



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 01:52 PM UTC

PDB ID : 4R5J / pdb_00004r5j
Title : Crystal structure of the DnaK C-terminus (Dnak-SBD-A)
Authors : Leu, J.I.; Zhang, P.; Murphy, M.E.; Marmorstein, R.; George, D.L.
Deposited on : 2014-08-21
Resolution : 2.36 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
Mogul	:	2022.3.0, CSD as543be (2022)
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

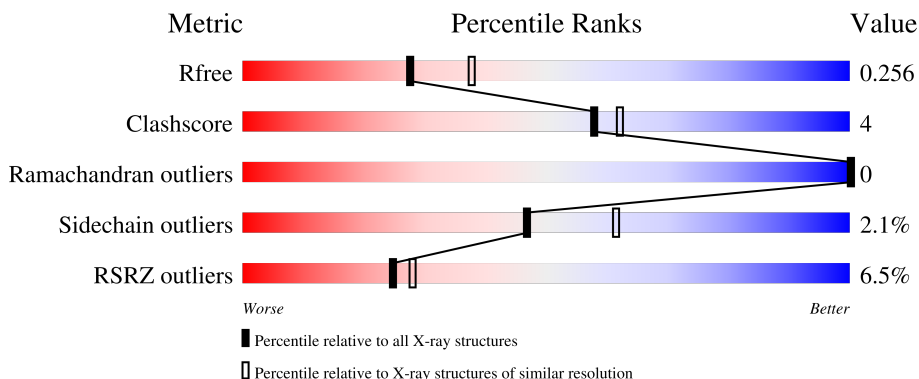
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.36 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	228	8% 91% • •
1	B	228	10% 82% 13% • •
1	C	228	5% 85% 13% • •
1	D	228	2% 87% 10% •

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6700 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 Chaperone protein DnaK.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	218	Total	C	N	O	S	0	0	0
			1631	1005	290	330	6			
1	B	218	Total	C	N	O	S	0	0	0
			1620	1003	291	320	6			
1	C	224	Total	C	N	O	S	0	0	0
			1668	1026	300	336	6			
1	D	221	Total	C	N	O	S	0	0	0
			1623	1000	284	333	6			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	380	MET	-	expression tag	UNP P0A6Y8
A	381	HIS	-	expression tag	UNP P0A6Y8
A	382	HIS	-	expression tag	UNP P0A6Y8
A	383	HIS	-	expression tag	UNP P0A6Y8
A	384	HIS	-	expression tag	UNP P0A6Y8
A	385	HIS	-	expression tag	UNP P0A6Y8
A	386	HIS	-	expression tag	UNP P0A6Y8
A	387	ILE	-	expression tag	UNP P0A6Y8
A	388	GLU	-	expression tag	UNP P0A6Y8
B	380	MET	-	expression tag	UNP P0A6Y8
B	381	HIS	-	expression tag	UNP P0A6Y8
B	382	HIS	-	expression tag	UNP P0A6Y8
B	383	HIS	-	expression tag	UNP P0A6Y8
B	384	HIS	-	expression tag	UNP P0A6Y8
B	385	HIS	-	expression tag	UNP P0A6Y8
B	386	HIS	-	expression tag	UNP P0A6Y8
B	387	ILE	-	expression tag	UNP P0A6Y8
B	388	GLU	-	expression tag	UNP P0A6Y8
C	380	MET	-	expression tag	UNP P0A6Y8
C	381	HIS	-	expression tag	UNP P0A6Y8
C	382	HIS	-	expression tag	UNP P0A6Y8

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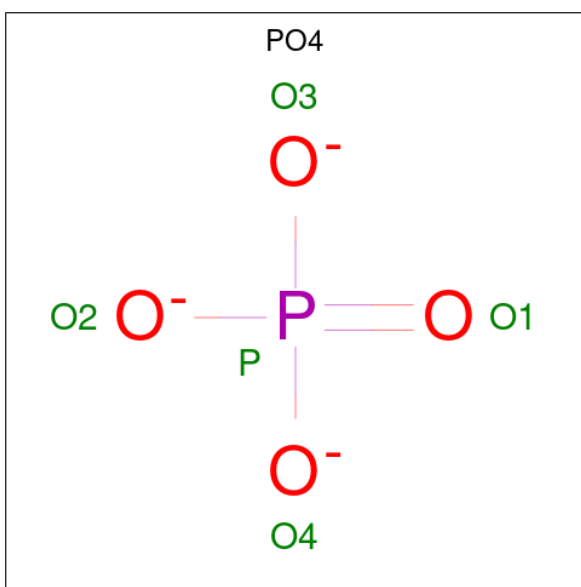
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Chain	Residue	Modelled	Actual	Comment	Reference
C	383	HIS	-	expression tag	UNP P0A6Y8
C	384	HIS	-	expression tag	UNP P0A6Y8
C	385	HIS	-	expression tag	UNP P0A6Y8
C	386	HIS	-	expression tag	UNP P0A6Y8
C	387	ILE	-	expression tag	UNP P0A6Y8
C	388	GLU	-	expression tag	UNP P0A6Y8
D	380	MET	-	expression tag	UNP P0A6Y8
D	381	HIS	-	expression tag	UNP P0A6Y8
D	382	HIS	-	expression tag	UNP P0A6Y8
D	383	HIS	-	expression tag	UNP P0A6Y8
D	384	HIS	-	expression tag	UNP P0A6Y8
D	385	HIS	-	expression tag	UNP P0A6Y8
D	386	HIS	-	expression tag	UNP P0A6Y8
D	387	ILE	-	expression tag	UNP P0A6Y8
D	388	GLU	-	expression tag	UNP P0A6Y8

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Ca 1 1	0	0
2	B	1	Total Ca 1 1	0	0
2	C	2	Total Ca 2 2	0	0
2	D	1	Total Ca 1 1	0	0

- Molecule 3 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total	O	P	0	0
			5	4	1		
3	D	1	Total	O	P	0	0
			5	4	1		

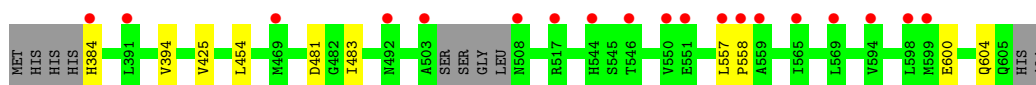
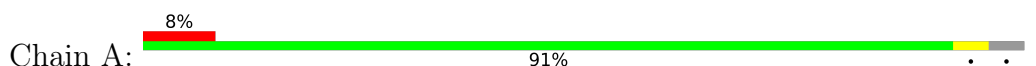
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	29	Total	O	0	0
			29	29		
4	B	34	Total	O	0	0
			34	34		
4	C	39	Total	O	0	0
			39	39		
4	D	41	Total	O	0	0
			41	41		

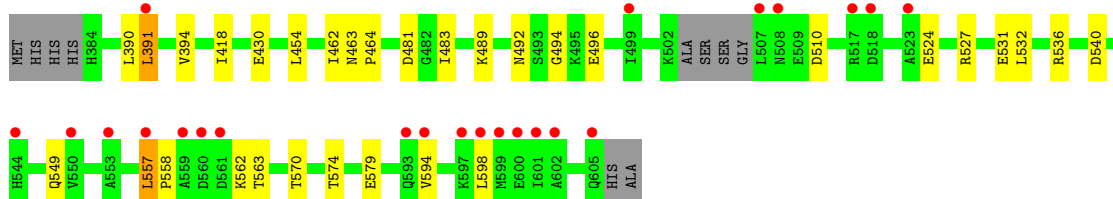
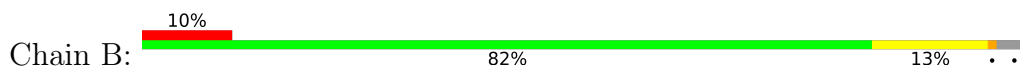
3 Residue-property plots [i](#)

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.

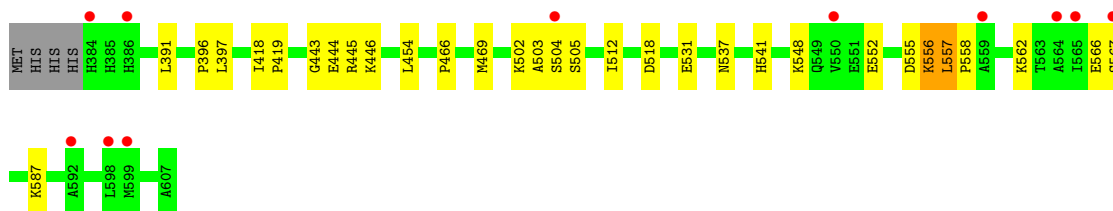
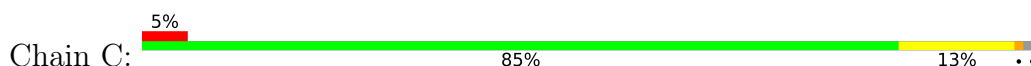
- Molecule 1: Chaperone protein DnaK



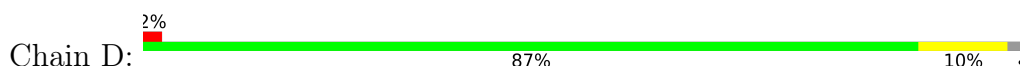
- Molecule 1: Chaperone protein DnaK



- Molecule 1: Chaperone protein DnaK



- Molecule 1: Chaperone protein DnaK



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	44.66Å 69.41Å 75.77Å 102.12° 104.20° 92.96°	Depositor
Resolution (Å)	44.25 – 2.36 44.25 – 2.36	Depositor EDS
% Data completeness (in resolution range)	97.8 (44.25-2.36) 97.9 (44.25-2.36)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.85 (at 2.37Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.215 , 0.258 0.216 , 0.256	Depositor DCC
R_{free} test set	1723 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	41.1	Xtriage
Anisotropy	0.288	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 39.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.36$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6700	wwPDB-VP
Average B, all atoms (Å ²)	61.0	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 37.65 % 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 4.1545e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

Bond lengths and bond angles in the following residue types are not validated in this section: PO4, CA

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	0.38	0/1647	0.83	0/2226
1	B	0.38	0/1636	0.86	0/2210
1	C	0.39	0/1685	0.88	3/2278 (0.1%)
1	D	0.38	0/1638	0.82	1/2218 (0.0%)
All	All	0.38	0/6606	0.85	4/8932 (0.0%)

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	C	0	1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	C	556	LYS	N-CA-C	-8.22	102.81	113.17
1	C	557	LEU	CA-C-N	6.39	127.83	119.84
1	C	557	LEU	C-N-CA	6.39	127.83	119.84
1	D	556	LYS	N-CA-C	-6.14	105.78	113.28

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	555	ASP	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	1631	0	1604	5	0
1	B	1620	0	1607	18	0
1	C	1668	0	1648	22	1
1	D	1623	0	1584	15	1
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	2	0	0	0	0
2	D	1	0	0	0	0
3	C	5	0	0	0	0
3	D	5	0	0	0	0
4	A	29	0	0	1	0
4	B	34	0	0	3	0
4	C	39	0	0	2	0
4	D	41	0	0	6	0
All	All	6700	0	6443	58	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 4.

All (58) 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:D:445:ARG:HG2	1:D:515:MET:HE1	1.49	0.94
1:D:498:LYS:NZ	4:D:1040:HOH:O	2.04	0.89
1:D:561:ASP:OD2	4:D:1028:HOH:O	1.91	0.86
1:D:497:GLN:NE2	4:D:1015:HOH:O	2.12	0.81
1:B:430:GLU:O	4:B:1003:HOH:O	2.06	0.72
1:D:538:GLN:OE1	4:D:1041:HOH:O	2.09	0.71
1:A:384:HIS:N	4:A:1029:HOH:O	2.27	0.67
1:D:394:VAL:O	4:D:1014:HOH:O	2.11	0.67
1:D:524:GLU:OE1	1:D:527:ARG:NH2	2.30	0.64
1:D:502:LYS:O	1:D:505:SER:OG	2.17	0.58
1:C:444:GLU:OE1	4:C:1021:HOH:O	2.17	0.58
1:A:425:VAL:HB	1:C:419:PRO:HG2	1.86	0.57
1:B:527:ARG:NH1	1:B:531:GLU:OE2	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:462:ILE:O	4:B:1023:HOH:O	2.18	0.55
1:B:557:LEU:N	1:B:558:PRO:HD3	2.23	0.54
1:D:449:ALA:O	4:D:1024:HOH:O	2.19	0.53
1:B:558:PRO:O	1:B:562:LYS:HB3	2.09	0.53
1:A:481:ASP:HB2	1:A:483:ILE:HG12	1.90	0.51
1:C:445:ARG:NH1	1:C:518:ASP:OD2	2.43	0.51
1:C:397:LEU:HD11	1:C:512:ILE:HG23	1.91	0.51
1:C:504:SER:OG	4:C:1028:HOH:O	2.19	0.51
1:B:540:ASP:OD2	4:B:1029:HOH:O	2.19	0.51
1:C:502:LYS:O	1:C:505:SER:OG	2.26	0.50
1:B:532:LEU:HD21	1:B:536:ARG:CZ	2.42	0.50
1:D:454:LEU:HB3	1:D:501:ILE:HD13	1.94	0.49
1:B:570:THR:O	1:B:574:THR:HG23	2.13	0.49
1:D:589:GLN:O	1:D:593:GLN:HG3	2.13	0.48
1:D:518:ASP:O	1:D:522:ASN:ND2	2.37	0.47
1:B:489:LYS:NZ	1:C:531:GLU:OE1	2.43	0.47
1:C:396:PRO:O	1:C:397:LEU:HD12	2.16	0.46
1:B:489:LYS:HG3	1:B:496:GLU:HB2	1.97	0.46
1:B:549:GLN:HE21	1:B:598:LEU:HD13	1.81	0.46
1:C:503:ALA:O	1:C:504:SER:OG	2.26	0.46
1:B:532:LEU:HD11	1:B:579:GLU:HA	1.98	0.45
1:B:489:LYS:HE2	1:B:494:GLY:HA2	1.98	0.45
1:D:557:LEU:HD23	1:D:562:LYS:HB2	1.99	0.45
1:C:418:ILE:HG23	1:C:419:PRO:HA	1.99	0.44
1:D:515:MET:O	1:D:515:MET:HE3	2.18	0.44
1:B:524:GLU:OE1	1:B:527:ARG:NH2	2.51	0.44
1:C:537:ASN:O	1:C:541:HIS:ND1	2.40	0.44
1:C:556:LYS:HE2	1:C:556:LYS:HB3	1.64	0.44
1:C:396:PRO:C	1:C:397:LEU:HD12	2.41	0.44
1:C:557:LEU:HA	1:C:558:PRO:HD3	1.64	0.44
1:A:600:GLU:O	1:A:604:GLN:HG2	2.18	0.43
1:C:548:LYS:O	1:C:552:GLU:N	2.52	0.43
1:B:391:LEU:HB3	1:B:418:ILE:O	2.18	0.43
1:A:557:LEU:HA	1:A:558:PRO:HD3	1.80	0.43
1:B:481:ASP:HB2	1:B:483:ILE:HG12	2.01	0.42
1:C:397:LEU:CD1	1:C:512:ILE:HG12	2.50	0.42
1:B:463:ASN:HA	1:B:464:PRO:HD3	1.95	0.42
1:C:446:LYS:HA	1:C:446:LYS:HD3	1.85	0.42
1:C:587:LYS:HD3	1:C:587:LYS:HA	1.83	0.42
1:C:548:LYS:HE2	1:C:548:LYS:HB2	1.80	0.41
1:C:562:LYS:HE3	1:C:566:GLU:OE2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:466:PRO:HD2	1:C:469:MET:HG3	2.02	0.41
1:B:598:LEU:HD23	1:B:598:LEU:HA	1.91	0.41
1:C:397:LEU:HD23	1:C:443:GLY:HA2	2.03	0.41
1:D:446:LYS:HD3	1:D:446:LYS:HA	1.88	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:C:587:LYS:NZ	1:D:491:LYS:O[1_655]	2.17	0.03

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	214/228 (94%)	209 (98%)	5 (2%)	0	100	100
1	B	214/228 (94%)	211 (99%)	3 (1%)	0	100	100
1	C	222/228 (97%)	216 (97%)	6 (3%)	0	100	100
1	D	219/228 (96%)	215 (98%)	4 (2%)	0	100	100
All	All	869/912 (95%)	851 (98%)	18 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	171/190 (90%)	169 (99%)	2 (1%)	63	77
1	B	168/190 (88%)	159 (95%)	9 (5%)	20	24
1	C	175/190 (92%)	172 (98%)	3 (2%)	53	68
1	D	168/190 (88%)	168 (100%)	0	100	100
All	All	682/760 (90%)	668 (98%)	14 (2%)	47	61

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	394	VAL
1	A	454	LEU
1	B	390	LEU
1	B	391	LEU
1	B	394	VAL
1	B	454	LEU
1	B	492	ASN
1	B	510	ASP
1	B	557	LEU
1	B	563	THR
1	B	594	VAL
1	C	391	LEU
1	C	454	LEU
1	C	567	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	432	ASN
1	B	456	GLN
1	B	492	ASN

5.3.3 RNA ⓘ

There are no RNA molecules 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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 5 are monoatomic - leaving 2 for Mogul analysis.

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	$\# Z > 2$
3	PO4	D	901	-	4,4,4	0.96	0	6,6,6	0.43	0
3	PO4	C	902	-	4,4,4	0.97	0	6,6,6	0.39	0

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.

No monomer is involved in short contacts.

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, 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	218/228 (95%)	0.76	19 (8%) 16 18	27, 62, 97, 115	0
1	B	218/228 (95%)	0.85	23 (10%) 11 13	30, 64, 118, 134	0
1	C	224/228 (98%)	0.55	11 (4%) 35 41	28, 57, 96, 110	0
1	D	221/228 (96%)	0.48	4 (1%) 67 72	28, 57, 77, 94	0
All	All	881/912 (96%)	0.66	57 (6%) 25 28	27, 60, 98, 134	0

All (57) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	599	MET	4.3
1	B	550	VAL	3.8
1	B	557	LEU	3.8
1	B	601	ILE	3.7
1	C	599	MET	3.6
1	C	564	ALA	3.6
1	C	567	SER	3.5
1	B	593	GLN	3.5
1	C	598	LEU	3.3
1	B	560	ASP	3.1
1	B	594	VAL	3.1
1	A	503	ALA	3.0
1	A	557	LEU	2.9
1	B	598	LEU	2.9
1	A	544	HIS	2.9
1	B	508	ASN	2.9
1	D	604	GLN	2.8
1	A	517	ARG	2.8
1	A	598	LEU	2.8
1	B	559	ALA	2.8
1	B	605	GLN	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	561	ASP	2.7
1	B	518	ASP	2.7
1	B	602	ALA	2.6
1	C	504	SER	2.6
1	A	391	LEU	2.6
1	B	507	LEU	2.6
1	C	559	ALA	2.6
1	C	565	ILE	2.5
1	A	594	VAL	2.4
1	A	469	MET	2.4
1	A	569	LEU	2.4
1	B	517	ARG	2.4
1	D	603	GLN	2.4
1	D	481	ASP	2.4
1	B	599	MET	2.3
1	B	391	LEU	2.3
1	B	553	ALA	2.3
1	B	523	ALA	2.3
1	A	550	VAL	2.3
1	A	558	PRO	2.2
1	A	559	ALA	2.2
1	B	499	ILE	2.2
1	A	508	ASN	2.2
1	B	597	LYS	2.2
1	C	550	VAL	2.1
1	D	561	ASP	2.1
1	A	565	ILE	2.1
1	C	384	HIS	2.1
1	A	546	THR	2.1
1	C	592	ALA	2.1
1	B	600	GLU	2.1
1	A	492	ASN	2.1
1	C	386	HIS	2.1
1	A	551	GLU	2.0
1	B	544	HIS	2.0
1	A	384	HIS	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 [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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. 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	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	PO4	D	901	5/5	0.76	0.18	54,82,86,96	0
3	PO4	C	902	5/5	0.89	0.16	60,61,74,80	0
2	CA	B	901	1/1	0.90	0.13	64,64,64,64	0
2	CA	C	903	1/1	0.95	0.23	76,76,76,76	0
2	CA	C	901	1/1	0.96	0.08	49,49,49,49	0
2	CA	A	901	1/1	0.97	0.13	67,67,67,67	0
2	CA	D	902	1/1	0.97	0.10	55,55,55,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.