



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 3NCV / pdb_00003ncv
Title : NgoL
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Deposited on : 2010-06-05
Resolution : 2.40 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

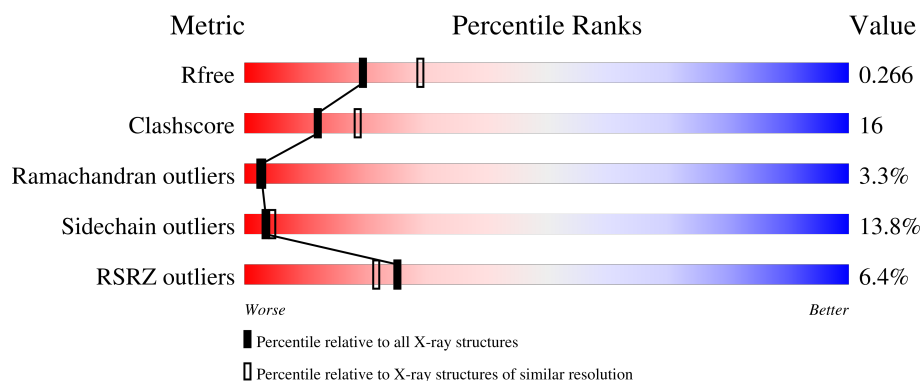
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	220	4% 57% 21% 7% 15%
1	B	220	7% 56% 21% 8% 15%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 2950 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 DNA mismatch repair protein mutL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	187	Total	C	N	O	S	0	0	0
			1427	888	260	269	10			
1	B	188	Total	C	N	O	S	0	0	0
			1415	884	256	265	10			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	439	THR	-	expression tag	UNP Q5F8M6
A	440	MET	-	expression tag	UNP Q5F8M6
A	441	GLY	-	expression tag	UNP Q5F8M6
A	442	SER	-	expression tag	UNP Q5F8M6
A	443	SER	-	expression tag	UNP Q5F8M6
A	444	HIS	-	expression tag	UNP Q5F8M6
A	445	HIS	-	expression tag	UNP Q5F8M6
A	446	HIS	-	expression tag	UNP Q5F8M6
A	447	HIS	-	expression tag	UNP Q5F8M6
A	448	HIS	-	expression tag	UNP Q5F8M6
A	449	HIS	-	expression tag	UNP Q5F8M6
A	450	SER	-	expression tag	UNP Q5F8M6
A	451	SER	-	expression tag	UNP Q5F8M6
A	452	GLY	-	expression tag	UNP Q5F8M6
A	453	LEU	-	expression tag	UNP Q5F8M6
A	454	VAL	-	expression tag	UNP Q5F8M6
A	455	PRO	-	expression tag	UNP Q5F8M6
A	456	ARG	-	expression tag	UNP Q5F8M6
A	457	GLY	-	expression tag	UNP Q5F8M6
A	458	SER	-	expression tag	UNP Q5F8M6
A	459	HIS	-	expression tag	UNP Q5F8M6
B	439	THR	-	expression tag	UNP Q5F8M6
B	440	MET	-	expression tag	UNP Q5F8M6
B	441	GLY	-	expression tag	UNP Q5F8M6
B	442	SER	-	expression tag	UNP Q5F8M6

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Chain	Residue	Modelled	Actual	Comment	Reference
B	443	SER	-	expression tag	UNP Q5F8M6
B	444	HIS	-	expression tag	UNP Q5F8M6
B	445	HIS	-	expression tag	UNP Q5F8M6
B	446	HIS	-	expression tag	UNP Q5F8M6
B	447	HIS	-	expression tag	UNP Q5F8M6
B	448	HIS	-	expression tag	UNP Q5F8M6
B	449	HIS	-	expression tag	UNP Q5F8M6
B	450	SER	-	expression tag	UNP Q5F8M6
B	451	SER	-	expression tag	UNP Q5F8M6
B	452	GLY	-	expression tag	UNP Q5F8M6
B	453	LEU	-	expression tag	UNP Q5F8M6
B	454	VAL	-	expression tag	UNP Q5F8M6
B	455	PRO	-	expression tag	UNP Q5F8M6
B	456	ARG	-	expression tag	UNP Q5F8M6
B	457	GLY	-	expression tag	UNP Q5F8M6
B	458	SER	-	expression tag	UNP Q5F8M6
B	459	HIS	-	expression tag	UNP Q5F8M6

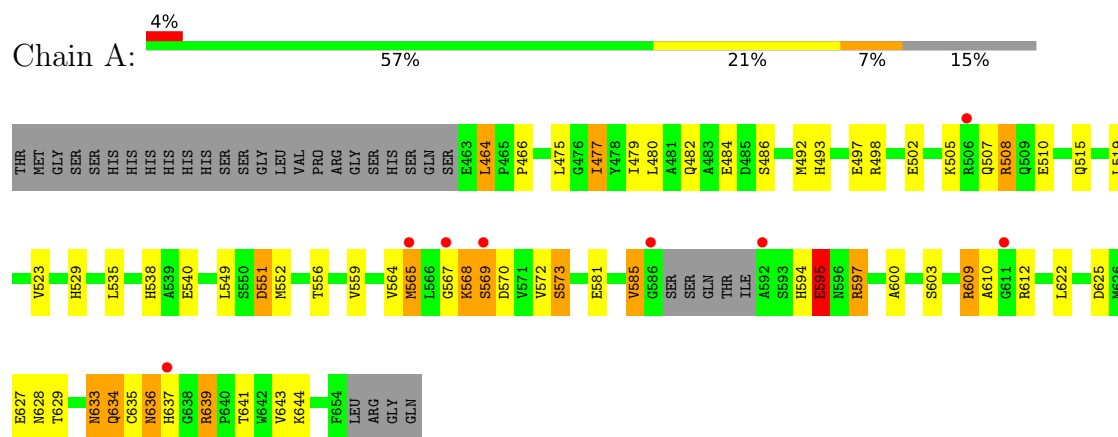
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	74	Total O 74 74	0	0
2	B	34	Total O 34 34	0	0

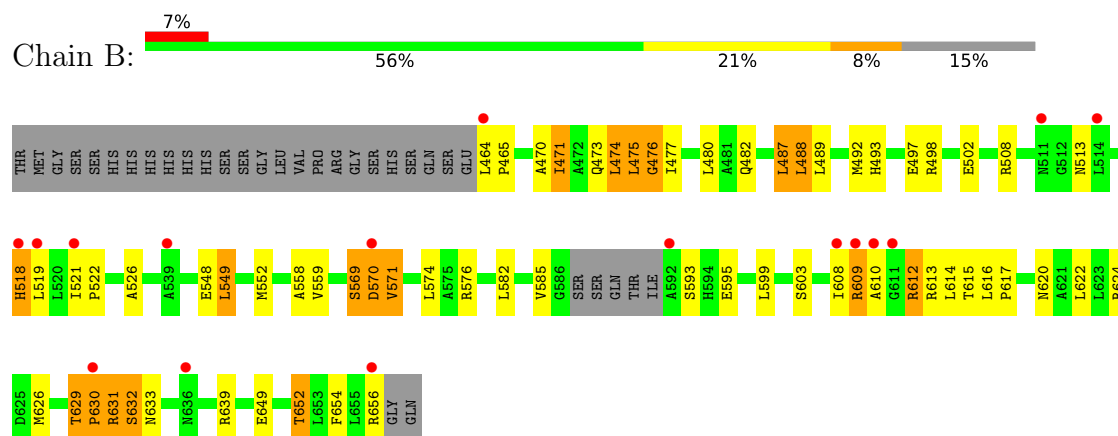
3 Residue-property plots [i](#)

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: DNA mismatch repair protein mutL



• Molecule 1: DNA mismatch repair protein mutL



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	49.50Å 62.10Å 92.10Å 90.00° 104.60° 90.00°	Depositor
Resolution (Å)	44.44 – 2.40 44.44 – 2.40	Depositor EDS
% Data completeness (in resolution range)	92.3 (44.44-2.40) 92.3 (44.44-2.40)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.10 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.216 , 0.272 0.217 , 0.266	Depositor DCC
R_{free} test set	1638 reflections (7.67%)	wwPDB-VP
Wilson B-factor (Å ²)	52.6	Xtriage
Anisotropy	0.166	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 40.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.035 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2950	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.30% 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	1.12	2/1447 (0.1%)	1.23	9/1956 (0.5%)
1	B	0.91	1/1435 (0.1%)	1.15	5/1943 (0.3%)
All	All	1.02	3/2882 (0.1%)	1.19	14/3899 (0.4%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	518	HIS	CE1-NE2	8.51	1.41	1.32
1	A	568	LYS	CA-C	5.46	1.58	1.52
1	A	559	VAL	CA-CB	5.18	1.60	1.54

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	629	THR	CA-C-N	7.57	129.30	119.84
1	B	629	THR	C-N-CA	7.57	129.30	119.84
1	A	486	SER	N-CA-C	6.56	119.03	109.07
1	A	464	LEU	CA-C-N	-6.51	113.68	120.38
1	A	464	LEU	C-N-CA	-6.51	113.68	120.38
1	A	629	THR	CA-C-N	-6.09	114.00	120.03
1	A	629	THR	C-N-CA	-6.09	114.00	120.03
1	B	616	LEU	CA-C-N	-5.73	113.11	119.19
1	B	616	LEU	C-N-CA	-5.73	113.11	119.19
1	A	551	ASP	N-CA-C	5.69	117.17	110.97
1	A	597	ARG	N-CA-C	-5.64	105.03	111.07
1	A	639	ARG	N-CA-C	-5.49	102.73	110.31
1	B	571	VAL	CB-CA-C	-5.34	104.94	112.14
1	A	477	ILE	N-CA-CB	-5.23	105.13	112.35

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	1427	0	1437	46	0
1	B	1415	0	1416	48	0
2	A	74	0	0	3	0
2	B	34	0	0	9	0
All	All	2950	0	2853	89	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 16.

All (89) 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:594:HIS:CD2	1:A:597:ARG:HH12	1.79	1.01
1:B:474:LEU:C	2:B:51:HOH:O	2.08	0.95
1:B:632:SER:HA	2:B:52:HOH:O	1.67	0.93
1:B:582:LEU:O	1:B:585:VAL:HG22	1.78	0.83
1:A:594:HIS:HD2	1:A:597:ARG:HH12	1.26	0.82
1:B:464:LEU:HB3	1:B:465:PRO:CD	2.12	0.80
1:B:474:LEU:HD22	1:B:475:LEU:HD22	1.63	0.80
1:A:569:SER:HA	1:A:609:ARG:HH21	1.48	0.77
1:A:568:LYS:O	1:A:569:SER:HB3	1.86	0.75
1:A:569:SER:HA	1:A:609:ARG:NH2	2.02	0.75
1:B:493:HIS:ND1	1:B:609:ARG:HA	2.01	0.75
1:B:470:ALA:H	1:B:620:ASN:HD21	1.34	0.74
1:B:474:LEU:HB3	2:B:51:HOH:O	1.91	0.69
1:B:526:ALA:O	1:B:576:ARG:NH2	2.25	0.69
1:A:565:MET:SD	1:A:565:MET:N	2.65	0.68
1:A:568:LYS:O	1:A:569:SER:CB	2.43	0.67
1:B:475:LEU:N	2:B:51:HOH:O	2.20	0.67
1:B:493:HIS:CE1	1:B:609:ARG:HA	2.29	0.67
1:B:474:LEU:CA	2:B:51:HOH:O	2.41	0.65
1:B:632:SER:O	1:B:633:ASN:CG	2.40	0.64
1:A:551:ASP:O	1:A:556:THR:O	2.15	0.64
1:B:464:LEU:HB3	1:B:465:PRO:HD3	1.79	0.64
1:B:631:ARG:C	1:B:632:SER:O	2.37	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:615:THR:HB	1:B:617:PRO:HD2	1.80	0.63
1:A:594:HIS:CD2	1:A:597:ARG:NH1	2.60	0.62
1:B:474:LEU:CB	2:B:51:HOH:O	2.46	0.60
1:B:480:LEU:HD23	1:B:489:LEU:HD12	1.85	0.59
1:B:569:SER:O	1:B:570:ASP:C	2.45	0.59
1:A:569:SER:O	1:A:570:ASP:HB3	2.06	0.56
1:A:568:LYS:HG2	1:A:569:SER:H	1.71	0.56
1:B:474:LEU:O	1:B:476:GLY:N	2.34	0.56
1:B:470:ALA:H	1:B:620:ASN:ND2	2.04	0.56
1:A:493:HIS:O	1:A:497:GLU:HG3	2.06	0.55
1:A:594:HIS:HD2	1:A:597:ARG:NH1	1.98	0.55
1:A:569:SER:O	1:A:570:ASP:CB	2.54	0.55
1:A:551:ASP:O	1:A:552:MET:HB2	2.07	0.54
1:A:551:ASP:O	1:A:552:MET:CB	2.55	0.53
1:A:637:HIS:CE1	1:B:656:ARG:CB	2.91	0.53
1:A:538:HIS:HA	1:A:540:GLU:OE2	2.09	0.52
1:B:548:GLU:C	1:B:549:LEU:HD23	2.35	0.52
1:A:508:ARG:HD2	1:A:595:GLU:OE2	2.10	0.51
1:A:594:HIS:CG	1:A:597:ARG:HH12	2.27	0.51
1:B:608:ILE:O	1:B:609:ARG:HB2	2.10	0.51
1:A:498:ARG:NH1	1:A:502:GLU:OE2	2.42	0.51
1:A:466:PRO:HG2	1:A:627:GLU:HG2	1.93	0.50
1:B:464:LEU:HB3	1:B:465:PRO:HD2	1.92	0.50
1:B:549:LEU:HD22	1:B:559:VAL:HA	1.94	0.50
1:A:480:LEU:HD13	1:B:480:LEU:HD13	1.94	0.49
1:A:507:GLN:HE22	1:A:515:GLN:HB3	1.78	0.48
1:A:585:VAL:HB	1:A:594:HIS:NE2	2.27	0.48
1:A:464:LEU:HD12	1:A:484:GLU:HB3	1.95	0.48
1:A:519:LEU:HD23	1:A:523:VAL:HG23	1.95	0.48
1:B:599:LEU:O	1:B:603:SER:N	2.47	0.48
1:B:608:ILE:O	1:B:609:ARG:CB	2.61	0.48
1:B:549:LEU:HA	1:B:558:ALA:O	2.15	0.47
1:A:540:GLU:CD	1:A:540:GLU:H	2.23	0.46
1:A:570:ASP:OD1	1:A:572:VAL:HB	2.15	0.46
1:B:593:SER:C	1:B:595:GLU:H	2.24	0.45
1:A:633:ASN:OD1	1:A:634:GLN:HG3	2.17	0.45
1:A:570:ASP:HA	2:A:55:HOH:O	2.16	0.45
1:A:564:VAL:HB	1:A:565:MET:CE	2.47	0.45
1:A:636:ASN:N	1:A:636:ASN:OD1	2.50	0.45
1:A:482:GLN:HE21	1:B:474:LEU:HD23	1.82	0.44
1:A:529:HIS:CE1	2:A:71:HOH:O	2.70	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:567:GLY:O	1:A:568:LYS:HB3	2.17	0.44
1:A:475:LEU:H	1:B:482:GLN:NE2	2.15	0.44
1:A:515:GLN:HB3	1:A:565:MET:HE1	1.99	0.44
1:B:498:ARG:NH1	1:B:502:GLU:OE2	2.50	0.44
1:B:493:HIS:HD1	1:B:609:ARG:HA	1.80	0.44
1:A:639:ARG:HG2	1:B:654:PHE:O	2.18	0.44
1:A:479:ILE:HD11	1:A:492:MET:HG3	1.99	0.43
1:A:600:ALA:O	1:A:603:SER:OG	2.25	0.43
1:B:471:ILE:HD13	1:B:482:GLN:HB2	2.01	0.43
1:B:629:THR:HA	1:B:630:PRO:HD3	1.60	0.43
1:A:637:HIS:ND1	1:A:637:HIS:O	2.52	0.42
1:B:649:GLU:O	1:B:652:THR:HG22	2.19	0.42
1:A:552:MET:HB3	1:A:552:MET:HE3	1.86	0.42
1:A:635:CYS:SG	1:A:639:ARG:HB2	2.60	0.42
1:A:628:ASN:HB2	2:A:65:HOH:O	2.19	0.42
1:A:570:ASP:HB3	1:A:573:SER:HB2	2.00	0.42
1:B:497:GLU:HG3	2:B:87:HOH:O	2.21	0.41
1:B:473:GLN:HE22	1:B:614:LEU:H	1.68	0.41
1:B:633:ASN:N	2:B:52:HOH:O	2.52	0.41
1:B:497:GLU:CG	2:B:87:HOH:O	2.68	0.41
1:B:502:GLU:OE2	1:B:631:ARG:NH1	2.54	0.40
1:B:608:ILE:HG23	1:B:614:LEU:HD11	2.02	0.40
1:B:612:ARG:HB2	1:B:613:ARG:H	1.55	0.40
1:B:622:LEU:O	1:B:626:MET:HG3	2.20	0.40
1:B:487:LEU:C	1:B:488:LEU:HD23	2.47	0.40

There are no symmetry-related clashes.

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	183/220 (83%)	169 (92%)	11 (6%)	3 (2%)	7 11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	184/220 (84%)	162 (88%)	13 (7%)	9 (5%)	1	1
All	All	367/440 (83%)	331 (90%)	24 (6%)	12 (3%)	3	2

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	569	SER
1	B	475	LEU
1	B	609	ARG
1	B	632	SER
1	A	610	ALA
1	B	569	SER
1	B	570	ASP
1	A	595	GLU
1	B	522	PRO
1	B	630	PRO
1	B	610	ALA
1	B	476	GLY

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	151/180 (84%)	130 (86%)	21 (14%)	3	4
1	B	147/180 (82%)	127 (86%)	20 (14%)	3	5
All	All	298/360 (83%)	257 (86%)	41 (14%)	3	4

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	477	ILE
1	A	505	LYS
1	A	508	ARG
1	A	510	GLU

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Mol	Chain	Res	Type
1	A	535	LEU
1	A	549	LEU
1	A	565	MET
1	A	573	SER
1	A	581	GLU
1	A	585	VAL
1	A	595	GLU
1	A	609	ARG
1	A	612	ARG
1	A	622	LEU
1	A	625	ASP
1	A	633	ASN
1	A	634	GLN
1	A	636	ASN
1	A	641	THR
1	A	643	VAL
1	A	644	LYS
1	B	471	ILE
1	B	474	LEU
1	B	477	ILE
1	B	487	LEU
1	B	488	LEU
1	B	492	MET
1	B	508	ARG
1	B	513	ASN
1	B	518	HIS
1	B	519	LEU
1	B	521	ILE
1	B	549	LEU
1	B	552	MET
1	B	571	VAL
1	B	574	LEU
1	B	612	ARG
1	B	624	ARG
1	B	631	ARG
1	B	639	ARG
1	B	652	THR

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	482	GLN

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Mol	Chain	Res	Type
1	A	507	GLN
1	A	529	HIS
1	A	594	HIS
1	B	473	GLN
1	B	482	GLN
1	B	507	GLN
1	B	513	ASN
1	B	555	ASN
1	B	594	HIS
1	B	620	ASN
1	B	634	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 [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	187/220 (85%)	0.05	8 (4%)	40 36	31, 46, 78, 96	0
1	B	188/220 (85%)	0.51	16 (8%)	16 13	38, 71, 105, 129	0
All	All	375/440 (85%)	0.28	24 (6%)	25 22	31, 57, 101, 129	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	592	ALA	7.1
1	A	592	ALA	4.7
1	A	569	SER	4.3
1	B	511	ASN	3.9
1	A	637	HIS	3.8
1	B	570	ASP	3.8
1	B	464	LEU	3.6
1	A	586	GLY	3.4
1	B	630	PRO	3.3
1	B	610	ALA	3.3
1	B	611	GLY	3.2
1	A	565	MET	3.0
1	A	506	ARG	2.8
1	B	609	ARG	2.7
1	B	608	ILE	2.7
1	B	521	ILE	2.6
1	A	611	GLY	2.5
1	B	656	ARG	2.3
1	B	519	LEU	2.2
1	B	636	ASN	2.2
1	A	567	GLY	2.2
1	B	518	HIS	2.1
1	B	539	ALA	2.0
1	B	514	LEU	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.