



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 01:51 PM UTC

PDB ID : 4G03 / pdb_00004g03
Title : High-resolution Crystal Structural Variance Analysis between Recombinant and Wild-type Human Serum Albumin
Authors : Cao, H.L.; Yin, D.C.
Deposited on : 2012-07-09
Resolution : 2.22 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

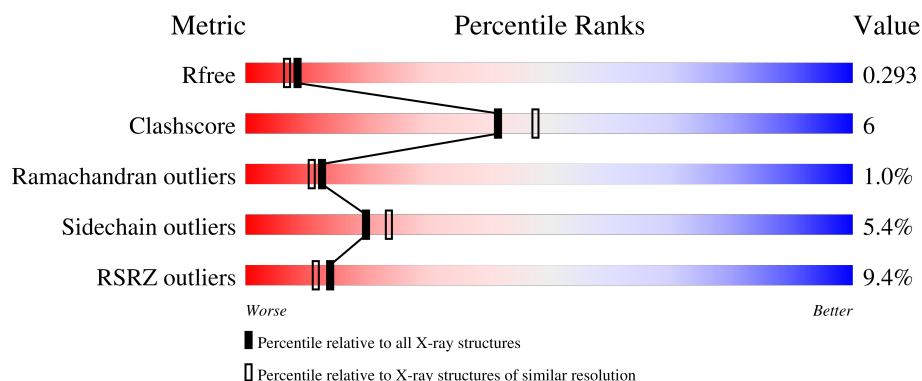
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.22 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	7682 (2.24-2.20)
Clashscore	190562	8402 (2.24-2.20)
Ramachandran outliers	187476	8303 (2.24-2.20)
Sidechain outliers	187428	8304 (2.24-2.20)
RSRZ outliers	180081	7683 (2.24-2.20)

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	585	8% 78% 20% ..
1	B	585	10% 79% 17% ..

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9279 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 Serum albumin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	578	Total	C	N	O	S	0	0	0
			4599	2903	776	879	41			
1	B	578	Total	C	N	O	S	0	0	0
			4599	2903	776	879	41			

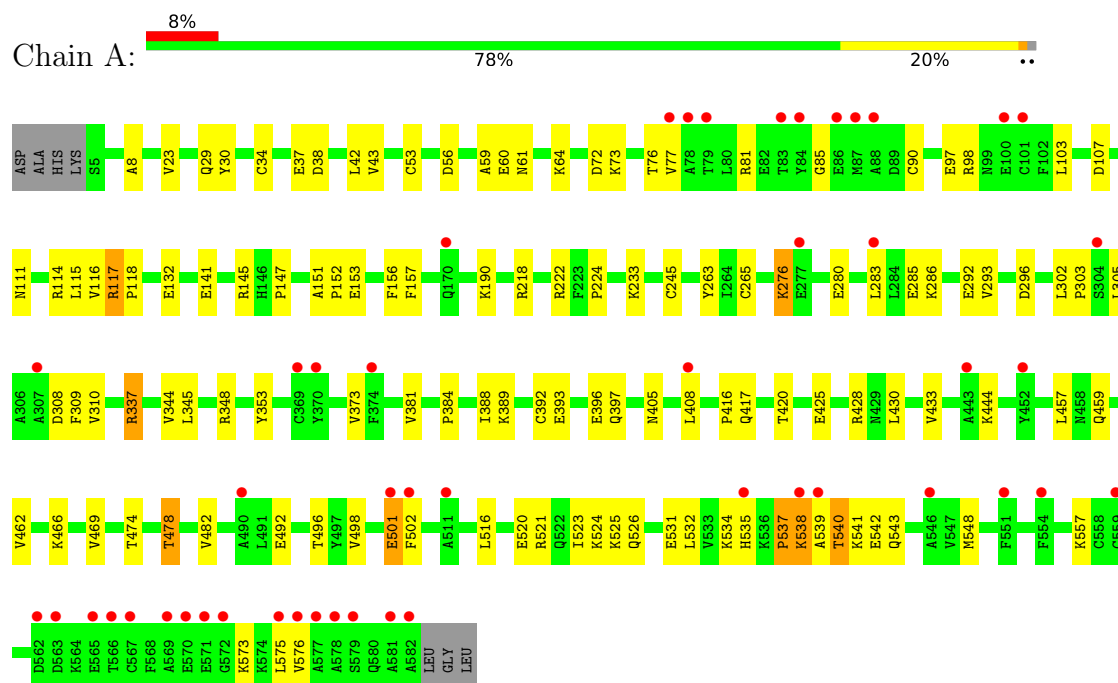
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	32	Total	O	0	0
			32	32		
2	B	49	Total	O	0	0
			49	49		

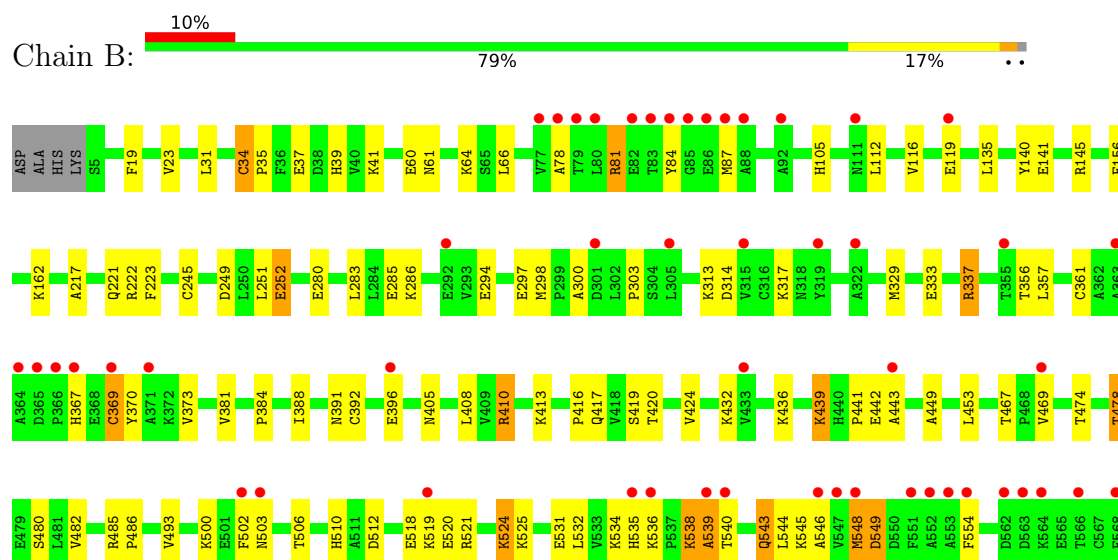
3 Residue-property plots

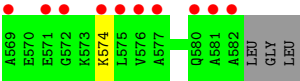
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Serum albumin



• Molecule 1: Serum albumin





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	58.57Å 58.67Å 95.67Å 75.71° 88.07° 73.63°	Depositor
Resolution (Å)	47.22 – 2.22 47.22 – 2.22	Depositor EDS
% Data completeness (in resolution range)	96.5 (47.22-2.22) 90.2 (47.22-2.22)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.54 (at 2.22Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.236 , 0.301 0.230 , 0.293	Depositor DCC
R_{free} test set	1999 reflections (3.52%)	wwPDB-VP
Wilson B-factor (Å ²)	38.5	Xtriage
Anisotropy	0.039	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 26.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9279	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.30% 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 [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	0.51	0/4688	0.87	3/6324 (0.0%)
1	B	0.54	0/4688	0.87	5/6324 (0.1%)
All	All	0.53	0/9376	0.87	8/12648 (0.1%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	444	LYS	N-CA-C	-5.12	107.71	114.31
1	B	300	ALA	N-CA-C	5.12	116.94	111.36
1	A	34	CYS	CA-C-N	5.11	125.04	119.78
1	A	34	CYS	C-N-CA	5.11	125.04	119.78
1	B	34	CYS	CA-C-N	5.05	124.81	119.76
1	B	34	CYS	C-N-CA	5.05	124.81	119.76
1	B	112	LEU	CA-C-N	5.01	126.11	119.84
1	B	112	LEU	C-N-CA	5.01	126.11	119.84

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	4599	0	4518	58	0
1	B	4599	0	4518	58	0
2	A	32	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	49	0	0	0	0
All	All	9279	0	9036	116	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 6.

All (116) 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:B:303:PRO:O	1:B:337:ARG:NH1	2.09	0.86
1:A:303:PRO:O	1:A:337:ARG:NH1	2.13	0.80
1:A:502:PHE:HZ	1:A:576:VAL:HB	1.54	0.73
1:A:525:LYS:HB3	1:A:548:MET:HE1	1.71	0.72
1:A:516:LEU:O	1:A:521:ARG:NH2	2.23	0.70
1:A:405:ASN:HA	1:A:408:LEU:HD12	1.75	0.68
1:B:156:PHE:HE1	1:B:285:GLU:HG3	1.58	0.67
1:A:417:GLN:HB3	1:A:469:VAL:HG12	1.78	0.64
1:B:135:LEU:HD21	1:B:162:LYS:HB2	1.80	0.64
1:B:356:THR:HG21	1:B:373:VAL:HG22	1.82	0.61
1:B:156:PHE:CE1	1:B:285:GLU:HG3	2.36	0.60
1:B:525:LYS:HB3	1:B:548:MET:HE1	1.83	0.60
1:B:531:GLU:O	1:B:535:HIS:ND1	2.35	0.59
1:A:224:PRO:HD2	1:A:296:ASP:HB3	1.85	0.59
1:A:353:TYR:HD1	1:A:373:VAL:HG11	1.68	0.58
1:B:384:PRO:O	1:B:388:ILE:HG12	2.04	0.58
1:B:416:PRO:O	1:B:534:LYS:HE2	2.04	0.58
1:B:313:LYS:HA	1:B:367:HIS:CE1	2.39	0.57
1:B:518:GLU:OE1	1:B:521:ARG:NH1	2.37	0.56
1:A:384:PRO:O	1:A:388:ILE:HG12	2.06	0.56
1:B:540:THR:HB	1:B:544:LEU:HG	1.86	0.56
1:A:392:CYS:O	1:A:396:GLU:HG2	2.05	0.56
1:A:474:THR:O	1:A:478:THR:OG1	2.20	0.56
1:B:392:CYS:O	1:B:396:GLU:HG2	2.05	0.56
1:A:531:GLU:O	1:A:535:HIS:ND1	2.39	0.55
1:B:417:GLN:HB3	1:B:469:VAL:HG12	1.89	0.55
1:B:405:ASN:HA	1:B:408:LEU:HD12	1.88	0.55
1:A:29:GLN:HG2	1:A:147:PRO:HA	1.88	0.54
1:B:369:CYS:SG	1:B:370:TYR:N	2.81	0.54
1:A:276:LYS:O	1:A:280:GLU:HG2	2.08	0.54
1:B:249:ASP:HB3	1:B:252:GLU:CG	2.38	0.53
1:A:540:THR:HA	1:A:543:GLN:HE21	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:ASP:HB3	1:A:59:ALA:HB2	1.92	0.52
1:B:536:LYS:O	1:B:540:THR:HG21	2.09	0.52
1:B:314:ASP:HB3	1:B:317:LYS:HB3	1.92	0.52
1:A:156:PHE:HE1	1:A:285:GLU:HG3	1.75	0.51
1:B:520:GLU:O	1:B:524:LYS:HG2	2.10	0.51
1:A:308:ASP:HB2	1:A:309:PHE:CD2	2.46	0.51
1:B:249:ASP:HB3	1:B:252:GLU:HG2	1.94	0.50
1:A:107:ASP:OD1	1:A:466:LYS:NZ	2.40	0.50
1:B:546:ALA:HA	1:B:549:ASP:HB2	1.93	0.50
1:B:391:ASN:OD1	1:B:410:ARG:NH2	2.43	0.50
1:A:81:ARG:HA	1:A:85:GLY:H	1.77	0.49
1:A:156:PHE:CE1	1:A:285:GLU:HG3	2.47	0.49
1:A:428:ARG:NE	1:A:526:GLN:OE1	2.45	0.49
1:A:348:ARG:HG3	1:A:482:VAL:CG1	2.42	0.49
1:B:441:PRO:O	1:B:443:ALA:N	2.42	0.49
1:A:233:LYS:HE3	1:A:263:TYR:CZ	2.48	0.49
1:A:23:VAL:HG12	1:A:43:VAL:HG22	1.95	0.48
1:B:502:PHE:HA	1:B:535:HIS:HD2	1.78	0.48
1:B:510:HIS:HB3	1:B:512:ASP:OD1	2.13	0.48
1:A:222:ARG:HD3	1:A:293:VAL:HG12	1.96	0.48
1:B:474:THR:O	1:B:478:THR:HB	2.13	0.48
1:A:302:LEU:HB3	1:A:337:ARG:NH1	2.29	0.48
1:A:153:GLU:O	1:A:157:PHE:HD1	1.96	0.48
1:B:538:LYS:O	1:B:540:THR:N	2.46	0.48
1:B:441:PRO:C	1:B:443:ALA:H	2.21	0.47
1:A:541:LYS:C	1:A:543:GLN:H	2.22	0.47
1:B:298:MET:HE3	1:B:298:MET:HB2	1.83	0.47
1:B:329:MET:O	1:B:333:GLU:HG2	2.15	0.47
1:A:42:LEU:HD22	1:A:73:LYS:HG3	1.97	0.47
1:A:353:TYR:CD1	1:A:373:VAL:HG11	2.48	0.47
1:B:544:LEU:C	1:B:546:ALA:H	2.23	0.47
1:A:265:CYS:SG	1:A:286:LYS:HD2	2.54	0.46
1:A:420:THR:OG1	1:A:531:GLU:OE2	2.23	0.46
1:B:313:LYS:HG3	1:B:367:HIS:HE1	1.81	0.46
1:B:432:LYS:O	1:B:436:LYS:HG3	2.16	0.46
1:A:61:ASN:HB3	1:A:64:LYS:HE2	1.97	0.45
1:B:34:CYS:HA	1:B:35:PRO:HD3	1.82	0.45
1:B:370:TYR:O	1:B:373:VAL:HG23	2.16	0.45
1:A:114:ARG:NH2	1:A:520:GLU:OE2	2.48	0.45
1:B:87:MET:HE1	1:B:105:HIS:HB3	1.98	0.45
1:B:217:ALA:O	1:B:221:GLN:HG3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:457:LEU:HD23	1:A:457:LEU:HA	1.80	0.45
1:A:141:GLU:OE1	1:A:145:ARG:NH1	2.36	0.45
1:A:537:PRO:HB2	1:A:538:LYS:H	1.66	0.45
1:A:30:TYR:HE1	1:A:103:LEU:HD23	1.82	0.44
1:A:416:PRO:O	1:A:534:LYS:HE2	2.16	0.44
1:A:90:CYS:O	1:A:98:ARG:HG3	2.17	0.44
1:A:537:PRO:O	1:A:539:ALA:N	2.50	0.44
1:B:19:PHE:O	1:B:23:VAL:HG23	2.18	0.44
1:B:81:ARG:HH11	1:B:81:ARG:HB2	1.83	0.44
1:B:449:ALA:O	1:B:453:LEU:HG	2.18	0.43
1:B:485:ARG:HB3	1:B:486:PRO:HD3	2.00	0.43
1:A:345:LEU:HD21	1:A:381:VAL:HG22	1.99	0.43
1:B:61:ASN:HB3	1:B:64:LYS:HD2	2.01	0.43
1:B:413:LYS:HB3	1:B:493:VAL:HG23	2.00	0.43
1:A:501:GLU:O	1:A:535:HIS:HB3	2.18	0.43
1:B:66:LEU:HD13	1:B:251:LEU:HD12	2.01	0.42
1:B:381:VAL:O	1:B:384:PRO:HD2	2.19	0.42
1:A:38:ASP:O	1:A:42:LEU:HG	2.20	0.42
1:A:72:ASP:O	1:A:76:THR:HG23	2.20	0.42
1:A:393:GLU:O	1:A:397:GLN:HG3	2.20	0.42
1:A:540:THR:HA	1:A:543:GLN:NE2	2.33	0.42
1:A:428:ARG:NE	1:A:523:ILE:HG12	2.35	0.42
1:B:39:HIS:HD2	1:B:140:TYR:HE1	1.68	0.42
1:B:503:ASN:HB2	1:B:506:THR:OG1	2.20	0.41
1:A:115:LEU:HD12	1:A:115:LEU:HA	1.79	0.41
1:A:425:GLU:HG2	1:A:459:GLN:NE2	2.36	0.41
1:B:539:ALA:O	1:B:543:GLN:NE2	2.54	0.41
1:B:78:ALA:HA	1:B:84:TYR:CD2	2.55	0.41
1:A:8:ALA:HB2	1:A:53:CYS:HB3	2.03	0.41
1:B:420:THR:O	1:B:424:VAL:HG23	2.21	0.41
1:B:439:LYS:O	1:B:439:LYS:NZ	2.39	0.41
1:A:190:LYS:HE2	1:A:190:LYS:HB3	1.88	0.41
1:A:459:GLN:HA	1:A:462:VAL:HG22	2.03	0.41
1:A:117:ARG:O	1:A:117:ARG:HG3	2.20	0.40
1:B:574:LYS:HA	1:B:574:LYS:HD3	1.88	0.40
1:A:151:ALA:HB3	1:A:152:PRO:HD3	2.02	0.40
1:B:78:ALA:HA	1:B:84:TYR:HD2	1.87	0.40
1:B:222:ARG:HG2	1:B:223:PHE:CE1	2.56	0.40
1:A:117:ARG:HA	1:A:118:PRO:HD3	1.82	0.40
1:A:430:LEU:O	1:A:433:VAL:HG12	2.21	0.40
1:B:141:GLU:OE1	1:B:145:ARG:NH1	2.30	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:357:LEU:O	1:B:361:CYS:HB2	2.21	0.40
1:B:500:LYS:HG2	1:B:535:HIS:CE1	2.57	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	576/585 (98%)	542 (94%)	29 (5%)	5 (1%)	14	13
1	B	576/585 (98%)	539 (94%)	31 (5%)	6 (1%)	12	11
All	All	1152/1170 (98%)	1081 (94%)	60 (5%)	11 (1%)	12	11

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	60	GLU
1	A	538	LYS
1	B	539	ALA
1	B	60	GLU
1	A	501	GLU
1	A	537	PRO
1	A	542	GLU
1	B	283	LEU
1	B	442	GLU
1	B	538	LYS
1	B	545	LYS

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	506/511 (99%)	479 (95%)	27 (5%)	20	24
1	B	506/511 (99%)	478 (94%)	28 (6%)	19	23
All	All	1012/1022 (99%)	957 (95%)	55 (5%)	20	23

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	GLU
1	A	77	VAL
1	A	97	GLU
1	A	111	ASN
1	A	116	VAL
1	A	117	ARG
1	A	132	GLU
1	A	218	ARG
1	A	245	CYS
1	A	276	LYS
1	A	283	LEU
1	A	292	GLU
1	A	305	LEU
1	A	310	VAL
1	A	337	ARG
1	A	344	VAL
1	A	389	LYS
1	A	478	THR
1	A	492	GLU
1	A	496	THR
1	A	498	VAL
1	A	524	LYS
1	A	532	LEU
1	A	540	THR
1	A	557	LYS
1	A	573	LYS
1	A	575	LEU

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Mol	Chain	Res	Type
1	B	31	LEU
1	B	37	GLU
1	B	41	LYS
1	B	81	ARG
1	B	116	VAL
1	B	119	GLU
1	B	245	CYS
1	B	252	GLU
1	B	280	GLU
1	B	286	LYS
1	B	294	GLU
1	B	297	GLU
1	B	337	ARG
1	B	369	CYS
1	B	410	ARG
1	B	419	SER
1	B	439	LYS
1	B	467	THR
1	B	478	THR
1	B	480	SER
1	B	482	VAL
1	B	519	LYS
1	B	524	LYS
1	B	532	LEU
1	B	543	GLN
1	B	548	MET
1	B	549	ASP
1	B	554	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	9	HIS
1	A	105	HIS
1	B	33	GLN
1	B	128	HIS
1	B	367	HIS
1	B	440	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

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	578/585 (98%)	0.75	48 (8%) 17 15	34, 49, 87, 124	0
1	B	578/585 (98%)	0.68	61 (10%) 11 9	29, 46, 90, 117	0
All	All	1156/1170 (98%)	0.71	109 (9%) 14 11	29, 48, 89, 124	0

All (109) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	78	ALA	6.4
1	A	539	ALA	5.6
1	B	539	ALA	4.9
1	A	83	THR	4.5
1	B	80	LEU	4.5
1	B	88	ALA	4.5
1	A	582	ALA	4.3
1	A	79	THR	4.3
1	A	576	VAL	4.3
1	A	577	ALA	4.2
1	B	569	ALA	4.2
1	A	575	LEU	4.0
1	B	582	ALA	4.0
1	A	77	VAL	3.9
1	B	581	ALA	3.7
1	B	78	ALA	3.6
1	A	565	GLU	3.6
1	B	575	LEU	3.5
1	B	548	MET	3.5
1	A	578	ALA	3.5
1	A	535	HIS	3.4
1	B	87	MET	3.4
1	B	369	CYS	3.4
1	B	552	ALA	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	87	MET	3.3
1	A	563	ASP	3.2
1	A	170	GLN	3.1
1	B	367	HIS	3.1
1	A	84	TYR	3.1
1	B	469	VAL	3.1
1	A	370	TYR	3.0
1	B	563	ASP	3.0
1	A	408	LEU	3.0
1	B	86	GLU	3.0
1	B	85	GLY	3.0
1	B	535	HIS	3.0
1	B	83	THR	2.9
1	B	576	VAL	2.9
1	A	369	CYS	2.9
1	A	86	GLU	2.9
1	B	364	ALA	2.9
1	B	551	PHE	2.9
1	A	88	ALA	2.9
1	A	554	PHE	2.9
1	B	562	ASP	2.8
1	B	366	PRO	2.8
1	B	119	GLU	2.8
1	A	538	LYS	2.8
1	B	564	LYS	2.8
1	A	567	CYS	2.7
1	B	84	TYR	2.7
1	A	559	CYS	2.7
1	B	540	THR	2.7
1	A	307	ALA	2.6
1	A	562	ASP	2.6
1	B	315	VAL	2.6
1	B	519	LYS	2.6
1	A	502	PHE	2.5
1	B	79	THR	2.5
1	B	547	VAL	2.5
1	B	319	TYR	2.5
1	A	283	LEU	2.5
1	B	371	ALA	2.5
1	B	553	ALA	2.5
1	A	501	GLU	2.4
1	B	82	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	396	GLU	2.4
1	A	277	GLU	2.4
1	B	355	THR	2.4
1	A	443	ALA	2.4
1	B	443	ALA	2.4
1	B	572	GLY	2.4
1	A	101	CYS	2.4
1	B	571	GLU	2.3
1	B	568	PHE	2.3
1	B	546	ALA	2.3
1	A	304	SER	2.3
1	B	580	GLN	2.3
1	B	111	ASN	2.2
1	B	503	ASN	2.2
1	A	100	GLU	2.2
1	A	571	GLU	2.2
1	B	577	ALA	2.2
1	B	292	GLU	2.2
1	B	363	ALA	2.2
1	B	566	THR	2.2
1	A	581	ALA	2.2
1	B	77	VAL	2.1
1	A	511	ALA	2.1
1	A	566	THR	2.1
1	A	569	ALA	2.1
1	B	322	ALA	2.1
1	A	570	GLU	2.1
1	B	301	ASP	2.1
1	B	365	ASP	2.1
1	B	433	VAL	2.1
1	A	572	GLY	2.1
1	B	574	LYS	2.1
1	A	374	PHE	2.1
1	B	502	PHE	2.1
1	B	536	LYS	2.0
1	A	490	ALA	2.0
1	B	92	ALA	2.0
1	B	305	LEU	2.0
1	A	452	TYR	2.0
1	A	551	PHE	2.0
1	B	554	PHE	2.0
1	A	579	SER	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	546	ALA	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.