



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 05:35 PM UTC

PDB ID : 4N7V / pdb_00004n7v
Title : Crystal structure of human Plk4 cryptic polo box (CPB) in complex with a Cep152 N-terminal fragment
Authors : Park, S.-Y.; Park, J.-E.; Tian, L.; Kim, T.-S.; Yang, W.; Lee, K.S.
Deposited on : 2013-10-16
Resolution : 2.76 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

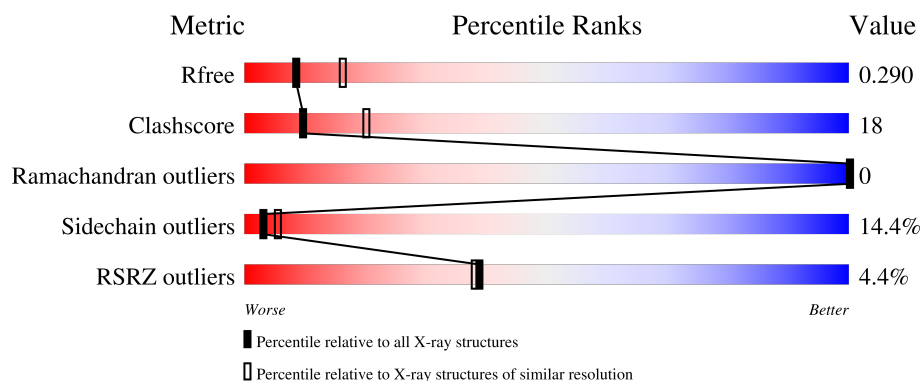
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.76 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	1009 (2.76-2.76)
Clashscore	190562	1044 (2.76-2.76)
Ramachandran outliers	187476	1024 (2.76-2.76)
Sidechain outliers	187428	1024 (2.76-2.76)
RSRZ outliers	180081	1009 (2.76-2.76)

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	229	3% 63% 28% 6% .
1	B	229	7% 60% 28% 8% ..
2	C	60	33% 18% . 45%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3920 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 Serine/threonine-protein kinase PLK4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	222	Total	C	N	O	S	0	0	0
			1810	1158	307	339	6			
1	B	222	Total	C	N	O	S	0	0	0
			1810	1158	307	339	6			

- Molecule 2 is a protein called Centrosomal protein of 152 kDa.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	33	Total	C	N	O	S	0	0	0
			284	171	41	71	1			

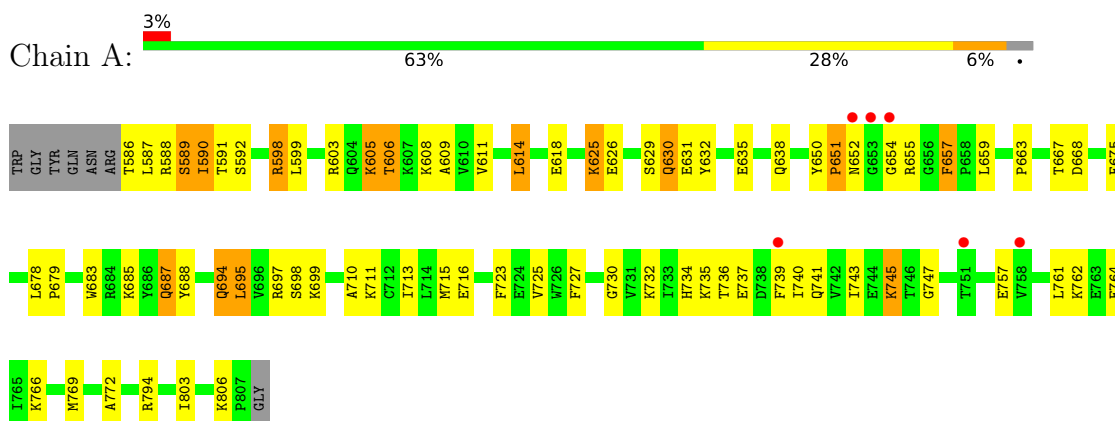
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	10	Total	O	0	0
			10	10		
3	B	3	Total	O	0	0
			3	3		
3	C	3	Total	O	0	0
			3	3		

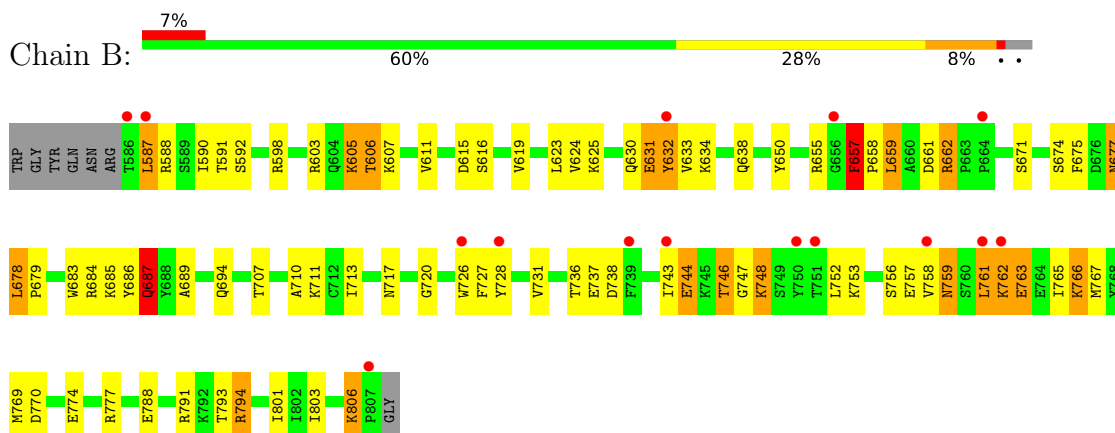
3 Residue-property plots [i](#)

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.

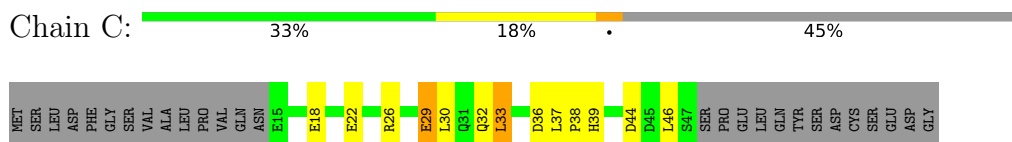
• Molecule 1: Serine/threonine-protein kinase PLK4



• Molecule 1: Serine/threonine-protein kinase PLK4



• Molecule 2: Centrosomal protein of 152 kDa



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	126.55Å 63.94Å 79.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.26 – 2.76 37.26 – 2.76	Depositor EDS
% Data completeness (in resolution range)	92.0 (37.26-2.76) 90.9 (37.26-2.76)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.28 (at 2.77Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.258 , 0.288 0.262 , 0.290	Depositor DCC
R_{free} test set	1586 reflections (10.00%)	wwPDB-VP
Wilson B-factor (Å ²)	75.5	Xtriage
Anisotropy	0.121	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 41.4	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	0.91	EDS
Total number of atoms	3920	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.20% 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 [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	0.36	0/1852	0.84	4/2501 (0.2%)
1	B	0.29	0/1852	0.84	10/2501 (0.4%)
2	C	0.30	0/287	0.80	0/387
All	All	0.33	0/3991	0.84	14/5389 (0.3%)

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	651	PRO	N-CA-C	-9.21	100.05	112.48
1	A	589	SER	N-CA-C	-9.08	100.95	111.03
1	B	747	GLY	N-CA-C	-6.57	97.61	113.18
1	B	746	THR	N-CA-C	6.48	120.49	107.41
1	B	746	THR	CB-CA-C	-6.45	100.45	111.41
1	B	662	ARG	CA-C-N	5.76	123.86	119.66
1	B	662	ARG	C-N-CA	5.76	123.86	119.66
1	A	747	GLY	N-CA-C	-5.47	106.98	114.64
1	A	592	SER	CB-CA-C	5.46	117.04	108.63
1	B	687	GLN	N-CA-C	-5.42	105.45	111.36
1	B	657	PHE	CA-C-N	5.08	126.19	119.84
1	B	657	PHE	C-N-CA	5.08	126.19	119.84
1	B	650	TYR	CA-C-N	5.02	125.02	119.90
1	B	650	TYR	C-N-CA	5.02	125.02	119.90

There are no chirality outliers.

There are no planarity outliers.

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	1810	0	1821	68	0
1	B	1810	0	1821	65	0
2	C	284	0	240	11	0
3	A	10	0	0	0	0
3	B	3	0	0	0	0
3	C	3	0	0	0	0
All	All	3920	0	3882	138	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 18.

All (138) 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:632:TYR:CD2	1:A:655:ARG:O	1.75	1.39
1:A:632:TYR:HD2	1:A:655:ARG:O	1.08	1.23
1:A:632:TYR:CE2	1:A:655:ARG:HB3	1.79	1.17
1:B:744:GLU:HB2	1:B:748:LYS:HB3	1.15	1.09
1:A:632:TYR:HE2	1:A:655:ARG:HB3	0.94	1.08
1:A:632:TYR:HE2	1:A:655:ARG:CB	1.74	0.99
1:B:761:LEU:O	1:B:762:LYS:HG2	1.67	0.95
1:B:746:THR:C	1:B:748:LYS:H	1.75	0.92
1:A:632:TYR:HD2	1:A:655:ARG:C	1.75	0.92
1:B:761:LEU:C	1:B:762:LYS:HG2	1.95	0.91
1:B:744:GLU:HB2	1:B:748:LYS:CB	2.03	0.88
1:B:752:LEU:HD13	1:B:758:VAL:HB	1.60	0.83
1:B:746:THR:C	1:B:748:LYS:N	2.35	0.81
1:A:587:LEU:HB2	1:A:683:TRP:CE2	2.17	0.79
1:B:746:THR:O	1:B:746:THR:HG23	1.81	0.78
1:A:688:TYR:HE2	2:C:38:PRO:O	1.67	0.78
1:B:763:GLU:HA	1:B:766:LYS:HB3	1.66	0.77
1:B:744:GLU:CB	1:B:748:LYS:HB3	2.07	0.76
1:B:746:THR:O	1:B:748:LYS:N	2.19	0.75
1:A:688:TYR:CE2	2:C:38:PRO:O	2.41	0.74
1:B:744:GLU:HB3	1:B:748:LYS:HE2	1.70	0.74
1:B:762:LYS:O	1:B:765:ILE:N	2.20	0.73
1:B:746:THR:CG2	1:B:748:LYS:HZ3	2.02	0.73
1:B:744:GLU:HG3	1:B:748:LYS:HG2	1.72	0.71
1:B:746:THR:HG22	1:B:748:LYS:HZ3	1.55	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:632:TYR:CE2	1:A:655:ARG:CB	2.61	0.71
1:B:736:THR:OG1	1:B:737:GLU:N	2.25	0.69
1:A:655:ARG:N	1:A:655:ARG:HD2	2.08	0.69
1:A:606:THR:HG23	1:A:608:LYS:H	1.59	0.68
1:A:654:GLY:C	1:A:655:ARG:HD2	2.19	0.68
2:C:22:GLU:OE2	2:C:26:ARG:NH1	2.27	0.67
1:B:632:TYR:OH	1:B:634:LYS:NZ	2.28	0.67
1:B:746:THR:CG2	1:B:748:LYS:NZ	2.59	0.66
1:A:588:ARG:HD2	1:A:675:PHE:HE2	1.62	0.64
1:A:586:THR:O	1:A:589:SER:OG	2.12	0.63
1:A:632:TYR:CD2	1:A:655:ARG:C	2.59	0.63
1:A:651:PRO:HA	1:A:667:THR:HG21	1.82	0.61
1:B:685:LYS:O	1:B:686:TYR:HB3	2.01	0.61
1:B:761:LEU:O	1:B:762:LYS:CG	2.47	0.61
2:C:37:LEU:O	2:C:39:HIS:ND1	2.33	0.60
1:A:590:ILE:HB	1:A:687:GLN:NE2	2.16	0.60
1:B:588:ARG:HE	1:B:675:PHE:HE2	1.49	0.60
1:A:611:VAL:HG21	1:A:688:TYR:HE1	1.67	0.60
1:A:699:LYS:HZ3	2:C:29:GLU:HB3	1.67	0.60
1:A:654:GLY:O	1:A:655:ARG:HB2	2.03	0.58
1:A:761:LEU:HD22	1:A:766:LYS:HB3	1.85	0.58
1:B:744:GLU:CB	1:B:748:LYS:HE2	2.32	0.58
1:A:618:GLU:OE1	1:A:638:GLN:NE2	2.36	0.58
1:A:635:GLU:OE1	1:A:685:LYS:NZ	2.37	0.57
1:B:711:LYS:HB3	1:B:726:TRP:HB2	1.88	0.56
1:B:746:THR:HG22	1:B:748:LYS:NZ	2.18	0.55
1:A:711:LYS:HE2	1:A:713:ILE:HD11	1.89	0.55
1:B:710:ALA:HB2	1:B:727:PHE:CD1	2.42	0.55
1:B:603:ARG:NH1	1:B:661:ASP:O	2.40	0.54
1:B:801:ILE:HD12	1:B:803:ILE:HD11	1.89	0.53
1:A:588:ARG:HB2	1:A:675:PHE:CE2	2.43	0.53
1:B:793:THR:OG1	1:B:794:ARG:N	2.40	0.53
1:A:606:THR:HG21	2:C:39:HIS:HD2	1.74	0.52
1:B:674:SER:OG	1:B:677:ASN:OD1	2.20	0.52
1:B:711:LYS:HE2	1:B:713:ILE:HD11	1.92	0.52
1:A:732:LYS:HB2	1:A:743:ILE:HB	1.91	0.51
1:B:774:GLU:OE2	1:B:777:ARG:NH2	2.39	0.51
1:A:590:ILE:H	1:A:590:ILE:HD12	1.75	0.51
1:A:625:LYS:O	1:A:632:TYR:N	2.25	0.51
1:A:587:LEU:O	1:A:588:ARG:HB3	2.10	0.51
1:A:650:TYR:C	1:A:652:ASN:N	2.68	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:598:ARG:NH2	1:A:716:GLU:OE1	2.34	0.50
1:B:806:LYS:HD3	1:B:806:LYS:H	1.75	0.50
1:B:743:ILE:HG22	1:B:744:GLU:O	2.11	0.50
1:A:740:ILE:HG21	1:A:769:MET:HE1	1.93	0.49
1:A:734:HIS:HB3	1:A:741:GLN:HB3	1.94	0.49
1:B:752:LEU:HD12	1:B:753:LYS:H	1.78	0.49
1:A:606:THR:HG22	1:A:609:ALA:O	2.13	0.49
1:A:606:THR:HG22	1:A:609:ALA:H	1.78	0.48
1:A:654:GLY:C	1:A:655:ARG:CD	2.86	0.48
1:B:678:LEU:HD23	1:B:679:PRO:HD2	1.94	0.48
1:B:631:GLU:HB3	1:B:659:LEU:HB2	1.95	0.48
1:A:588:ARG:HB2	1:A:675:PHE:HE2	1.78	0.48
1:A:803:ILE:HG12	1:B:801:ILE:HG22	1.95	0.48
1:B:717:ASN:ND2	1:B:720:GLY:O	2.47	0.48
1:B:763:GLU:HA	1:B:766:LYS:CB	2.41	0.48
1:A:606:THR:HG21	2:C:39:HIS:CD2	2.48	0.47
1:A:631:GLU:C	1:A:632:TYR:HD1	2.22	0.47
1:A:587:LEU:HB2	1:A:683:TRP:CD2	2.49	0.47
1:B:744:GLU:OE1	1:B:748:LYS:CE	2.62	0.47
1:A:632:TYR:CE2	1:A:655:ARG:O	2.54	0.47
1:A:723:PHE:HB3	1:A:735:LYS:HB2	1.97	0.47
1:B:686:TYR:C	1:B:686:TYR:CD1	2.92	0.47
1:B:619:VAL:HG11	1:B:689:ALA:HB1	1.96	0.46
1:A:586:THR:O	1:A:589:SER:N	2.43	0.46
1:B:657:PHE:HA	1:B:658:PRO:HD2	1.73	0.45
1:B:756:SER:N	1:B:759:ASN:HD21	2.15	0.45
1:A:632:TYR:CD2	1:A:655:ARG:CA	3.00	0.45
1:A:603:ARG:HH21	1:A:605:LYS:HD2	1.82	0.45
1:A:587:LEU:CB	1:A:683:TRP:CE2	2.95	0.45
1:A:695:LEU:HD12	1:A:695:LEU:HA	1.86	0.45
1:B:744:GLU:CG	1:B:748:LYS:HG2	2.44	0.45
1:A:588:ARG:HA	1:A:591:THR:O	2.17	0.44
1:A:730:GLY:HA3	1:A:745:LYS:HD2	2.00	0.44
1:B:615:ASP:O	1:B:616:SER:OG	2.31	0.44
1:A:651:PRO:HG3	1:A:657:PHE:CD2	2.52	0.44
1:B:788:GLU:HA	1:B:791:ARG:NH1	2.33	0.44
1:B:746:THR:HG23	1:B:748:LYS:HZ3	1.80	0.44
1:B:762:LYS:HB2	1:B:765:ILE:HB	2.00	0.44
1:B:763:GLU:C	1:B:765:ILE:N	2.76	0.44
1:A:678:LEU:HD12	1:A:679:PRO:HD2	2.00	0.44
2:C:37:LEU:O	2:C:38:PRO:C	2.61	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:587:LEU:HD23	1:B:683:TRP:CH2	2.54	0.43
1:B:605:LYS:HD3	1:B:605:LYS:H	1.83	0.43
1:B:759:ASN:ND2	1:B:759:ASN:H	2.16	0.43
1:A:698:SER:O	1:A:715:MET:HG2	2.19	0.43
1:A:725:VAL:HG21	1:A:772:ALA:HB1	2.01	0.43
1:B:659:LEU:HD22	1:B:659:LEU:HA	1.78	0.43
1:B:687:GLN:HE21	1:B:687:GLN:HB3	1.65	0.43
1:B:707:THR:HG1	1:B:710:ALA:N	2.16	0.43
1:A:590:ILE:H	1:A:590:ILE:CD1	2.28	0.43
1:B:625:LYS:HE3	1:B:625:LYS:HB2	1.83	0.43
1:A:599:LEU:HD21	1:A:697:ARG:HG2	2.01	0.43
1:A:694:GLN:OE1	1:A:697:ARG:NH1	2.51	0.42
1:B:591:THR:HG21	1:B:687:GLN:HG2	2.01	0.42
2:C:18:GLU:OE1	2:C:18:GLU:N	2.52	0.42
1:B:606:THR:HG22	1:B:607:LYS:H	1.85	0.42
1:B:767:MET:HE3	1:B:767:MET:HB2	1.96	0.42
1:B:625:LYS:HB3	1:B:632:TYR:HE1	1.85	0.42
2:C:32:GLN:NE2	2:C:36:ASP:OD2	2.53	0.42
1:B:752:LEU:HD12	1:B:753:LYS:N	2.35	0.42
1:A:710:ALA:HB2	1:A:727:PHE:CD1	2.55	0.42
1:A:586:THR:N	1:A:589:SER:OG	2.53	0.41
1:A:736:THR:HB	1:A:739:PHE:H	1.84	0.41
1:A:586:THR:HA	1:A:683:TRP:CH2	2.56	0.41
1:A:632:TYR:CE2	1:A:655:ARG:CA	3.03	0.41
1:A:629:SER:O	1:A:630:GLN:NE2	2.54	0.41
1:B:625:LYS:HB3	1:B:632:TYR:CE1	2.56	0.41
1:A:762:LYS:C	1:A:764:GLU:H	2.28	0.41
1:B:707:THR:OG1	1:B:710:ALA:N	2.50	0.41
1:A:614:LEU:HD11	1:A:663:PRO:HG2	2.02	0.40
2:C:33:LEU:HD12	2:C:33:LEU:HA	1.90	0.40
1:A:587:LEU:O	1:A:588:ARG:CB	2.69	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	220/229 (96%)	209 (95%)	11 (5%)	0	100	100
1	B	220/229 (96%)	196 (89%)	24 (11%)	0	100	100
2	C	31/60 (52%)	27 (87%)	4 (13%)	0	100	100
All	All	471/518 (91%)	432 (92%)	39 (8%)	0	100	100

There are no Ramachandran outliers to report.

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	203/208 (98%)	184 (91%)	19 (9%)	8	16
1	B	203/208 (98%)	164 (81%)	39 (19%)	1	2
2	C	33/57 (58%)	28 (85%)	5 (15%)	3	4
All	All	439/473 (93%)	376 (86%)	63 (14%)	3	5

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	590	ILE
1	A	598	ARG
1	A	605	LYS
1	A	606	THR
1	A	614	LEU
1	A	625	LYS
1	A	626	GLU
1	A	630	GLN
1	A	657	PHE
1	A	659	LEU
1	A	668	ASP
1	A	687	GLN
1	A	694	GLN

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Mol	Chain	Res	Type
1	A	695	LEU
1	A	737	GLU
1	A	745	LYS
1	A	757	GLU
1	A	794	ARG
1	A	806	LYS
1	B	587	LEU
1	B	590	ILE
1	B	592	SER
1	B	598	ARG
1	B	605	LYS
1	B	606	THR
1	B	611	VAL
1	B	623	LEU
1	B	624	VAL
1	B	630	GLN
1	B	631	GLU
1	B	632	TYR
1	B	633	VAL
1	B	638	GLN
1	B	655	ARG
1	B	657	PHE
1	B	659	LEU
1	B	662	ARG
1	B	671	SER
1	B	677	ASN
1	B	678	LEU
1	B	684	ARG
1	B	687	GLN
1	B	694	GLN
1	B	728	TYR
1	B	731	VAL
1	B	738	ASP
1	B	744	GLU
1	B	748	LYS
1	B	757	GLU
1	B	759	ASN
1	B	761	LEU
1	B	762	LYS
1	B	763	GLU
1	B	766	LYS
1	B	769	MET

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Mol	Chain	Res	Type
1	B	770	ASP
1	B	794	ARG
1	B	806	LYS
2	C	29	GLU
2	C	30	LEU
2	C	33	LEU
2	C	44	ASP
2	C	46	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	630	GLN
1	B	630	GLN
1	B	759	ASN
2	C	32	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 ⓘ

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	222/229 (96%)	0.08	6 (2%) 56 54	7, 32, 90, 108	0
1	B	222/229 (96%)	0.27	15 (6%) 23 23	13, 52, 108, 137	0
2	C	33/60 (55%)	0.08	0 100 100	19, 37, 96, 107	0
All	All	477/518 (92%)	0.17	21 (4%) 39 38	7, 44, 102, 137	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	652	ASN	6.0
1	A	654	GLY	3.7
1	B	758	VAL	3.5
1	B	750	TYR	3.1
1	B	743	ILE	3.0
1	A	653	GLY	2.9
1	A	758	VAL	2.8
1	B	761	LEU	2.8
1	B	656	GLY	2.7
1	B	751	THR	2.6
1	B	762	LYS	2.6
1	A	739	PHE	2.5
1	A	751	THR	2.5
1	B	586	THR	2.4
1	B	664	PRO	2.4
1	B	739	PHE	2.4
1	B	807	PRO	2.3
1	B	726	TRP	2.3
1	B	728	TYR	2.3
1	B	587	LEU	2.2
1	B	632	TYR	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.