



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 07:44 AM UTC

PDB ID : 5ME3 / pdb_00005me3
Title : Structure of the Scc2 C-terminus
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Deposited on : 2016-11-14
Resolution : 2.85 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

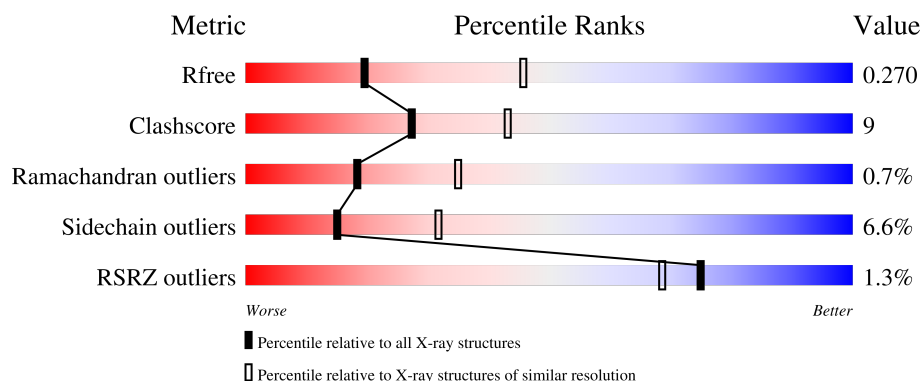
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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	1407 (2.88-2.84)
Clashscore	190562	1446 (2.88-2.84)
Ramachandran outliers	187476	1406 (2.88-2.84)
Sidechain outliers	187428	1407 (2.88-2.84)
RSRZ outliers	180081	1408 (2.88-2.84)

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	1143	66% 17% • 15%
1	B	1143	62% 20% • 16%
2	X	17	100%
3	Y	27	63% 37%
4	W	11	91% 9%

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Mol	Chain	Length	Quality of chain
4	Z	11	 100%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 16017 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 Sister chromatid cohesion protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	973	Total	C	N	O	S	0	0	0
			7931	5085	1341	1460	45			
1	B	960	Total	C	N	O	S	0	0	0
			7811	5009	1316	1442	44			

There are 82 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	377	MET	-	initiating methionine	UNP Q750S2
A	1480	LYS	-	expression tag	UNP Q750S2
A	1481	SER	-	expression tag	UNP Q750S2
A	1482	SER	-	expression tag	UNP Q750S2
A	1483	ILE	-	expression tag	UNP Q750S2
A	1484	PRO	-	expression tag	UNP Q750S2
A	1485	GLU	-	expression tag	UNP Q750S2
A	1486	ASN	-	expression tag	UNP Q750S2
A	1487	LEU	-	expression tag	UNP Q750S2
A	1488	TYR	-	expression tag	UNP Q750S2
A	1489	PHE	-	expression tag	UNP Q750S2
A	1490	GLN	-	expression tag	UNP Q750S2
A	1491	SER	-	expression tag	UNP Q750S2
A	1492	TRP	-	expression tag	UNP Q750S2
A	1493	SER	-	expression tag	UNP Q750S2
A	1494	HIS	-	expression tag	UNP Q750S2
A	1495	PRO	-	expression tag	UNP Q750S2
A	1496	GLN	-	expression tag	UNP Q750S2
A	1497	PHE	-	expression tag	UNP Q750S2
A	1498	GLU	-	expression tag	UNP Q750S2
A	1499	LYS	-	expression tag	UNP Q750S2
A	1500	GLY	-	expression tag	UNP Q750S2
A	1501	GLY	-	expression tag	UNP Q750S2
A	1502	GLY	-	expression tag	UNP Q750S2
A	1503	SER	-	expression tag	UNP Q750S2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1504	GLY	-	expression tag	UNP Q750S2
A	1505	GLY	-	expression tag	UNP Q750S2
A	1506	GLY	-	expression tag	UNP Q750S2
A	1507	SER	-	expression tag	UNP Q750S2
A	1508	GLY	-	expression tag	UNP Q750S2
A	1509	GLY	-	expression tag	UNP Q750S2
A	1510	GLY	-	expression tag	UNP Q750S2
A	1511	SER	-	expression tag	UNP Q750S2
A	1512	TRP	-	expression tag	UNP Q750S2
A	1513	SER	-	expression tag	UNP Q750S2
A	1514	HIS	-	expression tag	UNP Q750S2
A	1515	PRO	-	expression tag	UNP Q750S2
A	1516	GLN	-	expression tag	UNP Q750S2
A	1517	PHE	-	expression tag	UNP Q750S2
A	1518	GLU	-	expression tag	UNP Q750S2
A	1519	LYS	-	expression tag	UNP Q750S2
B	377	MET	-	initiating methionine	UNP Q750S2
B	1480	LYS	-	expression tag	UNP Q750S2
B	1481	SER	-	expression tag	UNP Q750S2
B	1482	SER	-	expression tag	UNP Q750S2
B	1483	ILE	-	expression tag	UNP Q750S2
B	1484	PRO	-	expression tag	UNP Q750S2
B	1485	GLU	-	expression tag	UNP Q750S2
B	1486	ASN	-	expression tag	UNP Q750S2
B	1487	LEU	-	expression tag	UNP Q750S2
B	1488	TYR	-	expression tag	UNP Q750S2
B	1489	PHE	-	expression tag	UNP Q750S2
B	1490	GLN	-	expression tag	UNP Q750S2
B	1491	SER	-	expression tag	UNP Q750S2
B	1492	TRP	-	expression tag	UNP Q750S2
B	1493	SER	-	expression tag	UNP Q750S2
B	1494	HIS	-	expression tag	UNP Q750S2
B	1495	PRO	-	expression tag	UNP Q750S2
B	1496	GLN	-	expression tag	UNP Q750S2
B	1497	PHE	-	expression tag	UNP Q750S2
B	1498	GLU	-	expression tag	UNP Q750S2
B	1499	LYS	-	expression tag	UNP Q750S2
B	1500	GLY	-	expression tag	UNP Q750S2
B	1501	GLY	-	expression tag	UNP Q750S2
B	1502	GLY	-	expression tag	UNP Q750S2
B	1503	SER	-	expression tag	UNP Q750S2
B	1504	GLY	-	expression tag	UNP Q750S2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1505	GLY	-	expression tag	UNP Q750S2
B	1506	GLY	-	expression tag	UNP Q750S2
B	1507	SER	-	expression tag	UNP Q750S2
B	1508	GLY	-	expression tag	UNP Q750S2
B	1509	GLY	-	expression tag	UNP Q750S2
B	1510	GLY	-	expression tag	UNP Q750S2
B	1511	SER	-	expression tag	UNP Q750S2
B	1512	TRP	-	expression tag	UNP Q750S2
B	1513	SER	-	expression tag	UNP Q750S2
B	1514	HIS	-	expression tag	UNP Q750S2
B	1515	PRO	-	expression tag	UNP Q750S2
B	1516	GLN	-	expression tag	UNP Q750S2
B	1517	PHE	-	expression tag	UNP Q750S2
B	1518	GLU	-	expression tag	UNP Q750S2
B	1519	LYS	-	expression tag	UNP Q750S2

- Molecule 2 is a protein called unassigned sequence of Scc2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	X	17	Total	C	N	O	0	0	0
			85	51	17	17			

- Molecule 3 is a protein called Scc2 unassigned sequence.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	Y	17	Total	C	N	O	0	0	0
			85	51	17	17			

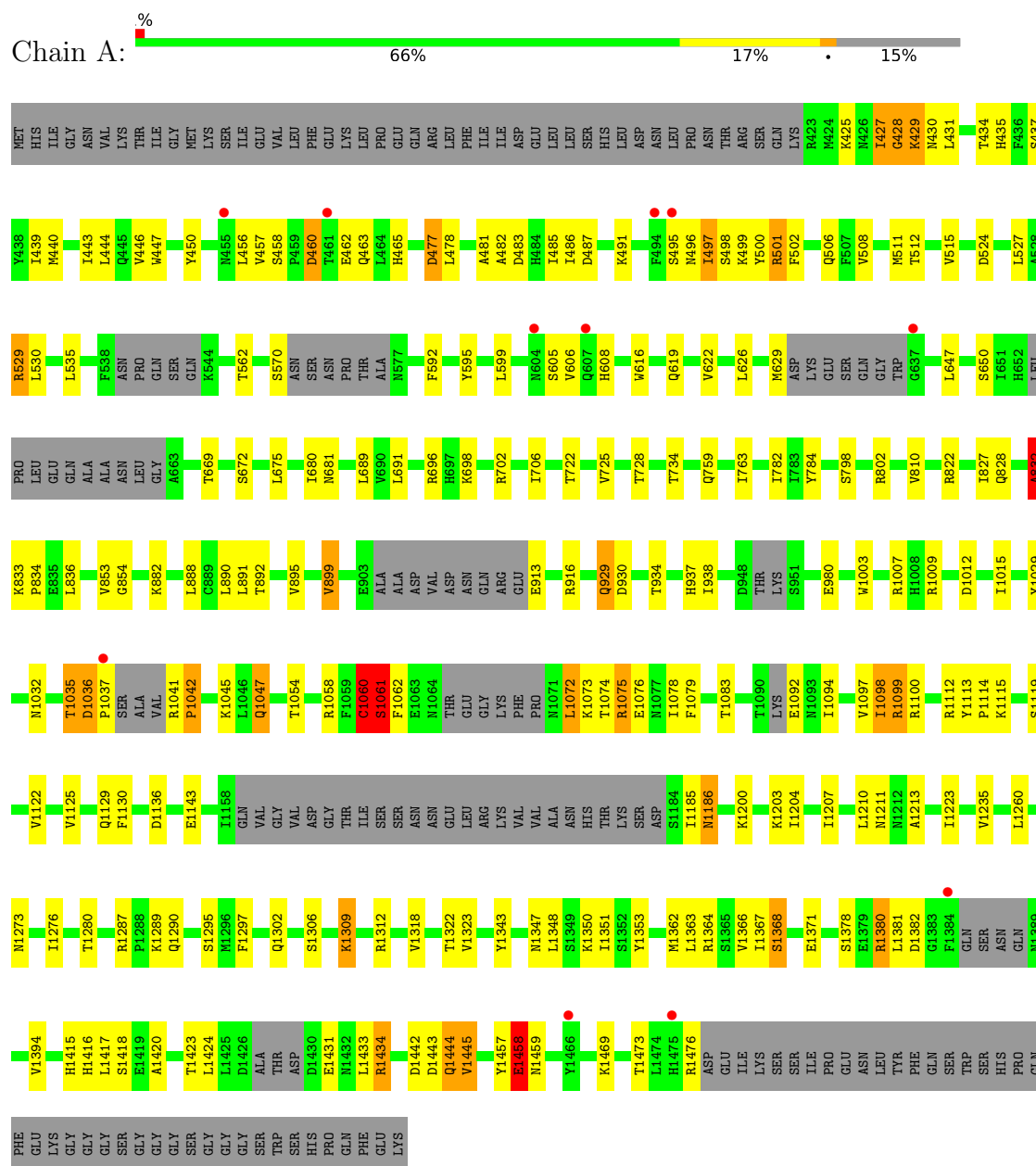
- Molecule 4 is a protein called Scc2 unassigned sequence.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	Z	11	Total	C	N	O	0	0	0
			55	33	11	11			
4	W	10	Total	C	N	O	0	0	0
			50	30	10	10			

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: Sister chromatid cohesion protein 2

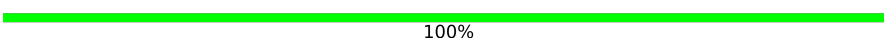


- Molecule 1: Sister chromatid cohesion protein 2





- Molecule 4: Scc2 unassigned sequence

Chain Z:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: Scc2 unassigned sequence

Chain W:  91% 9%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	98.05Å 106.44Å 143.18Å 90.00° 104.52° 90.00°	Depositor
Resolution (Å)	48.81 – 2.85 48.81 – 2.85	Depositor EDS
% Data completeness (in resolution range)	98.7 (48.81-2.85) 98.7 (48.81-2.85)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.21 (at 2.86Å)	Xtriage
Refinement program	PHENIX (1.11.1 _2575: ???)	Depositor
R, R_{free}	0.217 , 0.269 0.222 , 0.270	Depositor DCC
R_{free} test set	3386 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	90.5	Xtriage
Anisotropy	0.071	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 57.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	16017	wwPDB-VP
Average B, all atoms (Å ²)	93.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.28% 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	0.20	0/8071	0.52	9/10895 (0.1%)
1	B	0.18	0/7952	0.50	2/10741 (0.0%)
All	All	0.19	0/16023	0.51	11/21636 (0.1%)

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	A	0	1
1	B	0	2
All	All	0	3

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1458	GLU	CA-C-N	9.67	139.10	121.70
1	A	1458	GLU	C-N-CA	9.67	139.10	121.70
1	A	1444	GLN	CA-C-N	8.38	136.78	121.70
1	A	1444	GLN	C-N-CA	8.38	136.78	121.70
1	A	1060	CYS	CA-C-N	7.08	134.44	121.70
1	A	1060	CYS	C-N-CA	7.08	134.44	121.70
1	A	832	ALA	CA-C-N	5.36	131.34	121.70
1	A	832	ALA	C-N-CA	5.36	131.34	121.70
1	A	1036	ASP	N-CA-C	5.27	112.76	108.07
1	B	575	THR	CA-C-N	5.13	130.94	121.70
1	B	575	THR	C-N-CA	5.13	130.94	121.70

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1060	CYS	Peptide
1	B	458	SER	Peptide
1	B	460	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	7931	0	8056	139	0
1	B	7811	0	7928	157	0
2	X	85	0	19	0	0
3	Y	85	0	19	0	0
4	W	50	0	12	0	0
4	Z	55	0	13	0	0
All	All	16017	0	16047	293	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 9.

All (293) 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:1060:CYS:HA	1:A:1061:SER:HB2	1.39	1.01
1:B:1412:PHE:O	1:B:1416:HIS:HB2	1.70	0.91
1:B:1043:ASP:O	1:B:1045:LYS:N	2.07	0.86
1:A:1458:GLU:HB2	1:A:1459:ASN:HB2	1.61	0.83
1:B:501:ARG:NH1	1:B:505:ASP:OD2	2.13	0.80
1:B:981:THR:HG22	1:B:1014:ARG:HH22	1.47	0.80
1:A:832:ALA:HB1	1:A:833:LYS:HA	1.63	0.78
1:A:1416:HIS:HB3	1:A:1417:LEU:HA	1.66	0.77
1:A:1348:LEU:HD23	1:A:1362:MET:HE1	1.64	0.77
1:B:1299:ARG:NH2	1:B:1347:ASN:O	2.19	0.76
1:A:1287:ARG:HB3	1:A:1290:GLN:HG2	1.67	0.76
1:B:1387:ASN:O	1:B:1390:THR:OG1	2.06	0.72
1:A:929:GLN:CD	1:A:930:ASP:H	1.99	0.69
1:B:986:ARG:NH1	1:B:990:MET:SD	2.66	0.68
1:A:1458:GLU:HB2	1:A:1459:ASN:CB	2.22	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1075:ARG:NE	1:A:1075:ARG:O	2.27	0.68
1:A:1306:SER:HB2	1:A:1312:ARG:HG3	1.76	0.67
1:B:1421:LYS:H	1:B:1421:LYS:HD2	1.59	0.66
1:A:515:VAL:HG21	1:A:527:LEU:HD12	1.78	0.66
1:B:1377:ILE:HD11	1:B:1397:ILE:HG22	1.77	0.66
1:A:916:ARG:H	1:A:916:ARG:HD2	1.61	0.65
1:B:515:VAL:HG21	1:B:527:LEU:HD12	1.78	0.65
1:B:636:TRP:H	1:B:637:GLY:HA3	1.59	0.65
1:A:1060:CYS:CA	1:A:1061:SER:HB2	2.23	0.64
1:A:1420:ALA:O	1:A:1424:LEU:HD23	1.98	0.64
1:B:496:ASN:OD1	1:B:499:LYS:NZ	2.30	0.64
1:B:445:GLN:HE22	1:B:520:TRP:HA	1.63	0.63
1:B:483:ASP:OD2	1:B:529:ARG:NH2	2.32	0.62
1:A:1323:VAL:HG21	1:A:1348:LEU:HD21	1.81	0.62
1:B:1415:HIS:NE2	1:B:1442:ASP:OD2	2.20	0.62
1:B:1235:VAL:HA	1:B:1238:VAL:HG22	1.81	0.61
1:A:1037:PRO:HB3	1:A:1041:ARG:HG2	1.83	0.61
1:B:833:LYS:HB2	1:B:834:PRO:HD2	1.83	0.60
1:B:1282:TYR:CE1	1:B:1286:ILE:HD11	2.37	0.60
1:A:675:LEU:HA	1:A:680:ILE:HG12	1.83	0.60
1:A:1119:SER:HB3	1:A:1122:VAL:HG12	1.83	0.59
1:A:888:LEU:O	1:A:892:THR:HG23	2.03	0.59
1:A:1032:ASN:HA	1:A:1035:THR:HG23	1.86	0.58
1:B:1405:GLU:O	1:B:1408:LYS:HD3	2.02	0.58
1:B:1379:GLU:O	1:B:1381:LEU:N	2.34	0.58
1:A:1363:LEU:HA	1:A:1366:VAL:HG22	1.83	0.58
1:A:616:TRP:HA	1:A:619:GLN:NE2	2.19	0.58
1:A:1473:THR:HB	1:A:1476:ARG:HH21	1.68	0.58
1:B:636:TRP:N	1:B:637:GLY:HA3	2.18	0.58
1:B:788:GLU:OE1	1:B:788:GLU:N	2.36	0.57
1:A:1054:THR:O	1:A:1058:ARG:HG2	2.04	0.57
1:B:575:THR:OG1	1:B:577:ASN:N	2.37	0.57
1:A:427:ILE:HB	1:A:431:LEU:HG	1.84	0.57
1:B:1143:GLU:HG2	1:B:1215:VAL:HG11	1.86	0.56
1:B:511:MET:HE2	1:B:526:ILE:HB	1.86	0.56
1:A:511:MET:O	1:A:515:VAL:HG23	2.06	0.56
1:A:854:GLY:HA2	1:B:634:GLN:N	2.21	0.56
1:B:511:MET:O	1:B:515:VAL:HG23	2.06	0.56
1:B:1282:TYR:CZ	1:B:1286:ILE:HD11	2.41	0.56
1:A:980:GLU:OE1	1:A:1009:ARG:NH1	2.39	0.56
1:B:512:THR:HB	1:B:562:THR:HG21	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:508:VAL:HG22	1:B:530:LEU:HD21	1.88	0.55
1:A:535:LEU:HD23	1:A:689:LEU:HD22	1.88	0.55
1:B:935:LYS:NZ	1:B:969:SER:O	2.25	0.55
1:B:989:ARG:O	1:B:989:ARG:HG3	2.07	0.55
1:A:1353:TYR:HE2	1:A:1362:MET:HE2	1.72	0.55
1:B:1381:LEU:HA	1:B:1382:ASP:C	2.32	0.55
1:B:575:THR:HA	1:B:576:ALA:HB3	1.88	0.55
1:B:630:ASP:HB3	1:B:636:TRP:CD1	2.42	0.55
1:B:1139:LEU:HA	1:B:1142:LEU:HD23	1.87	0.54
1:B:1094:ILE:HD13	1:B:1098:ILE:HG22	1.87	0.54
1:B:736:SER:HB3	1:B:740:VAL:CG2	2.37	0.54
1:B:1235:VAL:HG22	1:B:1236:PRO:HD3	1.88	0.54
1:B:1308:ASN:OD1	1:B:1312:ARG:NH2	2.40	0.54
1:B:1416:HIS:NE2	1:B:1419:GLU:OE1	2.40	0.54
1:A:696:ARG:NH2	1:A:698:LYS:HD3	2.23	0.54
1:B:601:TYR:HA	1:B:604:ASN:HD21	1.72	0.54
1:A:457:VAL:HG23	1:A:458:SER:H	1.72	0.53
1:A:619:GLN:O	1:A:622:VAL:HG12	2.08	0.53
1:B:1343:TYR:O	1:B:1347:ASN:ND2	2.39	0.53
1:B:827:ILE:HD11	1:B:841:CYS:HB2	1.90	0.53
1:A:1003:TRP:CZ2	1:A:1061:SER:HB3	2.43	0.53
1:B:832:ALA:HB1	1:B:836:LEU:HD21	1.90	0.53
1:B:1095:HIS:CE1	1:B:1097:VAL:HB	2.44	0.53
1:A:462:GLU:HA	1:A:465:HIS:NE2	2.23	0.53
1:A:1302:GLN:O	1:A:1306:SER:OG	2.23	0.53
1:B:532:LYS:HB2	1:B:682:MET:HE1	1.90	0.53
1:A:1035:THR:OG1	1:A:1036:ASP:N	2.40	0.53
1:A:1047:GLN:HG3	1:A:1098:ILE:HD11	1.91	0.53
1:A:427:ILE:HG22	1:A:428:GLY:H	1.74	0.52
1:A:827:ILE:HD11	1:A:891:LEU:HD12	1.91	0.52
1:B:736:SER:HB3	1:B:740:VAL:HG23	1.90	0.52
1:A:497:ILE:HD12	1:A:501:ARG:HH12	1.74	0.52
1:B:602:CYS:O	1:B:606:VAL:HG22	2.09	0.52
1:B:1351:ILE:HD11	1:B:1353:TYR:CD2	2.45	0.52
1:B:1360:TYR:HA	1:B:1363:LEU:HD12	1.92	0.52
1:A:512:THR:HB	1:A:562:THR:HG21	1.92	0.52
1:A:913:GLU:HA	1:A:916:ARG:HD3	1.91	0.52
1:B:899:VAL:HG21	1:B:919:MET:HE2	1.92	0.52
1:B:753:SER:OG	1:B:754:TYR:N	2.43	0.51
1:B:1099:ARG:O	1:B:1103:THR:HG23	2.10	0.51
1:A:1276:ILE:O	1:A:1280:THR:HG23	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:977:TYR:O	1:B:981:THR:HG23	2.11	0.51
1:A:487:ASP:O	1:A:491:LYS:HG2	2.11	0.51
1:A:450:TYR:HD2	1:A:616:TRP:CD2	2.29	0.51
1:B:626:LEU:HA	1:B:629:MET:HE3	1.94	0.50
1:A:1072:LEU:O	1:A:1073:LYS:NZ	2.24	0.50
1:B:833:LYS:HG3	1:B:836:LEU:HD22	1.94	0.50
1:A:1378:SER:O	1:A:1382:ASP:HB2	2.12	0.50
1:A:1094:ILE:HB	1:A:1099:ARG:HH12	1.77	0.50
1:B:834:PRO:O	1:B:837:GLN:HB3	2.12	0.50
1:B:990:MET:HE2	1:B:995:LEU:HD23	1.93	0.50
1:B:1276:ILE:O	1:B:1280:THR:HG23	2.11	0.50
1:B:1351:ILE:HD11	1:B:1353:TYR:CE2	2.47	0.50
1:A:669:THR:O	1:A:672:SER:OG	2.26	0.50
1:B:439:ILE:HG13	1:B:440:MET:N	2.27	0.50
1:A:606:VAL:O	1:A:608:HIS:ND1	2.44	0.50
1:B:619:GLN:HB3	1:B:647:LEU:HD11	1.93	0.50
1:A:460:ASP:HB2	1:A:463:GLN:HB2	1.94	0.49
1:B:1214:MET:HG3	1:B:1248:TYR:OH	2.12	0.49
1:A:1204:ILE:O	1:A:1207:ILE:HG12	2.12	0.49
1:A:1125:VAL:O	1:A:1129:GLN:HG2	2.13	0.49
1:A:1186:ASN:N	1:A:1186:ASN:OD1	2.44	0.49
1:A:1235:VAL:HG22	1:A:1260:LEU:HD13	1.95	0.49
1:B:1380:ARG:HG2	1:B:1381:LEU:HG	1.93	0.49
1:A:483:ASP:OD1	1:A:529:ARG:HG2	2.12	0.49
1:A:1416:HIS:CB	1:A:1417:LEU:HA	2.40	0.49
1:A:1434:ARG:HA	1:A:1434:ARG:NE	2.27	0.49
1:B:1409:ARG:HG3	1:B:1410:PHE:N	2.26	0.49
1:B:1348:LEU:HA	1:B:1351:ILE:HG23	1.94	0.49
1:A:497:ILE:CD1	1:A:501:ARG:HH12	2.24	0.48
1:B:1357:LEU:O	1:B:1361:GLU:HB3	2.13	0.48
1:A:434:THR:HG23	1:A:437:SER:H	1.78	0.48
1:B:1125:VAL:O	1:B:1129:GLN:HG2	2.12	0.48
1:A:1442:ASP:OD1	1:A:1443:ASP:N	2.35	0.48
1:A:1457:TYR:HE1	1:A:1469:LYS:HE2	1.79	0.48
1:B:734:THR:HG22	1:B:763:ILE:HD13	1.95	0.48
1:A:1343:TYR:O	1:A:1347:ASN:ND2	2.45	0.48
1:A:691:LEU:HD11	1:A:725:VAL:HG12	1.95	0.48
1:A:854:GLY:HA2	1:B:634:GLN:H	1.77	0.48
1:B:1324:PHE:HE2	1:B:1362:MET:HE1	1.79	0.48
1:A:1416:HIS:HB3	1:A:1417:LEU:HD12	1.95	0.48
1:B:1204:ILE:O	1:B:1207:ILE:HG12	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1299:ARG:CZ	1:B:1351:ILE:HG22	2.44	0.48
1:B:752:SER:O	1:B:754:TYR:N	2.46	0.47
1:B:696:ARG:HH22	1:B:698:LYS:HD2	1.79	0.47
1:B:921:PHE:O	1:B:924:VAL:HG22	2.14	0.47
1:B:610:THR:HA	1:B:613:LYS:HB2	1.96	0.47
1:A:1273:ASN:OD1	1:A:1322:THR:HG22	2.14	0.47
1:A:1473:THR:O	1:A:1476:ARG:NE	2.48	0.47
1:A:435:HIS:O	1:A:439:ILE:HG22	2.14	0.47
1:A:500:TYR:N	1:A:501:ARG:HH21	2.13	0.47
1:B:1318:VAL:O	1:B:1322:THR:HG23	2.14	0.47
1:A:895:VAL:O	1:A:899:VAL:HG13	2.14	0.47
1:A:1029:TYR:OH	1:A:1045:LYS:HE2	2.15	0.47
1:B:900:ILE:HG22	1:B:944:TYR:HE2	1.79	0.47
1:A:499:LYS:N	1:A:501:ARG:HH21	2.12	0.47
1:A:672:SER:HA	1:A:675:LEU:HD12	1.97	0.47
1:B:1353:TYR:CD1	1:B:1359:LEU:HD12	2.51	0.46
1:A:1353:TYR:CE2	1:A:1362:MET:HE2	2.50	0.46
1:B:691:LEU:HD22	1:B:728:THR:HG21	1.97	0.46
1:A:1444:GLN:HA	1:A:1445:VAL:HB	1.97	0.46
1:B:608:HIS:CG	1:B:608:HIS:O	2.67	0.46
1:B:683:TYR:OH	1:B:719:MET:HE1	2.16	0.46
1:A:1297:PHE:HB3	1:A:1347:ASN:OD1	2.15	0.46
1:B:535:LEU:HD23	1:B:689:LEU:HD22	1.98	0.46
1:B:1302:GLN:HB2	1:B:1315:PHE:CE1	2.51	0.46
1:B:1210:LEU:HA	1:B:1213:ALA:HB3	1.98	0.46
1:B:1299:ARG:NE	1:B:1351:ILE:HA	2.31	0.46
1:A:929:GLN:NE2	1:A:930:ASP:H	2.14	0.46
1:A:1042:PRO:HB3	1:A:1098:ILE:HG12	1.98	0.46
1:B:1047:GLN:HG2	1:B:1101:ILE:HD12	1.97	0.45
1:B:618:LYS:O	1:B:622:VAL:HG13	2.17	0.45
1:B:990:MET:HE1	1:B:998:ALA:HB3	1.98	0.45
1:B:648:ILE:O	1:B:651:ILE:HD12	2.15	0.45
1:B:977:TYR:N	1:B:1009:ARG:HH12	2.14	0.45
1:B:990:MET:HE1	1:B:998:ALA:CB	2.46	0.45
1:A:1347:ASN:O	1:A:1351:ILE:HG23	2.17	0.45
1:B:702:ARG:O	1:B:706:ILE:HG12	2.17	0.45
1:B:1230:ASN:HD21	1:B:1232:SER:HB2	1.82	0.45
1:A:592:PHE:CE2	1:A:647:LEU:HD11	2.52	0.45
1:A:1350:LYS:HE2	1:A:1444:GLN:HG2	1.97	0.45
1:A:499:LYS:HE2	1:A:500:TYR:CZ	2.52	0.45
1:B:619:GLN:O	1:B:622:VAL:HG22	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:734:THR:HG22	1:A:763:ILE:HD13	1.98	0.45
1:B:447:TRP:CZ3	1:B:477:ASP:HB3	2.52	0.45
1:B:1042:PRO:HG3	1:B:1098:ILE:HD13	1.99	0.45
1:A:916:ARG:H	1:A:916:ARG:CD	2.30	0.44
1:A:1094:ILE:HB	1:A:1099:ARG:NH1	2.32	0.44
1:A:1290:GLN:OE1	1:A:1290:GLN:N	2.50	0.44
1:A:1469:LYS:O	1:A:1473:THR:HG23	2.17	0.44
1:A:784:TYR:CD1	1:A:822:ARG:HD3	2.51	0.44
1:B:481:ALA:O	1:B:485:ILE:HG22	2.17	0.44
1:B:943:PRO:HB2	1:B:944:TYR:CE1	2.52	0.44
1:B:957:ILE:O	1:B:960:VAL:HG22	2.17	0.44
1:A:443:ILE:O	1:A:446:VAL:HG22	2.18	0.44
1:B:440:MET:O	1:B:444:LEU:HD12	2.17	0.44
1:B:445:GLN:NE2	1:B:520:TRP:HA	2.31	0.44
1:A:1079:PHE:O	1:A:1083:THR:HG23	2.18	0.44
1:B:1297:PHE:HB3	1:B:1347:ASN:OD1	2.18	0.44
1:B:1299:ARG:CZ	1:B:1351:ILE:HA	2.47	0.44
1:B:1442:ASP:OD1	1:B:1443:ASP:N	2.34	0.44
1:A:482:ALA:O	1:A:486:ILE:HG12	2.18	0.44
1:B:986:ARG:CZ	1:B:990:MET:SD	3.06	0.44
1:B:1298:LEU:HB2	1:B:1299:ARG:HH22	1.82	0.44
1:A:502:PHE:O	1:A:506:GLN:HB2	2.18	0.44
1:B:1079:PHE:O	1:B:1083:THR:HG23	2.18	0.44
1:A:626:LEU:HA	1:A:629:MET:HE3	2.00	0.43
1:A:1348:LEU:CD2	1:A:1362:MET:HE1	2.42	0.43
1:B:773:ARG:NH1	1:B:806:ASP:OD2	2.51	0.43
1:B:1214:MET:HG3	1:B:1248:TYR:CE2	2.53	0.43
1:B:443:ILE:O	1:B:446:VAL:HG22	2.18	0.43
1:B:487:ASP:CG	1:B:533:LYS:HZ3	2.25	0.43
1:B:833:LYS:HB2	1:B:834:PRO:CD	2.46	0.43
1:B:934:THR:HG22	1:B:937:HIS:ND1	2.33	0.43
1:A:798:SER:O	1:A:802:ARG:HG3	2.18	0.43
1:A:1114:PRO:HG2	1:A:1186:ASN:ND2	2.33	0.43
1:B:552:ALA:O	1:B:556:ILE:HG23	2.18	0.43
1:B:609:HIS:HB3	1:B:611:PRO:HD2	1.99	0.43
1:B:1232:SER:OG	1:B:1267:MET:HE3	2.19	0.43
1:A:833:LYS:HB3	1:A:834:PRO:HD2	1.99	0.43
1:A:1041:ARG:HA	1:A:1042:PRO:HD3	1.71	0.43
1:B:896:ILE:O	1:B:899:VAL:HG12	2.19	0.43
1:B:708:CYS:O	1:B:712:LEU:HD13	2.18	0.43
1:B:1112:ARG:HD3	1:B:1112:ARG:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:616:TRP:HA	1:A:619:GLN:HE21	1.84	0.43
1:A:1210:LEU:HA	1:A:1213:ALA:HB3	2.00	0.43
1:B:1214:MET:HG3	1:B:1248:TYR:CZ	2.53	0.43
1:B:1299:ARG:NH1	1:B:1351:ILE:HG22	2.32	0.43
1:A:501:ARG:HG3	1:A:501:ARG:HH11	1.84	0.43
1:A:916:ARG:HD2	1:A:916:ARG:N	2.32	0.43
1:A:934:THR:HG22	1:A:937:HIS:ND1	2.34	0.43
1:A:1364:ARG:O	1:A:1368:SER:OG	2.35	0.43
1:A:1380:ARG:HG2	1:A:1394:VAL:CG1	2.49	0.43
1:B:1381:LEU:HA	1:B:1383:GLY:N	2.33	0.43
1:A:1367:ILE:HG13	1:A:1368:SER:N	2.32	0.43
1:B:633:SER:HB3	1:B:636:TRP:HB3	2.01	0.43
1:B:984:LEU:HA	1:B:987:LEU:HD13	2.00	0.43
1:A:696:ARG:HH22	1:A:698:LYS:HD3	1.84	0.43
1:A:1211:ASN:ND2	1:B:466:ASP:OD2	2.52	0.43
1:B:574:PRO:HA	1:B:576:ALA:HB3	2.01	0.43
1:B:1469:LYS:HE2	1:B:1469:LYS:HB2	1.80	0.43
1:B:609:HIS:ND1	1:B:610:THR:HG23	2.34	0.42
1:A:481:ALA:O	1:A:485:ILE:HG22	2.18	0.42
1:A:1078:ILE:H	1:A:1078:ILE:HD12	1.84	0.42
1:B:1450:MET:HB2	1:B:1450:MET:HE3	1.69	0.42
1:B:987:LEU:HD23	1:B:1052:LEU:HD11	2.01	0.42
1:B:1041:ARG:HG3	1:B:1042:PRO:N	2.34	0.42
1:A:702:ARG:O	1:A:706:ILE:HG12	2.19	0.42
1:B:439:ILE:O	1:B:443:ILE:HG12	2.18	0.42
1:B:598:CYS:HA	1:B:666:ILE:HD11	2.01	0.42
1:A:832:ALA:CB	1:A:833:LYS:HA	2.42	0.42
1:A:1318:VAL:O	1:A:1322:THR:HG23	2.20	0.42
1:B:634:GLN:O	1:B:638:SER:N	2.52	0.42
1:A:1098:ILE:HD12	1:A:1098:ILE:HA	1.73	0.42
1:A:1112:ARG:HD2	1:A:1113:TYR:CZ	2.54	0.42
1:A:440:MET:HG3	1:A:485:ILE:CD1	2.50	0.42
1:A:1114:PRO:HG2	1:A:1186:ASN:HD21	1.84	0.42
1:A:496:ASN:C	1:A:498:SER:H	2.28	0.42
1:B:980:GLU:HG3	1:B:984:LEU:CD1	2.50	0.42
1:A:447:TRP:CZ3	1:A:477:ASP:HB3	2.55	0.42
1:A:457:VAL:HG23	1:A:458:SER:N	2.34	0.42
1:B:986:ARG:HH22	1:B:998:ALA:CB	2.33	0.42
1:A:501:ARG:N	1:A:501:ARG:CZ	2.83	0.41
1:B:1363:LEU:HA	1:B:1366:VAL:HG22	2.02	0.41
1:A:497:ILE:C	1:A:501:ARG:NH2	2.78	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:604:ASN:OD1	1:B:605:SER:N	2.53	0.41
1:A:429:LYS:O	1:A:430:ASN:C	2.63	0.41
1:A:440:MET:O	1:A:444:LEU:HD12	2.20	0.41
1:B:1154:ARG:O	1:B:1155:ARG:HB2	2.20	0.41
1:A:722:THR:HG22	1:A:725:VAL:HG22	2.02	0.41
1:A:508:VAL:HG22	1:A:530:LEU:HD21	2.03	0.41
1:B:959:LYS:HB3	1:B:959:LYS:HE3	1.88	0.41
1:A:1130:PHE:HB3	1:A:1200:LYS:HD3	2.03	0.41
1:A:497:ILE:C	1:A:501:ARG:CZ	2.94	0.41
1:B:944:TYR:N	1:B:944:TYR:CD1	2.86	0.41
1:A:1363:LEU:O	1:A:1367:ILE:HG23	2.21	0.41
1:B:1360:TYR:CZ	1:B:1422:LEU:HD12	2.56	0.41
1:A:444:LEU:HA	1:A:447:TRP:CD1	2.56	0.41
1:A:1003:TRP:O	1:A:1007:ARG:HG2	2.20	0.41
1:B:956:HIS:O	1:B:959:LYS:HB2	2.20	0.41
1:B:1235:VAL:HG12	1:B:1260:LEU:HD13	2.03	0.41
1:A:511:MET:HB3	1:A:527:LEU:HG	2.03	0.40
1:A:595:TYR:O	1:A:599:LEU:HD12	2.21	0.40
1:A:1094:ILE:N	1:A:1099:ARG:HH12	2.19	0.40
1:A:1100:ARG:NH1	1:A:1136:ASP:OD1	2.54	0.40
1:A:1309:LYS:H	1:A:1309:LYS:HG2	1.38	0.40
1:B:1364:ARG:O	1:B:1367:ILE:HG13	2.20	0.40
1:B:450:TYR:HD2	1:B:616:TRP:CD2	2.39	0.40
1:B:1236:PRO:HG3	1:B:1271:CYS:HB3	2.02	0.40
1:B:1243:ALA:HB2	1:B:1297:PHE:CD1	2.56	0.40
1:B:1319:VAL:HG13	1:B:1320:LYS:HD3	2.03	0.40
1:B:1379:GLU:HG2	1:B:1380:ARG:H	1.85	0.40
1:B:1421:LYS:HD2	1:B:1421:LYS:N	2.32	0.40
1:B:497:ILE:HG21	1:B:547:ASN:HB3	2.03	0.40
1:B:527:LEU:HD23	1:B:527:LEU:HA	1.89	0.40
1:A:447:TRP:HZ3	1:A:477:ASP:HB3	1.87	0.40
1:B:1320:LYS:HD3	1:B:1320:LYS:N	2.35	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	947/1143 (83%)	901 (95%)	39 (4%)	7 (1%)	18	35
1	B	938/1143 (82%)	899 (96%)	33 (4%)	6 (1%)	21	38
All	All	1885/2286 (82%)	1800 (96%)	72 (4%)	13 (1%)	18	35

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1042	PRO
1	A	1061	SER
1	A	1445	VAL
1	B	1044	GLY
1	B	1385	GLN
1	A	428	GLY
1	A	832	ALA
1	A	1415	HIS
1	A	497	ILE
1	B	753	SER
1	B	1308	ASN
1	B	1380	ARG
1	B	459	PRO

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	906/1052 (86%)	845 (93%)	61 (7%)	15	31
1	B	891/1052 (85%)	833 (94%)	58 (6%)	15	32
All	All	1797/2104 (85%)	1678 (93%)	119 (7%)	15	32

All (119) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	425	LYS
1	A	427	ILE
1	A	429	LYS
1	A	456	LEU
1	A	460	ASP
1	A	477	ASP
1	A	478	LEU
1	A	495	SER
1	A	501	ARG
1	A	524	ASP
1	A	529	ARG
1	A	570	SER
1	A	605	SER
1	A	650	SER
1	A	681	ASN
1	A	728	THR
1	A	759	GLN
1	A	782	ILE
1	A	810	VAL
1	A	828	GLN
1	A	836	LEU
1	A	853	VAL
1	A	882	LYS
1	A	890	LEU
1	A	899	VAL
1	A	929	GLN
1	A	938	ILE
1	A	1012	ASP
1	A	1015	ILE
1	A	1035	THR
1	A	1047	GLN
1	A	1060	CYS
1	A	1061	SER
1	A	1062	PHE
1	A	1072	LEU
1	A	1074	THR
1	A	1075	ARG
1	A	1076	GLU
1	A	1092	GLU
1	A	1097	VAL
1	A	1098	ILE
1	A	1099	ARG
1	A	1115	LYS

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Mol	Chain	Res	Type
1	A	1143	GLU
1	A	1185	ILE
1	A	1186	ASN
1	A	1203	LYS
1	A	1223	ILE
1	A	1289	LYS
1	A	1295	SER
1	A	1309	LYS
1	A	1368	SER
1	A	1371	GLU
1	A	1380	ARG
1	A	1381	LEU
1	A	1418	SER
1	A	1423	THR
1	A	1431	GLU
1	A	1433	LEU
1	A	1434	ARG
1	A	1458	GLU
1	B	431	LEU
1	B	440	MET
1	B	456	LEU
1	B	458	SER
1	B	468	ILE
1	B	477	ASP
1	B	478	LEU
1	B	491	LYS
1	B	496	ASN
1	B	499	LYS
1	B	524	ASP
1	B	554	GLN
1	B	575	THR
1	B	578	LEU
1	B	606	VAL
1	B	609	HIS
1	B	650	SER
1	B	664	VAL
1	B	699	VAL
1	B	727	GLU
1	B	755	ILE
1	B	759	GLN
1	B	775	HIS
1	B	782	ILE

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Mol	Chain	Res	Type
1	B	827	ILE
1	B	853	VAL
1	B	857	LYS
1	B	885	SER
1	B	916	ARG
1	B	924	VAL
1	B	950	LYS
1	B	968	LEU
1	B	974	LYS
1	B	1007	ARG
1	B	1035	THR
1	B	1041	ARG
1	B	1045	LYS
1	B	1049	LEU
1	B	1097	VAL
1	B	1098	ILE
1	B	1132	LYS
1	B	1136	ASP
1	B	1142	LEU
1	B	1200	LYS
1	B	1203	LYS
1	B	1235	VAL
1	B	1246	ASN
1	B	1295	SER
1	B	1299	ARG
1	B	1310	ARG
1	B	1320	LYS
1	B	1362	MET
1	B	1381	LEU
1	B	1389	ASN
1	B	1408	LYS
1	B	1409	ARG
1	B	1416	HIS
1	B	1421	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	506	GLN
1	A	619	GLN
1	A	837	GLN
1	A	874	ASN

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Mol	Chain	Res	Type
1	A	963	ASN
1	A	1064	ASN
1	A	1246	ASN
1	A	1340	HIS
1	A	1459	ASN
1	B	445	GLN
1	B	506	GLN
1	B	874	ASN
1	B	954	GLN
1	B	1186	ASN
1	B	1230	ASN
1	B	1246	ASN
1	B	1444	GLN
1	B	1459	ASN

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	973/1143 (85%)	-0.16	11 (1%) 78 73	49, 80, 142, 192	0
1	B	960/1143 (83%)	-0.03	14 (1%) 72 65	57, 93, 142, 223	0
2	X	0/17	-	-	-	-
3	Y	0/27	-	-	-	-
4	W	0/11	-	-	-	-
4	Z	0/11	-	-	-	-
All	All	1933/2352 (82%)	-0.09	25 (1%) 75 68	49, 87, 142, 223	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	505	ASP	3.9
1	A	604	ASN	3.7
1	B	986	ARG	3.7
1	A	1384	PHE	3.4
1	A	495	SER	3.3
1	B	1037	PRO	3.2
1	A	1475	HIS	3.1
1	A	494	PHE	2.9
1	A	637	GLY	2.8
1	B	461	THR	2.8
1	A	607	GLN	2.7
1	B	708	CYS	2.5
1	B	1248	TYR	2.5
1	A	1037	PRO	2.5
1	B	1096	HIS	2.4
1	B	644	PHE	2.2
1	B	494	PHE	2.2
1	A	455	ASN	2.2
1	B	904	ALA	2.2
1	A	461	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	1441	LEU	2.0
1	B	716	ASP	2.0
1	B	1033	ALA	2.0
1	A	1466	TYR	2.0
1	B	1132	LYS	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.