



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 01:23 AM UTC

PDB ID : 1QB3 / pdb_00001qb3
Title : CRYSTAL STRUCTURE OF THE CELL CYCLE REGULATORY PROTEIN CKS1
Authors : Bourne, Y.; Watson, M.H.; Arvai, A.S.; Bernstein, S.L.; Reed, S.I.; Tainer, J.A.
Deposited on : 1999-04-30
Resolution : 3.00 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

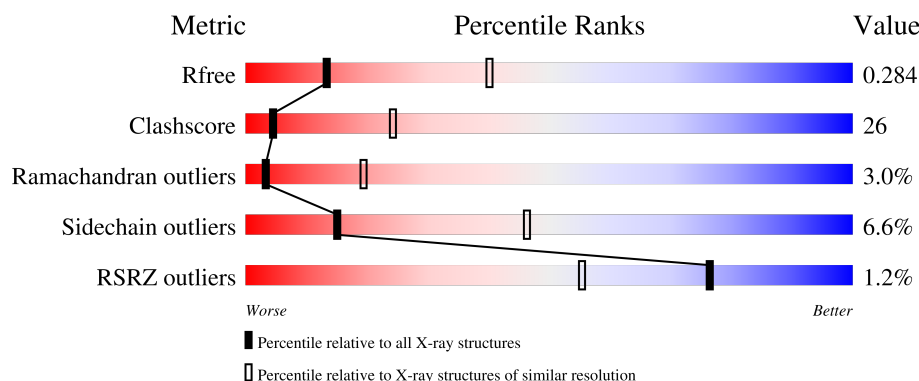
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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 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	150	39% 29% 8% 25%
1	B	150	47% 27% 6% 21%
1	C	150	33% 31% 9% 27%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2829 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 CYCLIN-DEPENDENT KINASES REGULATORY SUB-UNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	113	Total	C	N	O	S	0	0	0
			925	588	163	171	3			
1	B	119	Total	C	N	O	S	0	0	0
			975	616	174	182	3			
1	C	109	Total	C	N	O	S	0	0	0
			905	576	159	167	3			

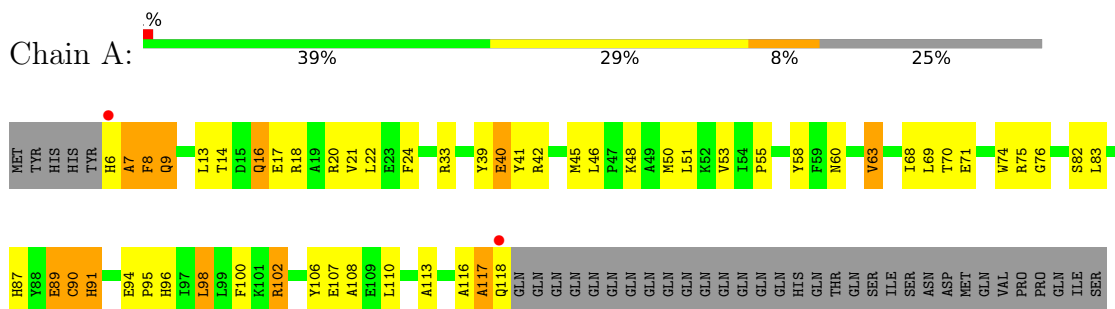
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	7	Total	O	0	0
			7	7		
2	B	15	Total	O	0	0
			15	15		
2	C	2	Total	O	0	0
			2	2		

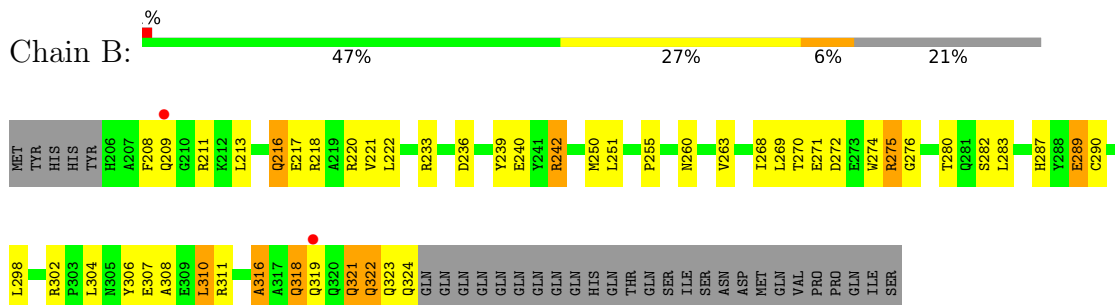
3 Residue-property plots

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.

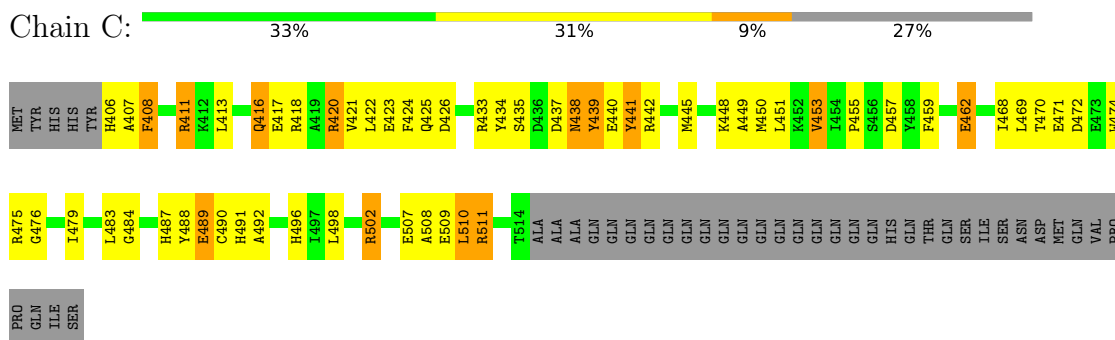
- Molecule 1: CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT



- Molecule 1: CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT



- Molecule 1: CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT



4 Data and refinement statistics

Property	Value	Source
Space group	P 62 2 2	Depositor
Cell constants a, b, c, α , β , γ	105.81Å 105.81Å 165.88Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	12.00 – 3.00 12.00 – 3.00	Depositor EDS
% Data completeness (in resolution range)	89.9 (12.00-3.00) 88.1 (12.00-3.00)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.77 (at 2.98Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.216 , 0.291 0.213 , 0.284	Depositor DCC
R_{free} test set	539 reflections (5.20%)	wwPDB-VP
Wilson B-factor (Å ²)	43.2	Xtriage
Anisotropy	0.349	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 54.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	2829	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.95% 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	0.78	0/950	1.24	8/1288 (0.6%)
1	B	0.88	0/1000	1.32	12/1355 (0.9%)
1	C	0.84	0/930	1.25	8/1260 (0.6%)
All	All	0.84	0/2880	1.27	28/3903 (0.7%)

There are no bond length outliers.

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	483	LEU	N-CA-C	8.46	121.70	110.53
1	B	321	GLN	N-CA-C	-8.05	99.49	110.68
1	B	322	GLN	N-CA-C	-8.04	103.93	114.31
1	C	489	GLU	N-CA-C	7.65	119.40	111.14
1	B	289	GLU	N-CA-C	7.48	119.22	111.14
1	A	40	GLU	N-CA-C	-7.46	97.58	109.59
1	C	511	ARG	N-CA-C	-7.21	102.61	111.40
1	B	318	GLN	N-CA-C	-7.06	103.02	113.61
1	A	89	GLU	N-CA-C	6.85	118.82	111.36
1	B	283	LEU	N-CA-C	6.81	119.75	110.55
1	C	475	ARG	N-CA-C	-6.80	103.95	111.36
1	A	83	LEU	N-CA-C	6.79	119.72	110.55
1	A	70	THR	N-CA-C	-6.44	102.49	110.41
1	C	470	THR	N-CA-C	-6.40	102.54	110.41
1	A	39	TYR	N-CA-C	6.32	119.32	109.52
1	B	275	ARG	N-CA-C	-6.27	104.53	111.36
1	A	75	ARG	N-CA-C	-6.07	104.22	111.69
1	C	441	TYR	N-CA-C	5.93	118.87	109.50
1	A	91	HIS	N-CA-C	5.71	118.01	108.02
1	B	208	PHE	N-CA-C	5.70	117.72	108.26
1	B	239	TYR	N-CA-C	5.68	118.32	109.52
1	B	311	ARG	N-CA-C	-5.66	105.11	111.28
1	C	439	TYR	N-CA-C	5.43	117.23	109.14
1	B	270	THR	N-CA-C	-5.38	103.79	110.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	240	GLU	N-CA-C	-5.37	100.94	109.59
1	B	280	THR	N-CA-C	5.37	117.16	108.41
1	A	58	TYR	N-CA-C	-5.29	106.67	113.02
1	C	479	ILE	N-CA-C	-5.28	102.70	109.30

There are no chirality outliers.

There are no planarity outliers.

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	925	0	879	55	0
1	B	975	0	921	35	1
1	C	905	0	862	67	0
2	A	7	0	0	0	0
2	B	15	0	0	0	0
2	C	2	0	0	0	0
All	All	2829	0	2662	142	1

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 26.

All (142) 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:C:469:LEU:H	1:C:487:HIS:HD2	1.15	0.94
1:A:40:GLU:OE2	1:C:502:ARG:HD2	1.69	0.92
1:C:411:ARG:HD3	1:C:457:ASP:OD2	1.71	0.90
1:B:242:ARG:HH22	1:C:507:GLU:HG3	1.39	0.85
1:B:316:ALA:HA	1:B:319:GLN:NE2	1.91	0.85
1:A:69:LEU:H	1:A:87:HIS:HD2	1.30	0.80
1:A:45:MET:HE2	1:C:496:HIS:HE1	1.47	0.79
1:C:468:ILE:CD1	1:C:489:GLU:HG3	2.14	0.78
1:A:45:MET:HE2	1:C:496:HIS:CE1	2.19	0.77
1:A:68:ILE:CD1	1:A:89:GLU:HG3	2.16	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:102:ARG:HD3	1:C:440:GLU:OE2	1.86	0.76
1:A:21:VAL:HG13	1:A:50:MET:HE3	1.67	0.75
1:C:468:ILE:HD11	1:C:489:GLU:HG3	1.70	0.73
1:B:268:ILE:CD1	1:B:289:GLU:HG3	2.20	0.71
1:A:33:ARG:NH1	1:A:40:GLU:OE1	2.23	0.70
1:C:469:LEU:H	1:C:487:HIS:CD2	2.04	0.70
1:B:269:LEU:H	1:B:287:HIS:HD2	1.38	0.69
1:B:322:GLN:O	1:B:324:GLN:N	2.27	0.68
1:B:218:ARG:NE	1:B:222:LEU:HD11	2.10	0.67
1:A:6:HIS:O	1:A:7:ALA:HB3	1.93	0.67
1:A:68:ILE:HD11	1:A:89:GLU:HG3	1.76	0.66
1:B:221:VAL:HG13	1:B:250:MET:HE3	1.77	0.65
1:B:260:ASN:OD1	1:B:263:VAL:HG23	1.97	0.65
1:A:96:HIS:CD2	1:A:96:HIS:H	2.15	0.63
1:A:100:PHE:CE1	1:C:487:HIS:HB2	2.32	0.63
1:B:268:ILE:HD11	1:B:289:GLU:HG3	1.81	0.62
1:A:60:ASN:OD1	1:A:63:VAL:HG23	2.00	0.62
1:C:418:ARG:NE	1:C:422:LEU:HD11	2.14	0.62
1:C:469:LEU:N	1:C:487:HIS:HD2	1.94	0.61
1:A:18:ARG:NE	1:A:22:LEU:HD11	2.15	0.60
1:A:21:VAL:CG1	1:A:50:MET:HE3	2.31	0.60
1:B:218:ARG:CZ	1:B:222:LEU:HD11	2.33	0.59
1:C:411:ARG:NH1	1:C:413:LEU:HA	2.16	0.59
1:C:420:ARG:NH2	1:C:423:GLU:OE1	2.35	0.59
1:A:68:ILE:HD13	1:A:89:GLU:HG3	1.84	0.59
1:B:218:ARG:NH1	1:B:276:GLY:O	2.35	0.59
1:A:14:THR:OG1	1:A:17:GLU:HG3	2.01	0.59
1:C:437:ASP:O	1:C:438:ASN:HB2	2.02	0.59
1:A:24:PHE:CE2	1:A:50:MET:HA	2.37	0.59
1:C:411:ARG:NH1	1:C:417:GLU:OE1	2.31	0.58
1:C:498:LEU:HD12	1:C:498:LEU:N	2.19	0.58
1:A:90:CYS:SG	1:C:490:CYS:CB	2.91	0.58
1:A:102:ARG:HB2	1:C:484:GLY:O	2.04	0.57
1:B:209:GLN:HG2	1:B:272:ASP:OD2	2.03	0.57
1:A:18:ARG:NH1	1:A:76:GLY:O	2.38	0.57
1:B:268:ILE:HD13	1:B:289:GLU:HG3	1.87	0.57
1:C:468:ILE:HD13	1:C:489:GLU:HG3	1.87	0.56
1:B:221:VAL:CG1	1:B:250:MET:HE3	2.35	0.56
1:C:508:ALA:O	1:C:511:ARG:N	2.39	0.56
1:B:269:LEU:N	1:B:287:HIS:HD2	2.05	0.55
1:B:321:GLN:HG2	1:B:321:GLN:O	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:421:VAL:CG1	1:C:450:MET:HE3	2.37	0.54
1:C:408:PHE:CE1	1:C:472:ASP:HB3	2.43	0.54
1:A:90:CYS:SG	1:C:490:CYS:HB3	2.48	0.53
1:A:13:LEU:CD2	1:A:55:PRO:HG2	2.39	0.53
1:A:18:ARG:CZ	1:A:22:LEU:HD11	2.38	0.53
1:C:421:VAL:HG13	1:C:450:MET:HE3	1.91	0.53
1:C:413:LEU:CD2	1:C:455:PRO:HG2	2.39	0.53
1:A:6:HIS:O	1:A:7:ALA:CB	2.57	0.53
1:B:319:GLN:C	1:B:321:GLN:H	2.15	0.53
1:C:508:ALA:O	1:C:509:GLU:C	2.52	0.52
1:A:48:LYS:O	1:A:51:LEU:HB2	2.10	0.52
1:C:418:ARG:NH1	1:C:476:GLY:O	2.42	0.52
1:A:9:GLN:N	1:A:9:GLN:CD	2.68	0.51
1:A:96:HIS:CE1	1:C:445:MET:HE2	2.45	0.51
1:B:211:ARG:HD2	1:B:211:ARG:C	2.36	0.51
1:B:302:ARG:HD3	1:B:306:TYR:CD2	2.46	0.50
1:C:424:PHE:CE2	1:C:450:MET:HA	2.47	0.50
1:C:424:PHE:CG	1:C:450:MET:HB2	2.46	0.50
1:A:69:LEU:H	1:A:87:HIS:CD2	2.20	0.50
1:C:424:PHE:CE1	1:C:449:ALA:HB3	2.47	0.50
1:C:434:TYR:CD1	1:C:441:TYR:HB2	2.47	0.49
1:C:434:TYR:CE1	1:C:441:TYR:HB2	2.47	0.49
1:C:420:ARG:HH21	1:C:423:GLU:CD	2.20	0.49
1:A:71:GLU:HA	1:A:74:TRP:NE1	2.28	0.48
1:A:116:ALA:O	1:A:117:ALA:C	2.56	0.48
1:C:433:ARG:NH1	1:C:440:GLU:OE1	2.47	0.48
1:A:102:ARG:O	1:A:102:ARG:HG2	2.11	0.48
1:A:106:TYR:O	1:A:110:LEU:HG	2.14	0.48
1:A:94:GLU:HB3	1:A:96:HIS:CD2	2.49	0.48
1:B:318:GLN:HA	1:B:321:GLN:OE1	2.14	0.47
1:B:271:GLU:OE2	1:B:275:ARG:NH2	2.40	0.47
1:C:411:ARG:CD	1:C:457:ASP:OD2	2.53	0.47
1:A:16:GLN:HE21	1:A:16:GLN:HB2	1.48	0.47
1:C:510:LEU:HD12	1:C:510:LEU:O	2.14	0.47
1:B:271:GLU:HA	1:B:274:TRP:NE1	2.29	0.47
1:C:448:LYS:O	1:C:449:ALA:C	2.58	0.47
1:C:406:HIS:O	1:C:407:ALA:HB3	2.15	0.47
1:B:216:GLN:H	1:B:216:GLN:HE21	1.63	0.46
1:C:491:HIS:O	1:C:492:ALA:C	2.58	0.46
1:C:488:TYR:OH	1:C:491:HIS:HD2	1.98	0.46
1:B:216:GLN:O	1:B:220:ARG:HG3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:98:LEU:HD12	1:A:98:LEU:N	2.31	0.45
1:A:7:ALA:O	1:A:8:PHE:C	2.59	0.45
1:C:422:LEU:HA	1:C:422:LEU:HD23	1.65	0.45
1:A:100:PHE:HE1	1:C:487:HIS:HB2	1.76	0.45
1:A:96:HIS:HE1	1:C:445:MET:HE2	1.80	0.45
1:A:69:LEU:N	1:A:87:HIS:HD2	2.05	0.44
1:A:14:THR:HG23	1:A:17:GLU:OE1	2.17	0.44
1:A:116:ALA:O	1:A:118:GLN:N	2.51	0.44
1:C:471:GLU:HA	1:C:474:TRP:CD1	2.52	0.44
1:C:451:LEU:HA	1:C:451:LEU:HD23	1.84	0.44
1:A:113:ALA:HA	1:A:116:ALA:CB	2.48	0.44
1:A:46:LEU:O	1:C:496:HIS:HB2	2.18	0.43
1:B:236:ASP:OD1	1:B:236:ASP:C	2.61	0.43
1:B:316:ALA:HA	1:B:319:GLN:CD	2.42	0.43
1:C:498:LEU:N	1:C:498:LEU:CD1	2.80	0.43
1:A:20:ARG:HG2	1:A:53:VAL:HB	2.01	0.43
1:C:435:SER:HB2	1:C:439:TYR:O	2.18	0.43
1:C:448:LYS:O	1:C:451:LEU:HB2	2.19	0.43
1:C:471:GLU:HA	1:C:474:TRP:NE1	2.33	0.43
1:A:13:LEU:HD22	1:A:55:PRO:HG2	1.99	0.43
1:A:22:LEU:HD23	1:A:22:LEU:HA	1.71	0.43
1:C:508:ALA:O	1:C:510:LEU:N	2.51	0.43
1:A:107:GLU:O	1:A:108:ALA:C	2.61	0.42
1:B:222:LEU:HD23	1:B:222:LEU:HA	1.85	0.42
1:C:433:ARG:HA	1:C:441:TYR:O	2.19	0.42
1:A:71:GLU:HA	1:A:74:TRP:CD1	2.54	0.42
1:B:307:GLU:O	1:B:308:ALA:C	2.63	0.42
1:A:13:LEU:HB3	1:A:17:GLU:HB2	2.02	0.42
1:C:468:ILE:HD11	1:C:489:GLU:CG	2.46	0.42
1:C:508:ALA:C	1:C:510:LEU:N	2.75	0.42
1:C:416:GLN:O	1:C:417:GLU:C	2.61	0.42
1:A:33:ARG:HA	1:A:41:TYR:O	2.19	0.42
1:C:451:LEU:HD22	1:C:459:PHE:CZ	2.55	0.42
1:B:251:LEU:HD23	1:B:251:LEU:HA	1.77	0.41
1:B:310:LEU:N	1:B:310:LEU:CD1	2.83	0.41
1:B:319:GLN:C	1:B:321:GLN:N	2.79	0.41
1:A:91:HIS:C	1:C:490:CYS:SG	3.03	0.41
1:C:407:ALA:O	1:C:408:PHE:C	2.62	0.41
1:C:421:VAL:HG22	1:C:453:VAL:HG23	2.01	0.41
1:A:94:GLU:HA	1:A:95:PRO:HD3	1.94	0.41
1:B:213:LEU:HB3	1:B:217:GLU:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:418:ARG:CZ	1:C:422:LEU:HD11	2.49	0.41
1:B:213:LEU:HD22	1:B:255:PRO:HG2	2.02	0.41
1:C:424:PHE:O	1:C:425:GLN:C	2.62	0.41
1:C:462:GLU:CD	1:C:462:GLU:N	2.78	0.41
1:B:298:LEU:HD23	1:B:298:LEU:HA	1.75	0.40
1:A:96:HIS:H	1:A:96:HIS:HD2	1.64	0.40
1:C:421:VAL:C	1:C:423:GLU:N	2.79	0.40
1:B:304:LEU:HD23	1:B:304:LEU:HA	1.89	0.40
1:A:100:PHE:C	1:C:488:TYR:HE1	2.30	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:290:CYS:SG	1:B:290:CYS:SG[4_555]	1.35	0.85

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	111/150 (74%)	96 (86%)	11 (10%)	4 (4%)	2	16
1	B	117/150 (78%)	104 (89%)	10 (8%)	3 (3%)	4	23
1	C	107/150 (71%)	88 (82%)	16 (15%)	3 (3%)	4	21
All	All	335/450 (74%)	288 (86%)	37 (11%)	10 (3%)	3	19

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	8	PHE
1	A	117	ALA
1	B	323	GLN

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Mol	Chain	Res	Type
1	C	438	ASN
1	A	82	SER
1	B	282	SER
1	C	408	PHE
1	A	7	ALA
1	B	316	ALA
1	C	426	ASP

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	95/135 (70%)	88 (93%)	7 (7%)	13	42
1	B	100/135 (74%)	96 (96%)	4 (4%)	28	62
1	C	95/135 (70%)	87 (92%)	8 (8%)	10	37
All	All	290/405 (72%)	271 (93%)	19 (7%)	15	46

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	GLN
1	A	16	GLN
1	A	42	ARG
1	A	63	VAL
1	A	90	CYS
1	A	98	LEU
1	A	102	ARG
1	B	216	GLN
1	B	233	ARG
1	B	242	ARG
1	B	310	LEU
1	C	411	ARG
1	C	416	GLN
1	C	420	ARG
1	C	442	ARG

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Mol	Chain	Res	Type
1	C	453	VAL
1	C	462	GLU
1	C	502	ARG
1	C	510	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	16	GLN
1	A	87	HIS
1	A	96	HIS
1	B	216	GLN
1	B	287	HIS
1	B	319	GLN
1	B	322	GLN
1	C	409	GLN
1	C	416	GLN
1	C	487	HIS
1	C	491	HIS
1	C	496	HIS

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 [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	113/150 (75%)	-0.35	2 (1%) 67 44	14, 44, 89, 93	0
1	B	119/150 (79%)	-0.58	2 (1%) 69 45	3, 28, 91, 99	0
1	C	109/150 (72%)	-0.55	0 100 100	15, 37, 72, 99	0
All	All	341/450 (75%)	-0.49	4 (1%) 76 55	3, 37, 88, 99	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	319	GLN	5.0
1	A	6	HIS	2.3
1	B	209	GLN	2.3
1	A	118	GLN	2.1

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.