



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 11:26 PM UTC

PDB ID : 3WS0 / pdb_00003ws0
Title : N288Q-N321Q mutant BETA-LACTAMASE DERIVED FROM CHROMO-HALOBACTER SP.560 (Condition-1A)
Authors : Arai, S.; Yonezawa, Y.; Okazaki, N.; Matsumoto, F.; Shimizu, R.; Yamada, M.; Adachi, M.; Tamada, T.; Tokunaga, H.; Ishibashi, M.; Tokunaga, M.; Kuroki, R.
Deposited on : 2014-02-27
Resolution : 2.00 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

<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

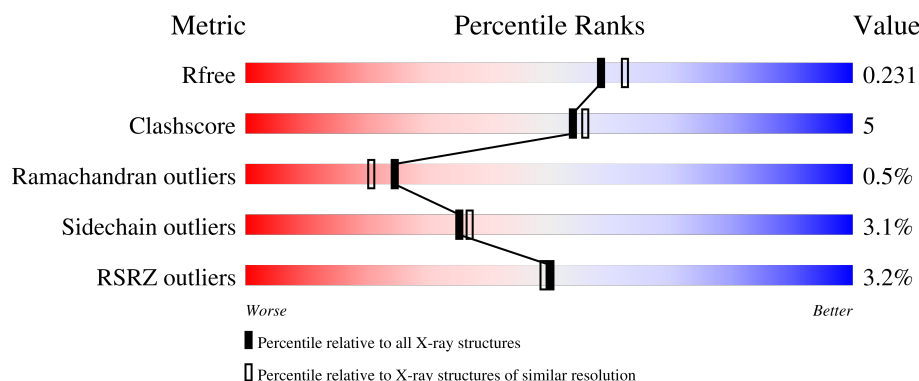
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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 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	367	3% 88% 8% ..
1	B	367	5% 88% 8% ..
1	C	367	2% 87% 8% ..

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8691 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 Beta-lactamase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	357	Total	C	N	O	S	0	0	0
			2704	1698	454	541	11			
1	B	357	Total	C	N	O	S	0	0	0
			2707	1698	457	541	11			
1	C	357	Total	C	N	O	S	0	0	0
			2703	1697	453	542	11			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	288	GLN	ASN	engineered mutation	UNP Q76LX5
A	321	GLN	ASN	engineered mutation	UNP Q76LX5
B	288	GLN	ASN	engineered mutation	UNP Q76LX5
B	321	GLN	ASN	engineered mutation	UNP Q76LX5
C	288	GLN	ASN	engineered mutation	UNP Q76LX5
C	321	GLN	ASN	engineered mutation	UNP Q76LX5

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	4	Total	Ca	0	0
			4	4		
2	B	3	Total	Ca	0	0
			3	3		
2	C	3	Total	Ca	0	0
			3	3		

- Molecule 3 is CESIUM ION (CCD ID: CS) (formula: Cs).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Cs	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	1	Total 1	Cs 1	0	0

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total 1	Cl 1	0	0
4	B	1	Total 1	Cl 1	0	0
4	C	2	Total 2	Cl 2	0	0

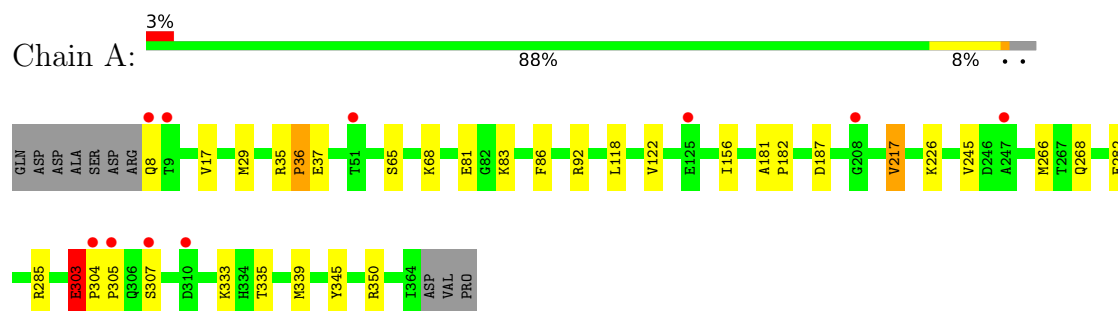
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	210	Total 210	O 210	0	0
5	B	127	Total 127	O 127	0	0
5	C	224	Total 224	O 224	0	0

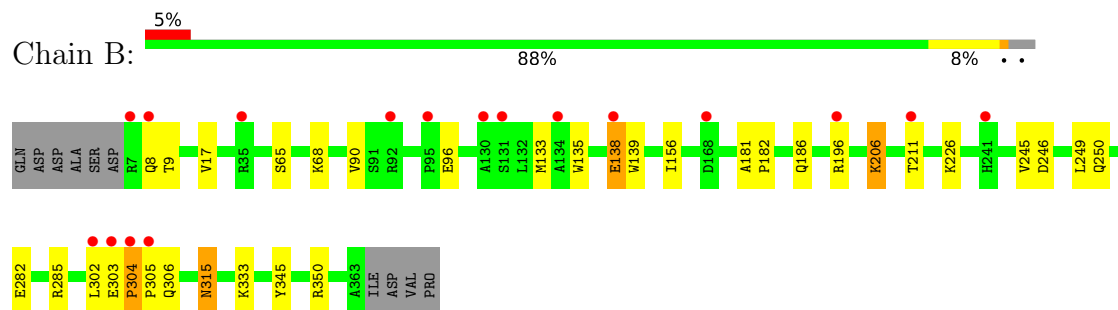
3 Residue-property plots [i](#)

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.

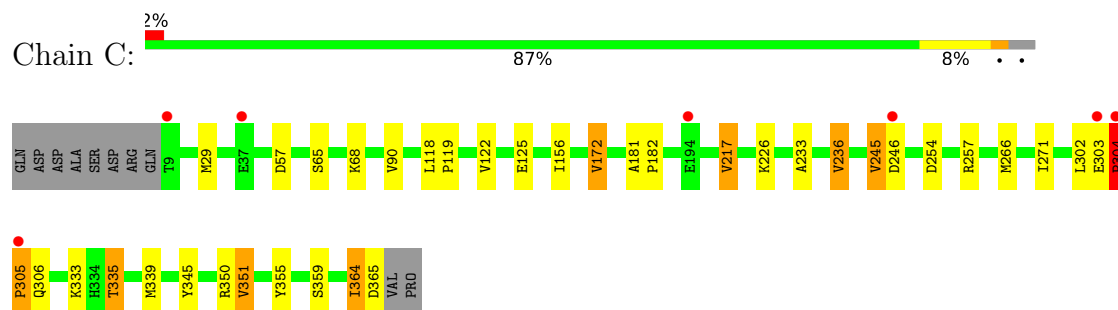
• Molecule 1: Beta-lactamase



• Molecule 1: Beta-lactamase



• Molecule 1: Beta-lactamase



4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	115.39Å 115.39Å 67.65Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.88 – 2.00 29.88 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.6 (29.88-2.00) 97.7 (29.88-2.00)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	7.67 (at 1.99Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.190 , 0.224 0.199 , 0.231	Depositor DCC
R_{free} test set	3389 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	23.5	Xtriage
Anisotropy	0.044	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 39.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.013 for -h,-k,l 0.022 for h,-h-k,-l 0.014 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8691	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.19% 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 ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: CS, CA, CL

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	0.67	0/2760	0.87	3/3764 (0.1%)
1	B	0.61	0/2763	0.84	0/3767
1	C	0.75	2/2759 (0.1%)	0.88	7/3763 (0.2%)
All	All	0.68	2/8282 (0.0%)	0.86	10/11294 (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	2
1	B	0	1
1	C	0	1
All	All	0	4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	245	VAL	C-N	14.60	1.53	1.33
1	C	246	ASP	C-N	8.94	1.45	1.33

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	303	GLU	CA-C-N	-11.39	108.65	120.38
1	A	303	GLU	C-N-CA	-11.39	108.65	120.38
1	C	245	VAL	CA-C-N	-10.52	98.95	121.45
1	C	245	VAL	C-N-CA	-10.52	98.95	121.45
1	C	303	GLU	CA-C-N	-6.77	113.41	120.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	303	GLU	C-N-CA	-6.77	113.41	120.38
1	A	36	PRO	N-CA-C	-6.30	102.32	111.33
1	C	245	VAL	O-C-N	6.25	129.89	122.95
1	C	351	VAL	N-CA-CB	5.51	118.03	110.54
1	C	172	VAL	N-CA-CB	5.03	118.26	111.21

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	303	GLU	Peptide
1	A	8	GLN	Peptide
1	B	8	GLN	Peptide
1	C	304	PRO	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	2704	0	2636	19	0
1	B	2707	0	2638	29	0
1	C	2703	0	2632	31	0
2	A	4	0	0	0	0
2	B	3	0	0	0	0
2	C	3	0	0	0	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	2	0	0	0	0
5	A	210	0	0	3	0
5	B	127	0	0	7	0
5	C	224	0	0	9	1
All	All	8691	0	7906	78	1

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 5.

All (78) 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:302:LEU:C	1:B:304:PRO:HD3	1.76	1.09
1:C:266:MET:HG2	5:C:688:HOH:O	1.51	1.07
1:C:305:PRO:HA	5:C:696:HOH:O	1.53	1.07
1:C:305:PRO:C	5:C:696:HOH:O	2.07	0.97
1:C:266:MET:HE3	5:C:688:HOH:O	1.73	0.87
1:B:304:PRO:HD2	1:B:305:PRO:HA	1.57	0.85
1:A:303:GLU:O	1:A:305:PRO:HD3	1.77	0.83
1:B:196:ARG:NH1	5:B:525:HOH:O	2.11	0.82
1:B:302:LEU:C	1:B:304:PRO:CD	2.54	0.81
1:C:304:PRO:O	1:C:305:PRO:O	2.07	0.73
1:B:135:TRP:O	1:B:138:GLU:OE1	2.06	0.72
1:A:303:GLU:O	1:A:305:PRO:CD	2.38	0.72
1:B:282:GLU:OE1	1:B:285:ARG:NH2	2.20	0.72
1:B:245:VAL:HG22	5:B:599:HOH:O	1.90	0.71
1:B:249:LEU:HB3	5:B:599:HOH:O	1.91	0.70
1:C:305:PRO:CA	5:C:696:HOH:O	2.17	0.69
1:A:266:MET:HE3	5:A:681:HOH:O	1.95	0.67
1:C:305:PRO:CB	1:C:306:GLN:HA	2.25	0.67
1:B:246:ASP:O	5:B:599:HOH:O	2.13	0.66
1:B:304:PRO:CD	1:B:305:PRO:HA	2.26	0.65
1:C:68:LYS:HE3	1:C:156:ILE:HG21	1.79	0.65
1:C:266:MET:CE	5:C:688:HOH:O	2.38	0.65
1:B:68:LYS:HE3	1:B:156:ILE:HG21	1.81	0.63
1:C:304:PRO:CD	1:C:305:PRO:HD3	2.28	0.63
1:A:68:LYS:HE3	1:A:156:ILE:HG21	1.80	0.62
1:B:302:LEU:O	1:B:304:PRO:HD3	1.98	0.62
1:C:304:PRO:HD2	1:C:305:PRO:HD3	1.83	0.60
1:B:250:GLN:N	5:B:599:HOH:O	2.34	0.60
1:A:92:ARG:HD3	1:B:186:GLN:OE1	2.01	0.60
1:B:303:GLU:N	1:B:304:PRO:CD	2.66	0.59
1:C:254:ASP:OD1	1:C:257:ARG:NH2	2.36	0.59
1:A:282:GLU:OE1	1:A:285:ARG:NH2	2.26	0.57
1:C:305:PRO:HB3	1:C:306:GLN:HA	1.86	0.57
1:C:302:LEU:C	1:C:305:PRO:HD2	2.30	0.56
1:A:36:PRO:O	1:A:37:GLU:CD	2.49	0.56
1:C:68:LYS:CE	1:C:156:ILE:HG21	2.36	0.55
1:C:305:PRO:CB	1:C:306:GLN:CA	2.84	0.55
1:B:304:PRO:HB2	1:B:305:PRO:C	2.32	0.53
1:B:245:VAL:HG13	5:B:599:HOH:O	2.08	0.53
1:B:138:GLU:OE1	1:B:139:TRP:N	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:68:LYS:CE	1:B:156:ILE:HG21	2.39	0.51
1:B:304:PRO:HG2	1:B:306:GLN:N	2.26	0.51
1:A:68:LYS:CE	1:A:156:ILE:HG21	2.41	0.50
1:C:65:SER:OG	1:C:68:LYS:NZ	2.45	0.50
1:C:335:THR:HG21	5:C:669:HOH:O	2.10	0.50
1:B:206:LYS:NZ	5:B:569:HOH:O	1.98	0.50
1:A:122:VAL:HG11	1:A:217:VAL:HG22	1.94	0.49
1:A:268:GLN:HA	5:A:681:HOH:O	2.12	0.49
1:C:359:SER:HB3	1:C:364:ILE:HD11	1.94	0.49
1:B:245:VAL:CG2	1:B:249:LEU:HD23	2.42	0.48
1:C:122:VAL:HG11	1:C:217:VAL:HG22	1.96	0.47
1:B:65:SER:OG	1:B:68:LYS:NZ	2.48	0.47
1:A:35:ARG:C	1:A:36:PRO:O	2.55	0.46
1:B:206:LYS:HA	1:B:206:LYS:HD2	1.66	0.46
1:A:81:GLU:OE1	1:A:83:LYS:HE2	2.15	0.46
1:B:181:ALA:HB3	1:B:182:PRO:HD3	1.98	0.46
1:A:36:PRO:O	1:A:37:GLU:CG	2.64	0.46
1:C:181:ALA:HB3	1:C:182:PRO:HD3	1.98	0.46
1:A:181:ALA:HB3	1:A:182:PRO:HD3	1.99	0.45
1:A:65:SER:OG	1:A:68:LYS:NZ	2.49	0.45
1:C:345:TYR:CZ	1:C:350:ARG:HG2	2.52	0.45
1:C:355:TYR:CZ	1:C:364:ILE:HD13	2.53	0.44
1:C:29:MET:HE1	1:C:339:MET:HE2	1.99	0.43
1:A:29:MET:HE1	1:A:339:MET:HE2	2.00	0.43
1:C:226:LYS:N	1:C:226:LYS:HD3	2.33	0.43
1:C:364:ILE:HD12	1:C:365:ASP:HB2	1.99	0.43
1:A:83:LYS:HE3	5:A:696:HOH:O	2.19	0.42
1:B:226:LYS:N	1:B:226:LYS:HD2	2.34	0.42
1:C:233:ALA:HA	1:C:236:VAL:HG13	2.01	0.42
1:A:226:LYS:N	1:A:226:LYS:HD2	2.34	0.42
1:C:306:GLN:N	5:C:696:HOH:O	2.40	0.42
1:A:345:TYR:CZ	1:A:350:ARG:HG2	2.55	0.41
1:B:315:ASN:C	1:B:315:ASN:HD22	2.27	0.41
1:C:57:ASP:HB2	5:C:700:HOH:O	2.20	0.41
1:B:345:TYR:CZ	1:B:350:ARG:HG2	2.55	0.41
1:B:96:GLU:OE2	1:B:133:MET:HE2	2.21	0.41
1:C:118:LEU:HA	1:C:119:PRO:HD3	1.89	0.40
1:C:156:ILE:HD13	1:C:271:ILE:HD11	2.04	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:530:HOH:O	5:C:707:HOH:O[2_555]	2.19	0.01

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	355/367 (97%)	345 (97%)	9 (2%)	1 (0%)	36	35
1	B	355/367 (97%)	346 (98%)	7 (2%)	2 (1%)	21	17
1	C	355/367 (97%)	347 (98%)	6 (2%)	2 (1%)	21	17
All	All	1065/1101 (97%)	1038 (98%)	22 (2%)	5 (0%)	24	21

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	305	PRO
1	B	9	THR
1	B	304	PRO
1	C	304	PRO
1	A	304	PRO

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	283/292 (97%)	274 (97%)	9 (3%)	34	35
1	B	283/292 (97%)	276 (98%)	7 (2%)	42	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	283/292 (97%)	273 (96%)	10 (4%)	32	32
All	All	849/876 (97%)	823 (97%)	26 (3%)	35	37

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	VAL
1	A	86	PHE
1	A	118	LEU
1	A	187	ASP
1	A	217	VAL
1	A	245	VAL
1	A	307	SER
1	A	333	LYS
1	A	335	THR
1	B	17	VAL
1	B	90	VAL
1	B	138	GLU
1	B	206	LYS
1	B	211	THR
1	B	315	ASN
1	B	333	LYS
1	C	90	VAL
1	C	125	GLU
1	C	172	VAL
1	C	217	VAL
1	C	236	VAL
1	C	245	VAL
1	C	333	LYS
1	C	335	THR
1	C	351	VAL
1	C	364	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	140	GLN
1	A	315	ASN
1	B	8	GLN
1	B	140	GLN
1	B	260	HIS

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Mol	Chain	Res	Type
1	C	209	GLN
1	C	315	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 16 ligands modelled in this entry, 16 are 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 ⓘ

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	357/367 (97%)	0.06	10 (2%) 55 54	14, 26, 46, 67	0
1	B	357/367 (97%)	0.40	17 (4%) 35 34	22, 33, 55, 82	0
1	C	357/367 (97%)	-0.05	7 (1%) 65 64	14, 24, 41, 65	0
All	All	1071/1101 (97%)	0.14	34 (3%) 50 49	14, 28, 51, 82	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	304	PRO	4.9
1	C	305	PRO	4.8
1	A	304	PRO	3.8
1	C	304	PRO	3.5
1	A	310	ASP	3.3
1	B	8	GLN	3.2
1	B	7	ARG	3.0
1	A	8	GLN	2.9
1	B	305	PRO	2.9
1	B	302	LEU	2.8
1	A	307	SER	2.8
1	B	35	ARG	2.8
1	B	138	GLU	2.7
1	A	125	GLU	2.7
1	B	130	ALA	2.7
1	B	134	ALA	2.7
1	B	92	ARG	2.7
1	A	9	THR	2.6
1	C	246	ASP	2.5
1	C	37	GLU	2.5
1	A	247	ALA	2.5
1	A	208	GLY	2.4
1	B	303	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	196	ARG	2.3
1	C	194	GLU	2.2
1	B	131	SER	2.2
1	A	51	THR	2.2
1	B	95	PRO	2.2
1	B	168	ASP	2.2
1	C	303	GLU	2.1
1	B	211	THR	2.1
1	C	9	THR	2.1
1	A	305	PRO	2.1
1	B	241	HIS	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	402	1/1	0.85	0.09	55,55,55,55	0
2	CA	B	401	1/1	0.92	0.07	41,41,41,41	0
2	CA	C	402	1/1	0.93	0.29	30,30,30,30	0
2	CA	B	402	1/1	0.95	0.05	43,43,43,43	0
2	CA	C	401	1/1	0.96	0.06	35,35,35,35	0
4	CL	B	404	1/1	0.96	0.07	42,42,42,42	0
2	CA	B	403	1/1	0.97	0.03	36,36,36,36	0
4	CL	C	405	1/1	0.97	0.04	26,26,26,26	0
2	CA	A	401	1/1	0.98	0.05	28,28,28,28	0
4	CL	A	406	1/1	0.98	0.06	33,33,33,33	0
2	CA	A	403	1/1	0.99	0.04	29,29,29,29	0
2	CA	C	403	1/1	0.99	0.03	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	CS	C	404	1/1	0.99	0.27	62,62,62,62	0
4	CL	C	406	1/1	0.99	0.06	29,29,29,29	0
3	CS	A	405	1/1	1.00	0.09	36,36,36,36	0
2	CA	A	404	1/1	1.00	0.04	25,25,25,25	0

6.5 Other polymers [i](#)

There are no such residues in this entry.