



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:35 PM UTC

PDB ID : 1MPR / pdb_00001mpr
Title : MALTOPORIN FROM SALMONELLA TYPHIMURIUM
Authors : Meyer, J.E.W.; Schulz, G.E.
Deposited on : 1996-12-18
Resolution : 2.80 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
Xtrriage (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

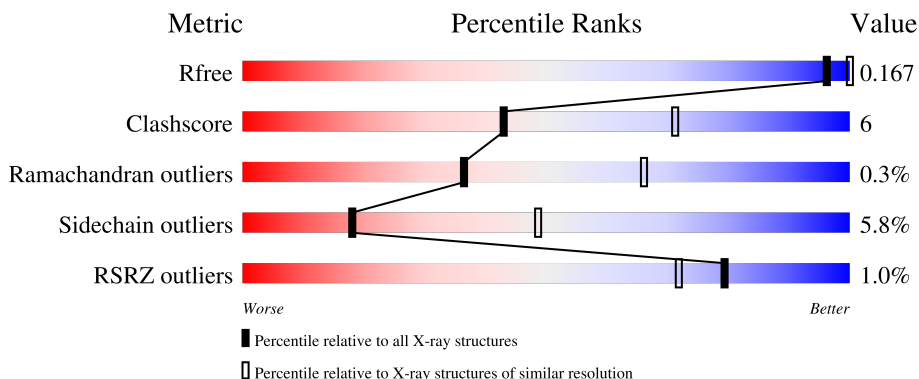
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



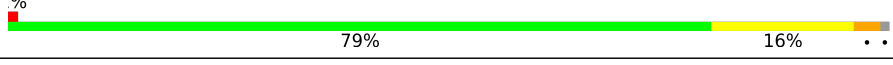
The reported resolution of this entry is 2.80 Å.

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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	427	 81% 15% ..
1	B	427	 83% 14% ..
1	C	427	 79% 16% ..

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10513 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 MALTOPORIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	421	3352	2110	571	659	12	10	0	0
1	B	421	3352	2110	571	659	12	10	0	0
1	C	421	3352	2110	571	659	12	11	0	0

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

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

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	153	Total	O	0	0
			153	153		
3	B	154	Total	O	0	0
			154	154		
3	C	149	Total	O	0	0
			149	149		



4 Data and refinement statistics i

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	124.50Å 211.80Å 184.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.80 10.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	94.8 (10.00-2.80) 92.6 (10.00-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtrriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.183 , 0.211 0.165 , 0.167	Depositor DCC
R_{free} test set	6992 reflections (10.09%)	wwPDB-VP
Wilson B-factor (Å ²)	30.6	Xtrriage
Anisotropy	0.026	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 84.8	EDS
L-test for twinning ¹	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.013 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.018 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10513	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.02% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Theoretical 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

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.58	1/3440 (0.0%)	0.97	13/4664 (0.3%)
1	B	0.57	0/3440	0.96	14/4664 (0.3%)
1	C	0.57	1/3440 (0.0%)	0.97	14/4664 (0.3%)
All	All	0.58	2/10320 (0.0%)	0.97	41/13992 (0.3%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	297	MET	SD-CE	-5.63	1.65	1.79
1	A	297	MET	SD-CE	-5.21	1.66	1.79

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	33	ARG	N-CA-C	11.40	125.05	111.82
1	A	33	ARG	N-CA-C	11.39	125.03	111.82
1	B	33	ARG	N-CA-C	11.12	124.72	111.82
1	C	274	ASN	N-CA-C	8.98	121.91	110.33
1	B	274	ASN	N-CA-C	8.61	121.44	110.33
1	A	274	ASN	N-CA-C	8.41	121.18	110.33
1	A	414	SER	N-CA-C	7.21	117.76	108.24
1	A	375	ILE	N-CA-C	-7.10	97.89	108.12
1	B	82	ARG	N-CA-C	7.10	121.17	112.23
1	B	375	ILE	N-CA-C	-7.08	97.93	108.12
1	B	414	SER	N-CA-C	7.07	117.57	108.24
1	C	160	ILE	N-CA-C	-6.97	98.40	108.36
1	C	414	SER	N-CA-C	6.95	117.41	108.24
1	C	375	ILE	N-CA-C	-6.68	98.50	108.12
1	A	82	ARG	N-CA-C	6.43	120.33	112.23
1	B	23	PHE	N-CA-C	6.17	118.57	108.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	23	PHE	N-CA-C	6.10	118.46	108.52
1	A	113	HIS	N-CA-C	6.04	118.36	111.11
1	B	107	TYR	N-CA-C	6.00	118.07	108.41
1	A	404	SER	N-CA-C	-5.76	101.75	110.28
1	C	164	VAL	CB-CA-C	-5.76	103.87	111.70
1	C	299	VAL	CB-CA-C	-5.75	100.41	110.71
1	A	107	TYR	N-CA-C	5.70	117.59	108.41
1	A	38	CYS	N-CA-C	5.69	119.53	112.59
1	C	404	SER	N-CA-C	-5.67	102.01	110.23
1	B	158	GLN	CB-CA-C	-5.66	110.07	116.63
1	B	299	VAL	CB-CA-C	-5.65	100.60	110.71
1	C	23	PHE	N-CA-C	5.64	117.72	108.52
1	B	113	HIS	N-CA-C	5.63	117.87	111.11
1	A	114	MET	N-CA-C	5.59	118.14	111.71
1	A	299	VAL	CB-CA-C	-5.59	100.71	110.71
1	C	114	MET	N-CA-C	5.51	118.05	111.71
1	B	114	MET	N-CA-C	5.50	119.09	112.38
1	B	249	GLY	N-CA-C	5.50	121.03	113.99
1	B	404	SER	N-CA-C	-5.46	102.31	110.23
1	C	249	GLY	N-CA-C	5.37	120.86	113.99
1	C	107	TYR	N-CA-C	5.33	116.99	108.41
1	B	164	VAL	CB-CA-C	-5.23	104.03	111.19
1	C	211	ASP	N-CA-C	5.16	116.14	108.86
1	C	82	ARG	N-CA-C	5.09	119.57	112.90
1	A	294	TRP	N-CA-C	5.08	117.35	108.76

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	3352	0	3107	43	0
1	B	3352	0	3107	39	0
1	C	3352	0	3107	46	0
2	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	153	0	0	3	0
3	B	154	0	0	5	0
3	C	149	0	0	2	0
All	All	10513	0	9321	119	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 (119) 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:C:165:LYS:HE2	1:C:199:THR:OG1	1.86	0.75
1:B:165:LYS:HE2	1:B:199:THR:OG1	1.88	0.73
1:C:173:ASP:OD1	1:C:175:ARG:HD2	1.89	0.73
1:A:71:GLN:O	1:C:147:THR:HG23	1.89	0.72
1:B:147:THR:HG23	1:C:71:GLN:O	1.91	0.71
1:B:173:ASP:OD1	1:B:175:ARG:HD2	1.90	0.70
1:A:173:ASP:OD1	1:A:175:ARG:HD2	1.94	0.68
1:A:147:THR:HG21	3:B:453:HOH:O	1.94	0.67
1:A:160:ILE:HA	1:A:267:ASN:O	1.95	0.66
1:B:147:THR:HG21	3:B:469:HOH:O	1.95	0.66
3:A:572:HOH:O	1:C:147:THR:HG21	1.96	0.65
1:A:147:THR:HG23	1:B:71:GLN:O	1.95	0.65
1:A:165:LYS:HE2	1:A:199:THR:OG1	1.97	0.65
1:A:71:GLN:HB2	1:C:147:THR:HG21	1.80	0.64
1:A:195:ARG:HG3	1:A:195:ARG:HH11	1.64	0.63
1:C:297:MET:HG3	1:C:367:ILE:HD13	1.84	0.60
1:A:71:GLN:HB2	1:C:147:THR:CG2	2.33	0.59
1:A:63:ASN:HD22	1:A:64:VAL:N	2.00	0.58
1:C:63:ASN:HD22	1:C:64:VAL:N	2.02	0.58
1:B:147:THR:HG21	1:C:71:GLN:HB2	1.86	0.56
1:B:147:THR:CG2	1:C:71:GLN:HB2	2.36	0.56
1:A:63:ASN:HD22	1:A:63:ASN:C	2.14	0.56
1:B:63:ASN:HD22	1:B:64:VAL:N	2.03	0.55
1:A:147:THR:HG21	1:B:71:GLN:HB2	1.88	0.55
1:A:297:MET:HG3	1:A:367:ILE:HD13	1.88	0.55
1:B:213:TRP:H	1:B:236:THR:HG22	1.73	0.54
1:A:182:ASN:HB2	1:A:183:PRO:HD2	1.89	0.54
1:B:160:ILE:HA	1:B:267:ASN:O	2.07	0.54
1:B:297:MET:HG3	1:B:367:ILE:HD13	1.89	0.53
1:B:63:ASN:HD22	1:B:63:ASN:C	2.17	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:241:THR:HB	1:B:248:ARG:HG3	1.90	0.53
1:B:94:TRP:CD1	1:B:94:TRP:H	2.26	0.53
1:A:422:GLN:HG2	1:A:423:MET:N	2.24	0.52
1:B:182:ASN:HB2	1:B:183:PRO:HD2	1.90	0.52
1:C:160:ILE:HA	1:C:267:ASN:O	2.10	0.52
1:C:63:ASN:HD22	1:C:63:ASN:C	2.17	0.52
1:A:273:ILE:HG12	1:A:273:ILE:O	2.08	0.51
1:A:33:ARG:HD3	1:A:37:GLU:OE2	2.10	0.51
1:B:273:ILE:HG12	1:B:273:ILE:O	2.11	0.50
1:A:147:THR:CG2	1:B:71:GLN:HB2	2.41	0.49
1:A:275:ASN:HD22	1:A:275:ASN:C	2.19	0.49
1:C:155:PHE:CE1	1:C:159:ASN:HA	2.47	0.49
1:A:94:TRP:CD1	1:A:94:TRP:H	2.30	0.49
1:A:241:THR:HB	1:A:248:ARG:HG3	1.95	0.49
1:C:94:TRP:H	1:C:94:TRP:CD1	2.29	0.49
1:C:273:ILE:HG12	1:C:273:ILE:O	2.11	0.49
1:A:330:MET:HE2	1:A:359:GLN:OE1	2.13	0.49
1:A:195:ARG:HG3	1:A:195:ARG:NH1	2.26	0.48
1:C:182:ASN:HB2	1:C:183:PRO:HD2	1.95	0.48
1:C:33:ARG:HD3	1:C:37:GLU:OE2	2.13	0.48
1:C:330:MET:HE2	1:C:359:GLN:OE1	2.14	0.48
1:A:208:ALA:HA	1:A:272:VAL:HG11	1.96	0.47
1:C:195:ARG:HH12	1:C:210:LYS:HE2	1.78	0.47
1:B:161:TYR:CE1	1:B:164:VAL:HG22	2.49	0.47
1:A:161:TYR:O	1:A:267:ASN:HB2	2.13	0.47
1:B:422:GLN:HG2	1:B:423:MET:N	2.30	0.47
1:B:32:TYR:O	1:B:354:LYS:HE3	2.15	0.47
1:C:374:ARG:O	1:C:421:ALA:HA	2.15	0.47
1:B:33:ARG:HD3	1:B:37:GLU:OE2	2.15	0.46
1:B:378:THR:O	1:B:417:TRP:HA	2.15	0.46
1:C:120:TRP:CH2	1:C:175:ARG:HG2	2.51	0.45
1:A:32:TYR:O	1:A:354:LYS:HE3	2.16	0.45
1:A:161:TYR:CE1	1:A:164:VAL:HG22	2.52	0.45
1:C:378:THR:O	1:C:417:TRP:HA	2.16	0.45
1:B:12:GLY:HA3	1:B:20:GLN:HB2	1.98	0.45
1:C:161:TYR:CE1	1:C:164:VAL:HG22	2.52	0.45
1:C:161:TYR:CZ	1:C:267:ASN:HB3	2.51	0.45
1:A:246:GLN:HG2	3:A:523:HOH:O	2.17	0.44
1:B:374:ARG:O	1:B:421:ALA:HA	2.17	0.44
1:B:4:HIS:HA	1:B:427:TRP:CD1	2.53	0.44
1:C:241:THR:HB	1:C:248:ARG:HG3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:392:GLY:C	1:A:394:ASN:H	2.25	0.44
1:C:195:ARG:HB2	1:C:195:ARG:HH11	1.83	0.44
1:C:12:GLY:HA3	1:C:20:GLN:HB2	1.98	0.44
1:C:275:ASN:C	1:C:275:ASN:HD22	2.24	0.44
1:A:165:LYS:HB2	1:A:202:TYR:CE2	2.53	0.44
1:C:32:TYR:O	1:C:354:LYS:HE3	2.16	0.44
1:A:160:ILE:HG12	1:A:268:TYR:CE1	2.53	0.43
1:C:145:ARG:CG	1:C:146:SER:N	2.81	0.43
1:B:334:LEU:HD12	1:B:356:THR:O	2.18	0.43
1:C:145:ARG:HG3	1:C:146:SER:N	2.33	0.43
1:B:161:TYR:O	1:B:267:ASN:HB2	2.19	0.43
1:A:33:ARG:HD2	3:A:507:HOH:O	2.17	0.43
1:A:322:PRO:HD2	1:A:334:LEU:O	2.19	0.43
1:C:194:GLY:HA3	1:C:247:ALA:HB2	2.00	0.43
1:C:224:LEU:HD23	1:C:288:ILE:HD12	2.01	0.43
1:A:320:VAL:HG13	1:A:322:PRO:HD3	2.00	0.43
1:B:417:TRP:CZ3	1:B:419:PHE:CD2	3.07	0.43
1:B:170:ASP:O	1:B:194:GLY:HA2	2.19	0.43
1:C:198:THR:HA	3:C:529:HOH:O	2.19	0.43
1:B:275:ASN:ND2	1:B:275:ASN:H	2.16	0.43
1:A:378:THR:O	1:A:417:TRP:HA	2.18	0.42
1:B:165:LYS:HE2	1:B:199:THR:HG1	1.81	0.42
1:A:205:ALA:HB3	1:A:272:VAL:HG23	2.02	0.42
1:A:12:GLY:HA3	1:A:20:GLN:HB2	2.00	0.42
1:A:145:ARG:HG3	1:A:146:SER:N	2.34	0.42
1:A:161:TYR:CZ	1:A:267:ASN:HB3	2.54	0.42
1:C:161:TYR:O	1:C:267:ASN:HB2	2.18	0.42
1:C:322:PRO:HD2	1:C:334:LEU:O	2.20	0.42
1:A:19:GLU:H	1:A:19:GLU:CD	2.28	0.42
1:B:161:TYR:CZ	1:B:267:ASN:HB3	2.54	0.42
1:C:392:GLY:C	1:C:394:ASN:H	2.27	0.42
1:C:320:VAL:HG13	1:C:322:PRO:HD3	2.01	0.41
1:A:214:MET:HE3	1:A:235:ALA:HB2	2.00	0.41
1:C:227:TYR:CD1	1:C:227:TYR:C	2.97	0.41
1:C:323:MET:SD	1:C:367:ILE:HA	2.60	0.41
1:B:33:ARG:HD2	3:B:541:HOH:O	2.20	0.41
1:B:153:TYR:CD2	1:B:164:VAL:HG13	2.56	0.41
1:B:173:ASP:CG	1:B:175:ARG:HH11	2.29	0.41
1:B:275:ASN:HD22	1:B:275:ASN:C	2.29	0.41
1:C:246:GLN:HG2	3:C:553:HOH:O	2.19	0.41
1:C:205:ALA:HB3	1:C:272:VAL:HG23	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:19:GLU:HG2	3:B:453:HOH:O	2.21	0.41
1:B:227:TYR:CD1	1:B:227:TYR:C	2.99	0.41
1:A:195:ARG:NH1	1:A:197:ASN:HB2	2.35	0.41
1:C:92:ILE:HG21	1:C:95:LEU:HD12	2.03	0.40
3:B:469:HOH:O	1:C:19:GLU:HG2	2.20	0.40
1:A:374:ARG:O	1:A:421:ALA:HA	2.22	0.40
1:C:4:HIS:HA	1:C:427:TRP:CD1	2.56	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	417/427 (98%)	393 (94%)	23 (6%)	1 (0%)	43 72
1	B	417/427 (98%)	396 (95%)	20 (5%)	1 (0%)	43 72
1	C	417/427 (98%)	396 (95%)	19 (5%)	2 (0%)	24 55
All	All	1251/1281 (98%)	1185 (95%)	62 (5%)	4 (0%)	36 66

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	158	GLN
1	B	392	GLY
1	A	392	GLY
1	C	392	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	343/348 (99%)	324 (94%)	19 (6%)	19	51
1	B	343/348 (99%)	324 (94%)	19 (6%)	19	51
1	C	343/348 (99%)	321 (94%)	22 (6%)	16	44
All	All	1029/1044 (99%)	969 (94%)	60 (6%)	18	49

All (60) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	GLU
1	A	33	ARG
1	A	34	LEU
1	A	154	THR
1	A	164	VAL
1	A	175	ARG
1	A	189	LEU
1	A	224	LEU
1	A	236	THR
1	A	273	ILE
1	A	275	ASN
1	A	283	LEU
1	A	290	LEU
1	A	299	VAL
1	A	320	VAL
1	A	321	ARG
1	A	354	LYS
1	A	357	LEU
1	A	415	ASP
1	B	19	GLU
1	B	33	ARG
1	B	34	LEU
1	B	154	THR
1	B	164	VAL
1	B	175	ARG
1	B	189	LEU
1	B	224	LEU
1	B	236	THR
1	B	273	ILE
1	B	275	ASN

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Mol	Chain	Res	Type
1	B	283	LEU
1	B	290	LEU
1	B	299	VAL
1	B	320	VAL
1	B	321	ARG
1	B	354	LYS
1	B	357	LEU
1	B	415	ASP
1	C	19	GLU
1	C	33	ARG
1	C	34	LEU
1	C	154	THR
1	C	159	ASN
1	C	164	VAL
1	C	175	ARG
1	C	189	LEU
1	C	195	ARG
1	C	206	ASP
1	C	224	LEU
1	C	236	THR
1	C	273	ILE
1	C	275	ASN
1	C	283	LEU
1	C	290	LEU
1	C	299	VAL
1	C	320	VAL
1	C	321	ARG
1	C	354	LYS
1	C	357	LEU
1	C	415	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	29	GLN
1	A	63	ASN
1	A	70	GLN
1	A	85	ASN
1	A	87	GLN
1	A	275	ASN
1	A	278	ASN
1	A	304	ASN

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Mol	Chain	Res	Type
1	B	29	GLN
1	B	63	ASN
1	B	70	GLN
1	B	85	ASN
1	B	87	GLN
1	B	275	ASN
1	B	276	ASN
1	C	29	GLN
1	C	63	ASN
1	C	70	GLN
1	C	85	ASN
1	C	87	GLN
1	C	275	ASN
1	C	278	ASN
1	C	304	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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

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 [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	421/427 (98%)	-0.89	5 (1%) 76 68	3, 15, 53, 107	5 (1%)
1	B	421/427 (98%)	-0.91	3 (0%) 84 77	3, 16, 55, 107	5 (1%)
1	C	421/427 (98%)	-0.93	4 (0%) 79 72	3, 16, 53, 107	5 (1%)
All	All	1263/1281 (98%)	-0.91	12 (0%) 79 72	3, 16, 55, 107	15 (1%)

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	157	SER	3.2
1	A	254	SER	2.9
1	A	257	THR	2.8
1	B	393	ASP	2.6
1	A	256	PHE	2.5
1	C	268	TYR	2.4
1	A	258	GLU	2.3
1	C	157	SER	2.3
1	C	394	ASN	2.1
1	A	391	ASP	2.1
1	B	258	GLU	2.1
1	C	404	SER	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](#)

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(Å ²)	Q<0.9
2	CA	A	428	1/1	0.94	0.02	25,25,25,25	0

6.5 Other polymers [i](#)

There are no such residues in this entry.