2.33	0.61
1:D:769:LEU:HD23	1:D:808:TRP:HE3	1.66	0.61
1:C:502:ARG:NH2	1:C:663:MET:O	2.34	0.60
1:B:469:LYS:HE2	1:B:471:LYS:HE2	1.82	0.60
1:C:455:ASN:ND2	1:C:457:MET:SD	2.74	0.60
1:C:405:VAL:HG21	1:C:428:VAL:HG11	1.83	0.59
1:B:723:MET:HG2	1:B:842:PRO:HG3	1.83	0.59
1:B:727:ARG:HD3	1:B:831:ASP:HB3	1.84	0.59
1:A:797:ARG:NH1	1:A:799:SER:O	2.36	0.58
1:B:528:GLN:O	1:B:662:ARG:NH2	2.35	0.57
1:B:734:ARG:HD3	1:B:739:LEU:HD21	1.86	0.57
1:C:727:ARG:HD3	1:C:831:ASP:HB3	1.86	0.57
1:C:723:MET:HG2	1:C:842:PRO:HG3	1.86	0.57
1:D:511:GLY:O	1:D:805:LYS:NZ	2.34	0.57
1:D:723:MET:HG2	1:D:842:PRO:HG3	1.86	0.57
1:A:734:ARG:HD3	1:A:739:LEU:HD21	1.86	0.57
1:A:441:ARG:HG2	1:A:486:LEU:HD21	1.87	0.56
1:A:769:LEU:HD23	1:A:808:TRP:HE3	1.69	0.56
1:B:877:ALA:HB1	1:C:328:LYS:HG2	1.87	0.56
1:A:723:MET:HG2	1:A:842:PRO:HG3	1.88	0.55
1:C:335:ASP:OD1	1:C:744:ARG:NH2	2.37	0.55
1:B:307:TYR:HA	1:B:596:ILE:HG22	1.87	0.55
1:A:395:LEU:HD23	1:A:395:LEU:H	1.71	0.55
1:B:499:TRP:O	1:B:504:ASN:ND2	2.32	0.55
1:C:433:PHE:HE1	1:C:482:GLY:HA2	1.72	0.54
1:A:498:HIS:HB3	1:A:501:SER:HB3	1.88	0.54
1:B:441:ARG:HG2	1:B:486:LEU:HD21	1.90	0.54
1:C:499:TRP:O	1:C:504:ASN:ND2	2.37	0.54
1:D:742:ARG:HH22	1:D:800:TRP:HD1	1.54	0.54
1:C:819:ASN:HD21	1:C:834:PRO:HA	1.72	0.53
1:A:502:ARG:NH2	1:A:663:MET:O	2.38	0.53
1:A:335:ASP:OD1	1:A:744:ARG:NH2	2.38	0.53
1:B:511:GLY:O	1:B:805:LYS:NZ	2.38	0.53
1:A:357:PHE:O	1:A:362:ASP:N	2.33	0.53
1:D:734:ARG:HD3	1:D:739:LEU:HD21	1.90	0.53
1:C:359:GLU:HG3	1:C:360:LYS:HG2	1.90	0.53
1:B:584:ARG:NE	1:B:594:ASP:OD2	2.35	0.53
1:A:347:ASP:HB3	1:A:459:LYS:HG2	1.90	0.53
1:B:398:LYS:HE2	1:B:434:TRP:CD2	2.44	0.52
1:D:552:GLU:OE2	1:D:616:THR:OG1	2.23	0.52
1:D:380:THR:HG21	1:D:551:ASN:HB3	1.90	0.52
1:A:727:ARG:HD3	1:A:831:ASP:HB3	1.91	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:278:LYS:HD3	1:A:573:LEU:HD23	1.91	0.52
1:D:396:CYS:HB2	1:D:489:GLU:HA	1.92	0.52
1:D:723:MET:N	1:D:727:ARG:O	2.40	0.52
1:B:516:LYS:NZ	1:B:827:GLU:OE2	2.39	0.52
1:D:389:ARG:HH22	1:D:504:ASN:HA	1.74	0.51
1:A:306:THR:OG1	1:A:597:SER:OG	2.28	0.51
1:B:548:ASP:OD2	1:B:691:LYS:NZ	2.32	0.51
1:D:350:PRO:HG2	1:D:591:THR:HG21	1.93	0.51
1:B:769:LEU:HD23	1:B:808:TRP:HE3	1.76	0.50
1:B:776:ASP:OD1	1:B:861:ARG:NH1	2.41	0.50
1:A:606:GLN:HG2	1:A:609:THR:OG1	2.11	0.50
1:C:693:ARG:NH1	1:C:702:SER:OG	2.39	0.50
1:B:598:ARG:NH1	1:B:601:GLN:OE1	2.45	0.50
1:D:359:GLU:HG3	1:D:360:LYS:HG2	1.93	0.50
1:B:775:ARG:HD2	1:B:856:ILE:HG21	1.93	0.50
1:D:787:ALA:HB2	1:D:872:ILE:HG23	1.94	0.50
1:D:606:GLN:O	1:D:609:THR:OG1	2.28	0.50
1:B:324:ASN:HD22	1:B:759:LEU:HD12	1.78	0.49
1:B:549:LEU:HD13	1:B:602:ARG:HB2	1.95	0.49
1:C:430:ASP:O	1:C:433:PHE:HB3	2.13	0.49
1:A:552:GLU:OE1	1:A:602:ARG:NE	2.46	0.49
1:C:350:PRO:HG3	1:C:583:MET:SD	2.52	0.49
1:B:752:ASN:HB2	1:B:755:ASP:HB2	1.95	0.49
1:C:676:ASP:N	1:C:676:ASP:OD2	2.44	0.49
1:A:604:SER:OG	1:A:605:GLY:N	2.45	0.49
1:D:447:GLY:HA2	1:D:573:LEU:HD11	1.94	0.48
1:B:607:VAL:HG13	1:B:608:VAL:HG13	1.95	0.48
1:B:807:GLU:N	1:B:807:GLU:OE1	2.43	0.48
1:A:477:TRP:HB2	1:A:605:GLY:HA3	1.95	0.48
1:A:552:GLU:OE2	1:A:602:ARG:NH2	2.47	0.47
1:D:607:VAL:HG13	1:D:608:VAL:HG13	1.95	0.47
1:C:618:ILE:HG12	1:C:665:ILE:HG13	1.96	0.47
1:C:441:ARG:NH2	1:C:562:GLU:OE1	2.47	0.47
1:B:328:LYS:NZ	1:B:335:ASP:OD1	2.48	0.47
1:D:810:THR:OG1	1:D:811:THR:N	2.48	0.47
1:C:552:GLU:O	1:C:555:VAL:HG23	2.15	0.47
1:A:810:THR:OG1	1:A:811:THR:N	2.48	0.47
1:D:349:THR:O	1:D:353:GLN:HG3	2.14	0.47
1:A:306:THR:HG1	1:A:597:SER:HG	1.57	0.47
1:A:618:ILE:HG12	1:A:665:ILE:HG13	1.97	0.47
1:C:350:PRO:HB3	1:C:583:MET:HB3	1.95	0.47
1:A:375:VAL:HG22	1:A:640:LEU:HD22	1.97	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:551:ASN:HA	1:A:554:LYS:HE3	1.97	0.47
1:B:449:CYS:HB2	1:B:573:LEU:HB3	1.97	0.47
1:A:486:LEU:O	1:A:487:GLU:HB3	2.14	0.46
1:B:584:ARG:HA	1:B:585:PRO:HD3	1.79	0.46
1:C:540:TRP:NE1	1:C:613:ASN:OD1	2.42	0.46
1:A:282:ARG:HD2	1:A:579:VAL:HG21	1.98	0.46
1:B:470:ALA:O	1:B:694:LYS:NZ	2.35	0.46
1:A:347:ASP:OD1	1:A:349:THR:OG1	2.21	0.46
1:A:386:HIS:O	1:A:389:ARG:NH1	2.47	0.46
1:D:540:TRP:NE1	1:D:613:ASN:OD1	2.46	0.46
1:C:398:LYS:HG3	1:C:434:TRP:CZ3	2.50	0.46
1:C:347:ASP:HB3	1:C:459:LYS:HG2	1.97	0.46
1:A:877:ALA:HB1	1:D:328:LYS:HG2	1.98	0.46
1:C:486:LEU:O	1:C:487:GLU:HB3	2.16	0.45
1:D:571:ILE:HA	1:D:575:TYR:HD1	1.81	0.45
1:B:365:ALA:HB2	1:B:543:ARG:HA	1.99	0.45
1:D:819:ASN:HD21	1:D:834:PRO:HA	1.80	0.45
1:C:287:LYS:HG2	1:C:294:TRP:CZ2	2.52	0.45
1:C:604:SER:OG	1:C:605:GLY:N	2.50	0.45
1:C:460:ARG:HB3	1:C:474:ARG:HB2	1.98	0.45
1:D:398:LYS:HE2	1:D:434:TRP:CD2	2.51	0.45
1:B:338:ALA:O	1:B:342:THR:OG1	2.22	0.45
1:C:329:LEU:HD22	1:C:874:GLN:HE22	1.81	0.45
1:C:386:HIS:O	1:C:389:ARG:NH1	2.46	0.45
1:C:498:HIS:HB3	1:C:501:SER:HB3	1.98	0.45
1:A:775:ARG:HD2	1:A:856:ILE:HG21	1.99	0.45
1:C:797:ARG:HD2	1:C:800:TRP:CZ2	2.52	0.45
1:C:279:ILE:HG22	1:C:282:ARG:NH2	2.32	0.44
1:A:584:ARG:NE	1:A:594:ASP:OD2	2.39	0.44
1:B:723:MET:N	1:B:727:ARG:O	2.47	0.44
1:C:392:ARG:HA	1:C:393:PRO:HD3	1.85	0.44
1:A:759:LEU:O	1:A:762:ALA:HB3	2.18	0.44
1:A:345:MET:HG3	1:A:460:ARG:NH1	2.33	0.44
1:A:370:ALA:HA	1:A:373:ARG:HH11	1.83	0.44
1:C:279:ILE:HG22	1:C:282:ARG:HH21	1.82	0.44
1:D:510:GLU:HG2	1:D:610:TYR:HE2	1.83	0.44
1:A:359:GLU:HG3	1:A:360:LYS:HG2	2.00	0.44
1:C:517:LEU:HD22	1:C:713:PHE:HE2	1.83	0.44
1:D:714:CYS:O	1:D:716:ASN:ND2	2.49	0.44
1:A:307:TYR:HA	1:A:596:ILE:HG22	2.00	0.43
1:A:584:ARG:HA	1:A:585:PRO:HD3	1.83	0.43
1:C:651:TRP:CZ2	1:C:659:ARG:HG3	2.53	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:810:THR:OG1	1:C:811:THR:N	2.51	0.43
1:D:868:ILE:O	1:D:872:ILE:HG13	2.18	0.43
1:B:642:ARG:O	1:B:646:ILE:HG12	2.19	0.43
1:C:769:LEU:HD23	1:C:808:TRP:HE3	1.84	0.43
1:B:486:LEU:O	1:B:487:GLU:HB3	2.18	0.43
1:A:746:SER:HA	1:A:747:PRO:HD3	1.82	0.43
1:C:664:ALA:HB3	1:C:671:VAL:HB	2.01	0.43
1:D:584:ARG:HA	1:D:585:PRO:HD3	1.88	0.43
1:C:371:GLY:O	1:C:375:VAL:HG23	2.18	0.43
1:C:300:HIS:HA	1:C:301:PRO:HD3	1.87	0.43
1:C:300:HIS:HB2	1:C:302:TYR:CD2	2.54	0.43
1:D:855:LEU:O	1:D:858:THR:OG1	2.30	0.42
1:B:552:GLU:OE2	1:B:616:THR:OG1	2.25	0.42
1:D:629:GLU:HG3	1:D:631:VAL:HG23	2.01	0.42
1:C:694:LYS:HB3	1:C:694:LYS:HE2	1.81	0.42
1:C:746:SER:HA	1:C:747:PRO:HD3	1.84	0.42
1:B:347:ASP:HB3	1:B:459:LYS:HG2	2.01	0.42
1:B:552:GLU:O	1:B:555:VAL:HG23	2.19	0.42
1:C:525:ALA:O	1:C:673:LYS:NZ	2.51	0.42
1:A:658:GLU:OE2	1:A:662:ARG:NH1	2.52	0.42
1:C:398:LYS:HE2	1:C:434:TRP:CD2	2.55	0.42
1:A:394:ARG:NH2	1:A:400:GLU:OE2	2.50	0.42
1:A:398:LYS:HE2	1:A:434:TRP:CD2	2.55	0.42
1:B:604:SER:OG	1:B:605:GLY:N	2.53	0.42
1:D:769:LEU:HD23	1:D:808:TRP:CE3	2.50	0.42
1:C:444:HIS:CE1	1:C:486:LEU:HD13	2.55	0.42
1:B:347:ASP:OD1	1:B:349:THR:OG1	2.28	0.42
1:B:797:ARG:HD2	1:B:800:TRP:CZ2	2.54	0.42
1:C:570:ILE:O	1:C:574:THR:OG1	2.20	0.42
1:B:711:VAL:HA	1:B:712:PRO:HD3	1.88	0.42
1:D:437:VAL:O	1:D:441:ARG:HG3	2.20	0.42
1:A:392:ARG:HA	1:A:393:PRO:HD3	1.84	0.41
1:D:445:LEU:HD21	1:D:566:LEU:HD23	2.02	0.41
1:C:629:GLU:OE2	1:C:659:ARG:NE	2.32	0.41
1:D:316:THR:OG1	1:D:316:THR:O	2.20	0.41
1:C:759:LEU:O	1:C:762:ALA:HB3	2.20	0.41
1:B:787:ALA:HB2	1:B:872:ILE:HG23	2.02	0.41
1:B:651:TRP:CH2	1:B:659:ARG:HG3	2.55	0.41
1:A:778:ARG:NH2	1:A:838:TRP:O	2.53	0.41
1:C:754:LYS:HE3	1:C:792:TRP:CE2	2.55	0.41
1:B:551:ASN:HA	1:B:554:LYS:HE3	2.01	0.41
1:C:868:ILE:O	1:C:872:ILE:HG13	2.20	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:469:LYS:NZ	1:B:715:SER:H	2.18	0.41
1:D:279:ILE:O	1:D:283:ILE:HG12	2.19	0.41
1:C:734:ARG:HD3	1:C:739:LEU:HD21	2.03	0.41
1:A:365:ALA:HB2	1:A:543:ARG:HA	2.03	0.41
1:A:739:LEU:HA	1:A:739:LEU:HD23	1.90	0.41
1:C:548:ASP:OD2	1:C:691:LYS:NZ	2.37	0.41
1:C:552:GLU:OE2	1:C:616:THR:OG1	2.28	0.41
1:B:571:ILE:HA	1:B:575:TYR:HB2	2.02	0.41
1:B:727:ARG:HD2	1:B:829:MET:SD	2.61	0.40
1:A:723:MET:N	1:A:727:ARG:O	2.47	0.40
1:C:541:ASP:CG	1:C:604:SER:HB2	2.42	0.40
1:B:569:ALA:HB1	1:B:573:LEU:HD12	2.03	0.40
1:C:575:TYR:CE1	1:C:606:GLN:HG2	2.56	0.40
1:B:287:LYS:HG2	1:B:294:TRP:CZ2	2.56	0.40
1:B:746:SER:HA	1:B:747:PRO:HD3	1.82	0.40
1:A:552:GLU:O	1:A:555:VAL:HG23	2.21	0.40
1:C:651:TRP:CH2	1:C:659:ARG:HG3	2.57	0.40
1:D:440:GLU:HA	1:D:443:ASN:HD22	1.86	0.40
1:D:287:LYS:HE2	1:D:294:TRP:CZ2	2.56	0.40
1:B:849:ASP:OD1	1:B:854:SER:HB2	2.22	0.40
1:A:663:MET:HG2	1:A:672:VAL:HG22	2.03	0.40
1:B:810:THR:OG1	1:B:811:THR:N	2.54	0.40
1:A:571:ILE:O	1:A:575:TYR:HB2	2.22	0.40
1:D:548:ASP:OD2	1:D:691:LYS:NZ	2.49	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

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	583/634 (92%)	556 (95%)	26 (4%)	1 (0%)	56	94
1	B	583/634 (92%)	554 (95%)	28 (5%)	1 (0%)	56	94
1	C	575/634 (91%)	548 (95%)	26 (4%)	1 (0%)	56	94

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	534/634 (84%)	510 (96%)	22 (4%)	2 (0%)	43	90
All	All	2275/2536 (90%)	2168 (95%)	102 (4%)	5 (0%)	56	94

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	299	GLU
1	B	299	GLU
1	D	299	GLU
1	C	298	PRO
1	D	277	GLU

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	503/541 (93%)	497 (99%)	6 (1%)	82	96
1	B	503/541 (93%)	498 (99%)	5 (1%)	85	97
1	C	497/541 (92%)	494 (99%)	3 (1%)	92	98
1	D	466/541 (86%)	459 (98%)	7 (2%)	76	95
All	All	1969/2164 (91%)	1948 (99%)	21 (1%)	84	96

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

Mol	Chain	Res	Type
1	A	322	LEU
1	A	345	MET
1	A	579	VAL
1	A	606	GLN
1	A	819	ASN
1	A	861	ARG
1	B	322	LEU
1	B	669	ASP
1	B	676	ASP
1	B	819	ASN

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Mol	Chain	Res	Type
1	B	861	ARG
1	C	322	LEU
1	C	819	ASN
1	C	861	ARG
1	D	316	THR
1	D	322	LEU
1	D	542	THR
1	D	563	HIS
1	D	609	THR
1	D	676	ASP
1	D	819	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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	591/634 (93%)	0.08	2 (0%)	91	82	0, 22, 84, 142	0
1	B	591/634 (93%)	0.08	0	100	100	0, 35, 105, 139	0
1	C	585/634 (92%)	0.21	13 (2%)	59	36	1, 26, 111, 142	0
1	D	546/634 (86%)	0.48	32 (5%)	22	14	1, 66, 136, 190	0
All	All	2313/2536 (91%)	0.21	47 (2%)	62	38	0, 34, 119, 190	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	575	TYR	5.8
1	C	471	LYS	4.3
1	D	280	LYS	3.6
1	C	470	ALA	3.4
1	C	578	LYS	3.3
1	D	296	LYS	3.2
1	C	286	LEU	3.2
1	C	312	GLU	3.2
1	D	432	ARG	3.2
1	C	284	GLN	3.2
1	C	472	GLY	3.1
1	D	555	VAL	3.0
1	D	571	ILE	3.0
1	D	568	ARG	3.0
1	D	284	GLN	3.0
1	D	578	LYS	3.0
1	D	431	PRO	2.9
1	D	565	MET	2.9
1	C	280	LYS	2.8
1	D	607	VAL	2.8
1	D	485	TYR	2.7

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Mol	Chain	Res	Type	RSRZ
1	D	292	THR	2.7
1	D	577	HIS	2.6
1	C	426	GLU	2.6
1	C	588	GLU	2.6
1	D	552	GLU	2.6
1	D	672	VAL	2.6
1	C	282	ARG	2.5
1	D	295	HIS	2.5
1	D	553	ALA	2.5
1	C	283	ILE	2.4
1	D	569	ALA	2.4
1	D	277	GLU	2.4
1	D	387	LEU	2.4
1	D	484	ARG	2.3
1	D	310	SER	2.3
1	D	573	LEU	2.2
1	D	281	LYS	2.2
1	A	575	TYR	2.2
1	D	303	ARG	2.2
1	D	572	GLU	2.1
1	D	581	LYS	2.1
1	C	288	GLU	2.1
1	D	660	VAL	2.1
1	D	587	ALA	2.1
1	A	432	ARG	2.1
1	D	538	ALA	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	ZN	C	1002	1/1	0.21	-0.26	2,2,2,2	0
2	ZN	A	1002	1/1	0.21	-0.79	2,2,2,2	0
2	ZN	D	1002	1/1	0.17	-0.85	0,0,0,0	0
2	ZN	B	1002	1/1	0.19	-0.97	2,2,2,2	0
2	ZN	A	1001	1/1	0.08	-1.43	42,42,42,42	0
2	ZN	B	1001	1/1	0.06	-1.67	85,85,85,85	0
2	ZN	C	1001	1/1	0.09	-1.68	63,63,63,63	0
2	ZN	D	1001	1/1	0.09	-1.69	112,112,112,112	0

6.5　Other polymers ⓘ

There are no such residues in this entry.