



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 03:19 PM GMT

PDB ID : 4C4V
Title : Structure of the outer membrane protein insertase BamA with one POTRA domain.
Authors : Zeth, K.; Albrecht, R.; Diederichs, K.
Deposited on : 2013-09-09
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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

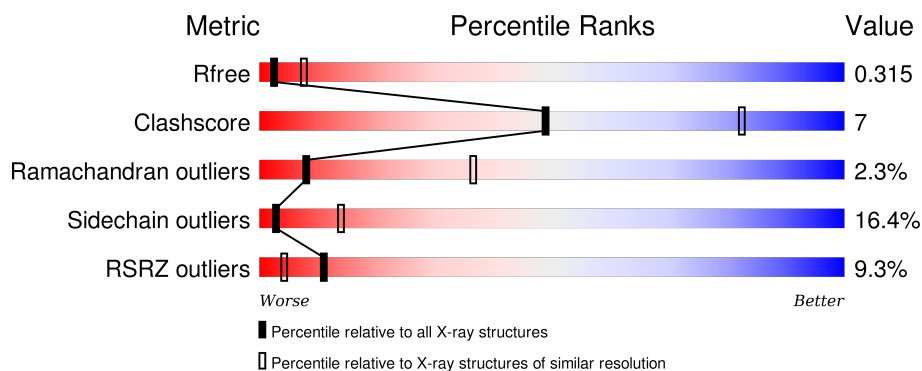
1 Overall quality at a glance

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}	91344	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	464	<div> <div>11%</div> <div> <div></div> <div>68%</div> <div>24%</div> <div>• •</div> </div> </div>
2	B	467	<div> <div>7%</div> <div> <div></div> <div>67%</div> <div>25%</div> <div>• •</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7147 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 OUTER MEMBRANE PROTEIN ASSEMBLY FACTOR BAMA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	445	Total	C	N	O	S	0	1	0
			3498	2210	580	697	11			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	501	SER	LEU	CONFLICT	UNP P0A940
A	522	GLU	TYR	CONFLICT	UNP P0A940
A	673	ILE	VAL	CONFLICT	UNP P0A940

- Molecule 2 is a protein called OUTER MEMBRANE PROTEIN ASSEMBLY FACTOR BAMA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	446	Total	C	N	O	S	0	0	0
			3528	2230	586	701	11			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	501	SER	LEU	CONFLICT	UNP P0A940
B	522	GLU	TYR	CONFLICT	UNP P0A940
B	673	ILE	VAL	CONFLICT	UNP P0A940

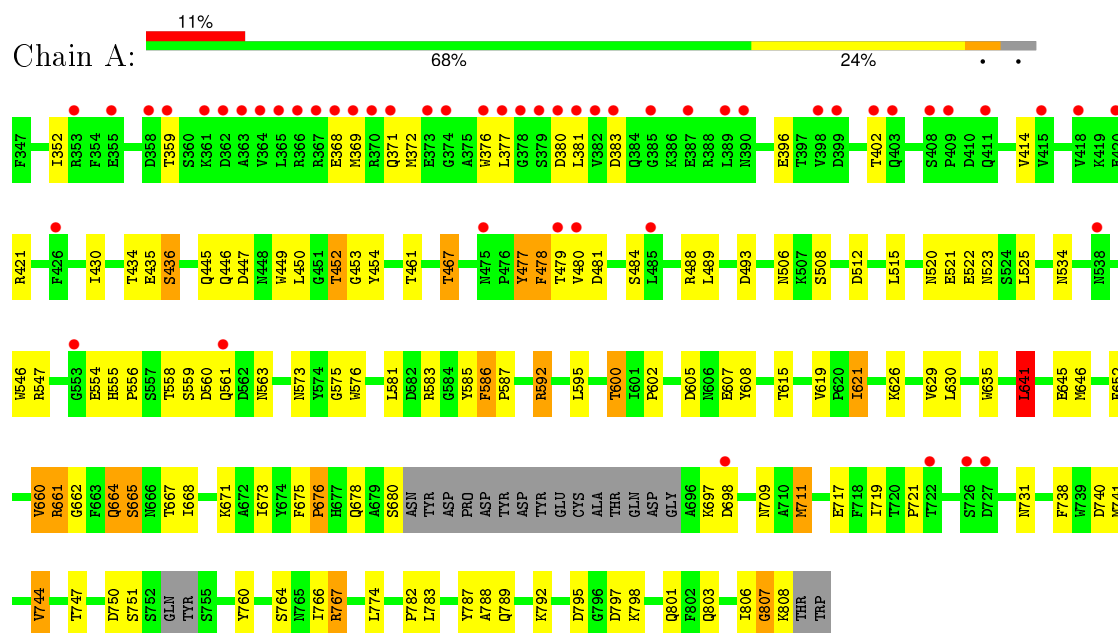
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	55	Total	O	0	0
			55	55		
3	B	66	Total	O	0	0
			66	66		

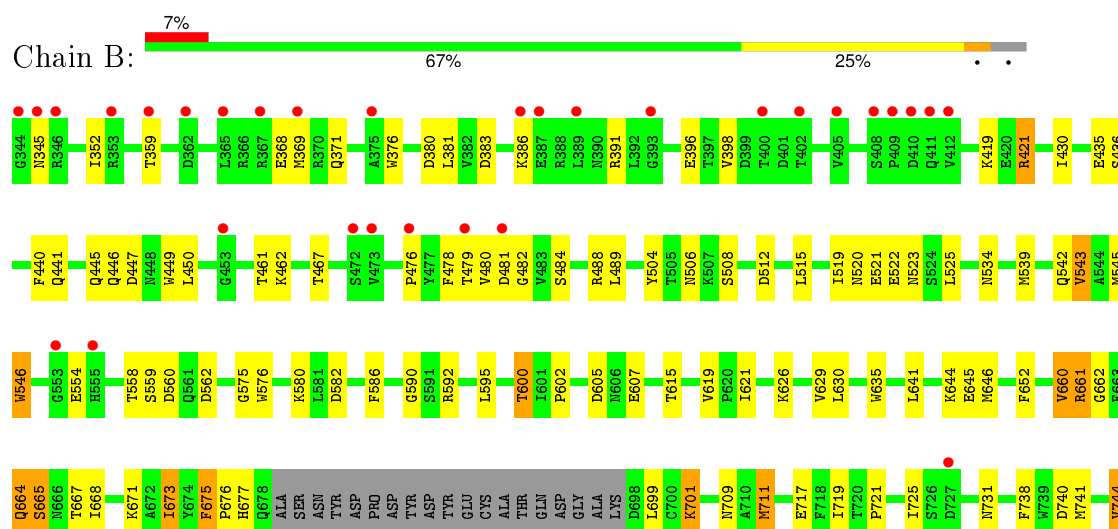
3 Residue-property plots

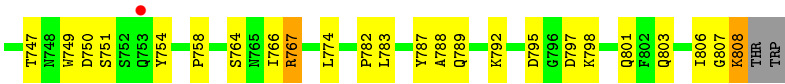
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: OUTER MEMBRANE PROTEIN ASSEMBLY FACTOR BAMA



• Molecule 2: OUTER MEMBRANE PROTEIN ASSEMBLY FACTOR BAMA





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	79.58 Å 67.35 Å 109.80 Å 90.00° 93.46° 90.00°	Depositor
Resolution (Å)	33.59 – 3.00 47.23 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.6 (33.59-3.00) 99.0 (47.23-2.80)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.16 (at 2.81 Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, R_{free}	0.234 , 0.292 0.251 , 0.315	Depositor DCC
R_{free} test set	1180 reflections (5.30%)	DCC
Wilson B-factor (Å ²)	73.2	Xtriage
Anisotropy	0.682	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 79.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 28589 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	7147	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 5.40% 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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.43	0/3596	0.73	1/4886 (0.0%)
2	B	0.43	0/3625	0.75	0/4922
All	All	0.43	0/7221	0.74	1/9808 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	585	TYR	C-N-CA	5.56	135.61	121.70

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	3498	0	3212	47	0
2	B	3528	0	3256	51	0
3	A	55	0	0	0	0
3	B	66	0	0	0	0
All	All	7147	0	6468	97	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 7.

All (97) 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)
2:B:481:ASP:H	2:B:482:GLY:HA2	1.18	1.09
2:B:435:GLU:HB2	2:B:665:SER:HB2	1.61	0.81
2:B:652:PHE:HB3	2:B:711:MET:HG2	1.65	0.79
1:A:652:PHE:HB3	1:A:711:MET:HG2	1.66	0.76
2:B:709:ASN:HD21	2:B:747:THR:HB	1.54	0.72
1:A:709:ASN:HD21	1:A:747:THR:HB	1.55	0.71
2:B:664:GLN:HG2	2:B:798:LYS:HB2	1.79	0.65
2:B:675:PHE:HB3	2:B:676:PRO:HD3	1.78	0.65
1:A:600:THR:HG21	1:A:607:GLU:HA	1.79	0.65
1:A:664:GLN:HG2	1:A:798:LYS:HB2	1.79	0.64
2:B:600:THR:HG21	2:B:607:GLU:HA	1.78	0.64
2:B:481:ASP:N	2:B:482:GLY:HA2	1.99	0.64
2:B:481:ASP:H	2:B:482:GLY:CA	2.05	0.63
1:A:396:GLU:HB2	1:A:421:ARG:HB3	1.79	0.63
2:B:626:LYS:HB3	2:B:721:PRO:HG3	1.81	0.62
2:B:396:GLU:HB2	2:B:421:ARG:HB3	1.80	0.62
2:B:675:PHE:CB	2:B:676:PRO:HD3	2.33	0.58
2:B:783:LEU:HD12	2:B:806:ILE:HD13	1.86	0.56
1:A:452:THR:HB	1:A:454:TYR:HD1	1.69	0.56
2:B:488:ARG:HB3	2:B:512:ASP:HB2	1.88	0.56
2:B:478:PHE:HD1	2:B:479:THR:HG23	1.71	0.56
1:A:660:VAL:HG13	1:A:668:ILE:HD12	1.89	0.55
1:A:488:ARG:HB3	1:A:512:ASP:HB2	1.89	0.55
1:A:782:PRO:HD2	1:A:807:GLY:HA2	1.91	0.53
2:B:660:VAL:HG13	2:B:668:ILE:HD12	1.90	0.53
2:B:675:PHE:HA	2:B:699:LEU:HD12	1.91	0.53
1:A:673:ILE:HD11	1:A:760:TYR:HE2	1.74	0.52
1:A:788:ALA:O	1:A:801:GLN:HG3	2.09	0.52
1:A:671:LYS:NZ	1:A:797:ASP:OD1	2.42	0.52
1:A:619:VAL:HB	1:A:629:VAL:HG13	1.92	0.51
2:B:782:PRO:HD2	2:B:807:GLY:HA3	1.91	0.51
2:B:788:ALA:O	2:B:801:GLN:HG3	2.10	0.51
1:A:402:THR:HG22	1:A:414:VAL:HG22	1.92	0.51
1:A:626:LYS:HB3	1:A:721:PRO:HG3	1.91	0.51
1:A:452:THR:N	1:A:453:GLY:HA2	2.27	0.50
2:B:619:VAL:HB	2:B:629:VAL:HG13	1.92	0.50
2:B:644:LYS:HB3	2:B:645:GLU:HG3	1.92	0.49
1:A:738:PHE:HZ	1:A:788:ALA:HB2	1.78	0.49
2:B:441:GLN:HE22	2:B:808:LYS:HG3	1.77	0.49
2:B:440:PHE:CD2	2:B:462:LYS:HE2	2.47	0.49
1:A:547:ARG:HD2	1:A:645:GLU:OE1	2.13	0.49
2:B:484:SER:O	2:B:515:LEU:HA	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:738:PHE:HZ	2:B:788:ALA:HB2	1.78	0.48
2:B:671:LYS:NZ	2:B:797:ASP:OD1	2.43	0.48
2:B:787:TYR:CE1	2:B:801:GLN:HB3	2.49	0.48
1:A:630:LEU:HB3	1:A:717:GLU:HB3	1.96	0.48
1:A:621:ILE:HG21	2:B:519:ILE:HD12	1.96	0.48
1:A:575:GLY:HA2	1:A:595:LEU:O	2.12	0.48
2:B:575:GLY:HA2	2:B:595:LEU:O	2.13	0.47
2:B:543:VAL:HG13	2:B:673:ILE:HB	1.96	0.47
1:A:711:MET:HB3	1:A:744:VAL:HB	1.97	0.47
1:A:787:TYR:CE1	1:A:801:GLN:HB3	2.50	0.47
1:A:608:TYR:HA	1:A:641:LEU:H	1.80	0.47
1:A:675:PHE:HB2	1:A:676:PRO:HD3	1.96	0.46
2:B:630:LEU:HB3	2:B:717:GLU:HB3	1.96	0.46
2:B:504:TYR:HB2	2:B:539:MET:HG2	1.97	0.46
2:B:545:MET:HG3	2:B:546:TRP:HE3	1.80	0.46
2:B:662:GLY:H	2:B:803:GLN:NE2	2.14	0.46
1:A:583:ARG:HH11	1:A:586:PHE:HB3	1.81	0.46
2:B:711:MET:HB3	2:B:744:VAL:HB	1.98	0.45
2:B:701:LYS:HZ2	2:B:758:PRO:HD2	1.80	0.45
1:A:484:SER:O	1:A:515:LEU:HA	2.16	0.45
1:A:583:ARG:HD2	1:A:586:PHE:O	2.16	0.45
1:A:586:PHE:H	1:A:587:PRO:HD3	1.80	0.45
1:A:738:PHE:CZ	1:A:788:ALA:HB2	2.52	0.44
2:B:580:LYS:HD3	2:B:590:GLY:HA2	1.99	0.44
1:A:435:GLU:HB2	1:A:665:SER:HB2	1.99	0.44
1:A:667:THR:HG21	1:A:798:LYS:O	2.18	0.44
2:B:386:LYS:HG3	2:B:398:VAL:HG22	1.99	0.44
1:A:371:GLN:HG2	1:A:381:LEU:HB3	1.99	0.44
2:B:661:ARG:HD2	2:B:740:ASP:OD2	2.18	0.44
2:B:738:PHE:CZ	2:B:788:ALA:HB2	2.53	0.43
1:A:661:ARG:HD2	1:A:740:ASP:OD2	2.18	0.43
1:A:660:VAL:CG1	1:A:668:ILE:HD12	2.47	0.43
1:A:523:ASN:HD22	1:A:576:TRP:HE1	1.67	0.43
2:B:371:GLN:HG2	2:B:381:LEU:HB3	1.99	0.43
1:A:662:GLY:H	1:A:803:GLN:NE2	2.16	0.43
2:B:767:ARG:HB2	2:B:792:LYS:O	2.19	0.43
1:A:783:LEU:HD12	1:A:806:ILE:HD13	2.00	0.42
2:B:717:GLU:HG3	2:B:738:PHE:HB3	2.02	0.42
2:B:667:THR:HG21	2:B:798:LYS:O	2.19	0.42
1:A:767:ARG:HB2	1:A:792:LYS:O	2.19	0.42
2:B:523:ASN:HD22	2:B:576:TRP:HE1	1.67	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:506:ASN:HD21	1:A:534:ASN:HB3	1.85	0.41
2:B:506:ASN:HD21	2:B:534:ASN:HB3	1.85	0.41
1:A:520:ASN:HD22	1:A:522:GLU:H	1.68	0.41
1:A:478:PHE:HA	1:A:478:PHE:HD1	1.73	0.41
2:B:660:VAL:CG1	2:B:668:ILE:HD12	2.49	0.41
2:B:449:TRP:CE3	2:B:449:TRP:HA	2.56	0.41
2:B:749:TRP:CZ2	2:B:754:TYR:HB2	2.56	0.41
2:B:520:ASN:HD22	2:B:522:GLU:H	1.67	0.41
1:A:467:THR:HG23	1:A:493:ASP:HB3	2.02	0.41
2:B:807:GLY:HA2	2:B:808:LYS:HB3	2.02	0.41
1:A:592:ARG:HH11	1:A:592:ARG:HB3	1.86	0.41
1:A:452:THR:HB	1:A:454:TYR:CD1	2.53	0.40
1:A:673:ILE:HD11	1:A:760:TYR:CE2	2.55	0.40
1:A:449:TRP:HA	1:A:450:LEU:HA	1.95	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	440/464 (95%)	385 (88%)	43 (10%)	12 (3%)	6	32
2	B	442/467 (95%)	389 (88%)	45 (10%)	8 (2%)	11	45
All	All	882/931 (95%)	774 (88%)	88 (10%)	20 (2%)	8	36

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	586	PHE
2	B	359	THR
2	B	436	SER
2	B	675	PHE

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Mol	Chain	Res	Type
1	A	436	SER
1	A	480	VAL
1	A	641	LEU
1	A	807	GLY
2	B	559	SER
2	B	562	ASP
1	A	559	SER
1	A	676	PRO
1	A	764	SER
2	B	764	SER
1	A	477	TYR
1	A	479	THR
1	A	556	PRO
1	A	602	PRO
2	B	476	PRO
2	B	602	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	370/392 (94%)	307 (83%)	63 (17%)	2	13
2	B	375/394 (95%)	316 (84%)	59 (16%)	3	15
All	All	745/786 (95%)	623 (84%)	122 (16%)	3	14

All (122) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	352	ILE
1	A	359	THR
1	A	368	GLU
1	A	369	MET
1	A	372	MET
1	A	376	TRP
1	A	377	LEU

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Mol	Chain	Res	Type
1	A	380	ASP
1	A	383	ASP
1	A	430	ILE
1	A	434	THR
1	A	436	SER
1	A	445	GLN
1	A	446	GLN
1	A	447	ASP
1	A	452	THR
1	A	461	THR
1	A	467	THR
1	A	477	TYR
1	A	478	PHE
1	A	481	ASP
1	A	489	LEU
1	A	508	SER
1	A	521	GLU
1	A	525	LEU
1	A	546	TRP
1	A	554	GLU
1	A	555	HIS
1	A	558	THR
1	A	560	ASP
1	A	561	GLN
1	A	563	ASN
1	A	573	ASN
1	A	581	LEU
1	A	592	ARG
1	A	600	THR
1	A	605	ASP
1	A	615	THR
1	A	621	ILE
1	A	635	TRP
1	A	641	LEU
1	A	646	MET
1	A	660	VAL
1	A	661	ARG
1	A	664	GLN
1	A	665	SER
1	A	678	GLN
1	A	680	SER
1	A	697	LYS

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Mol	Chain	Res	Type
1	A	698	ASP
1	A	711	MET
1	A	719	ILE
1	A	731	ASN
1	A	741	MET
1	A	744	VAL
1	A	750	ASP
1	A	751	SER
1	A	766	ILE
1	A	767	ARG
1	A	774	LEU
1	A	789	GLN
1	A	795	ASP
1	A	808	LYS
2	B	345	ASN
2	B	352	ILE
2	B	368	GLU
2	B	369	MET
2	B	376	TRP
2	B	380	ASP
2	B	383	ASP
2	B	391	ARG
2	B	419	LYS
2	B	421	ARG
2	B	430	ILE
2	B	445	GLN
2	B	446	GLN
2	B	447	ASP
2	B	450	LEU
2	B	461	THR
2	B	467	THR
2	B	480	VAL
2	B	489	LEU
2	B	508	SER
2	B	521	GLU
2	B	525	LEU
2	B	542	GLN
2	B	543	VAL
2	B	546	TRP
2	B	554	GLU
2	B	558	THR
2	B	560	ASP

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Mol	Chain	Res	Type
2	B	582	ASP
2	B	586	PHE
2	B	592	ARG
2	B	600	THR
2	B	605	ASP
2	B	615	THR
2	B	621	ILE
2	B	635	TRP
2	B	641	LEU
2	B	646	MET
2	B	660	VAL
2	B	661	ARG
2	B	664	GLN
2	B	665	SER
2	B	673	ILE
2	B	677	HIS
2	B	701	LYS
2	B	711	MET
2	B	719	ILE
2	B	725	ILE
2	B	731	ASN
2	B	741	MET
2	B	744	VAL
2	B	750	ASP
2	B	751	SER
2	B	766	ILE
2	B	767	ARG
2	B	774	LEU
2	B	789	GLN
2	B	795	ASP
2	B	808	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	459	ASN
1	A	506	ASN
1	A	520	ASN
1	A	555	HIS
1	A	563	ASN
1	A	803	GLN
2	B	441	GLN

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Mol	Chain	Res	Type
2	B	459	ASN
2	B	506	ASN
2	B	520	ASN
2	B	523	ASN
2	B	555	HIS
2	B	803	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 carbohydrates 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	445/464 (95%)	0.63	51 (11%) 6 2	50, 88, 167, 185	0
2	B	446/467 (95%)	0.40	32 (7%) 18 7	48, 87, 136, 163	0
All	All	891/931 (95%)	0.51	83 (9%) 11 4	48, 88, 151, 185	0

All (83) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	387	GLU	8.9
1	A	383	ASP	7.1
1	A	382	VAL	6.4
1	A	367	ARG	5.9
1	A	359	THR	5.3
1	A	368	GLU	5.3
1	A	389	LEU	4.9
1	A	355	GLU	4.9
1	A	479	THR	4.5
1	A	480	VAL	4.4
1	A	380	ASP	4.1
1	A	385	GLY	4.1
2	B	753	GLN	3.9
2	B	453	GLY	3.7
1	A	381	LEU	3.7
2	B	375	ALA	3.7
1	A	698	ASP	3.6
2	B	410	ASP	3.6
1	A	379	SER	3.6
1	A	358	ASP	3.6
2	B	365	LEU	3.5
2	B	553	GLY	3.5
2	B	367	ARG	3.5
1	A	408	SER	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	371	GLN	3.5
2	B	481	ASP	3.4
1	A	370	ARG	3.2
1	A	362	ASP	3.1
1	A	399	ASP	3.1
1	A	411	GLN	3.1
2	B	345	ASN	3.1
1	A	553	GLY	3.1
2	B	476	PRO	3.0
2	B	727	ASP	3.0
1	A	364	VAL	3.0
2	B	387	GLU	2.9
2	B	555	HIS	2.9
2	B	344	GLY	2.8
1	A	538	ASN	2.8
1	A	378	GLY	2.8
1	A	398	VAL	2.8
1	A	377	LEU	2.7
1	A	403	GLN	2.6
2	B	411	GLN	2.6
1	A	409	PRO	2.5
1	A	726	SER	2.5
1	A	369	MET	2.5
1	A	353	ARG	2.5
2	B	473	VAL	2.5
2	B	393	GLY	2.5
2	B	362	ASP	2.4
1	A	415	VAL	2.4
1	A	722	THR	2.4
2	B	402	THR	2.4
2	B	479	THR	2.4
2	B	389	LEU	2.4
2	B	409	PRO	2.4
2	B	408	SER	2.4
2	B	346	ARG	2.4
1	A	365	LEU	2.4
1	A	426	PHE	2.4
1	A	420	GLU	2.3
1	A	376	TRP	2.3
1	A	361	LYS	2.3
1	A	366	ARG	2.3
1	A	402	THR	2.3

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Mol	Chain	Res	Type	RSRZ
2	B	400	THR	2.3
1	A	727	ASP	2.2
1	A	390	ASN	2.2
2	B	412	VAL	2.2
2	B	472	SER	2.2
1	A	374	GLY	2.1
1	A	418	VAL	2.1
1	A	373	GLU	2.1
2	B	405	VAL	2.1
1	A	485	LEU	2.1
2	B	386	LYS	2.1
1	A	363	ALA	2.1
2	B	369	MET	2.1
1	A	561	GLN	2.0
2	B	353	ARG	2.0
1	A	475	ASN	2.0
2	B	359	THR	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 carbohydrates 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.