



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:02 AM UTC

PDB ID : 9FI4 / pdb_00009fi4
Title : Bacteroides ovatus polysaccharide lyase family 38 (BoPL38) mutant Q173N at pH 8
Authors : Tandrup, T.; Wilkens, C.
Deposited on : 2024-05-28
Resolution : 2.47 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

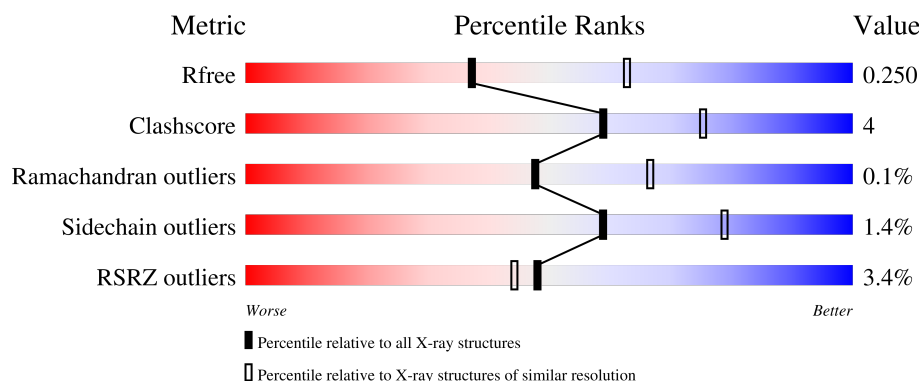
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.47 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	7589 (2.50-2.46)
Clashscore	190562	8295 (2.50-2.46)
Ramachandran outliers	187476	8164 (2.50-2.46)
Sidechain outliers	187428	8166 (2.50-2.46)
RSRZ outliers	180081	7593 (2.50-2.46)

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	404	
1	B	404	
1	C	404	
1	D	404	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12479 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 Alginate lyase family protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	380	Total	C	N	O	S	0	0	0
			3051	1951	516	571	13			
1	B	380	Total	C	N	O	S	0	0	0
			3051	1951	516	571	13			
1	C	380	Total	C	N	O	S	0	0	0
			3051	1951	516	571	13			
1	D	380	Total	C	N	O	S	0	0	0
			3051	1951	516	571	13			

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP A0A5M5BWR5
A	2	GLY	-	expression tag	UNP A0A5M5BWR5
A	3	SER	-	expression tag	UNP A0A5M5BWR5
A	4	SER	-	expression tag	UNP A0A5M5BWR5
A	5	HIS	-	expression tag	UNP A0A5M5BWR5
A	6	HIS	-	expression tag	UNP A0A5M5BWR5
A	7	HIS	-	expression tag	UNP A0A5M5BWR5
A	8	HIS	-	expression tag	UNP A0A5M5BWR5
A	9	HIS	-	expression tag	UNP A0A5M5BWR5
A	10	HIS	-	expression tag	UNP A0A5M5BWR5
A	11	SER	-	expression tag	UNP A0A5M5BWR5
A	12	SER	-	expression tag	UNP A0A5M5BWR5
A	13	GLY	-	expression tag	UNP A0A5M5BWR5
A	14	LEU	-	expression tag	UNP A0A5M5BWR5
A	15	VAL	-	expression tag	UNP A0A5M5BWR5
A	16	PRO	-	expression tag	UNP A0A5M5BWR5
A	17	ARG	-	expression tag	UNP A0A5M5BWR5
A	18	GLY	-	expression tag	UNP A0A5M5BWR5
A	19	SER	-	expression tag	UNP A0A5M5BWR5
A	20	HIS	-	expression tag	UNP A0A5M5BWR5
A	21	MET	-	expression tag	UNP A0A5M5BWR5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	22	ALA	-	expression tag	UNP A0A5M5BWR5
A	23	SER	-	expression tag	UNP A0A5M5BWR5
A	173	ASN	GLN	engineered mutation	UNP A0A5M5BWR5
B	1	MET	-	initiating methionine	UNP A0A5M5BWR5
B	2	GLY	-	expression tag	UNP A0A5M5BWR5
B	3	SER	-	expression tag	UNP A0A5M5BWR5
B	4	SER	-	expression tag	UNP A0A5M5BWR5
B	5	HIS	-	expression tag	UNP A0A5M5BWR5
B	6	HIS	-	expression tag	UNP A0A5M5BWR5
B	7	HIS	-	expression tag	UNP A0A5M5BWR5
B	8	HIS	-	expression tag	UNP A0A5M5BWR5
B	9	HIS	-	expression tag	UNP A0A5M5BWR5
B	10	HIS	-	expression tag	UNP A0A5M5BWR5
B	11	SER	-	expression tag	UNP A0A5M5BWR5
B	12	SER	-	expression tag	UNP A0A5M5BWR5
B	13	GLY	-	expression tag	UNP A0A5M5BWR5
B	14	LEU	-	expression tag	UNP A0A5M5BWR5
B	15	VAL	-	expression tag	UNP A0A5M5BWR5
B	16	PRO	-	expression tag	UNP A0A5M5BWR5
B	17	ARG	-	expression tag	UNP A0A5M5BWR5
B	18	GLY	-	expression tag	UNP A0A5M5BWR5
B	19	SER	-	expression tag	UNP A0A5M5BWR5
B	20	HIS	-	expression tag	UNP A0A5M5BWR5
B	21	MET	-	expression tag	UNP A0A5M5BWR5
B	22	ALA	-	expression tag	UNP A0A5M5BWR5
B	23	SER	-	expression tag	UNP A0A5M5BWR5
B	173	ASN	GLN	engineered mutation	UNP A0A5M5BWR5
C	1	MET	-	initiating methionine	UNP A0A5M5BWR5
C	2	GLY	-	expression tag	UNP A0A5M5BWR5
C	3	SER	-	expression tag	UNP A0A5M5BWR5
C	4	SER	-	expression tag	UNP A0A5M5BWR5
C	5	HIS	-	expression tag	UNP A0A5M5BWR5
C	6	HIS	-	expression tag	UNP A0A5M5BWR5
C	7	HIS	-	expression tag	UNP A0A5M5BWR5
C	8	HIS	-	expression tag	UNP A0A5M5BWR5
C	9	HIS	-	expression tag	UNP A0A5M5BWR5
C	10	HIS	-	expression tag	UNP A0A5M5BWR5
C	11	SER	-	expression tag	UNP A0A5M5BWR5
C	12	SER	-	expression tag	UNP A0A5M5BWR5
C	13	GLY	-	expression tag	UNP A0A5M5BWR5
C	14	LEU	-	expression tag	UNP A0A5M5BWR5
C	15	VAL	-	expression tag	UNP A0A5M5BWR5

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Chain	Residue	Modelled	Actual	Comment	Reference
C	16	PRO	-	expression tag	UNP A0A5M5BWR5
C	17	ARG	-	expression tag	UNP A0A5M5BWR5
C	18	GLY	-	expression tag	UNP A0A5M5BWR5
C	19	SER	-	expression tag	UNP A0A5M5BWR5
C	20	HIS	-	expression tag	UNP A0A5M5BWR5
C	21	MET	-	expression tag	UNP A0A5M5BWR5
C	22	ALA	-	expression tag	UNP A0A5M5BWR5
C	23	SER	-	expression tag	UNP A0A5M5BWR5
C	173	ASN	GLN	engineered mutation	UNP A0A5M5BWR5
D	1	MET	-	initiating methionine	UNP A0A5M5BWR5
D	2	GLY	-	expression tag	UNP A0A5M5BWR5
D	3	SER	-	expression tag	UNP A0A5M5BWR5
D	4	SER	-	expression tag	UNP A0A5M5BWR5
D	5	HIS	-	expression tag	UNP A0A5M5BWR5
D	6	HIS	-	expression tag	UNP A0A5M5BWR5
D	7	HIS	-	expression tag	UNP A0A5M5BWR5
D	8	HIS	-	expression tag	UNP A0A5M5BWR5
D	9	HIS	-	expression tag	UNP A0A5M5BWR5
D	10	HIS	-	expression tag	UNP A0A5M5BWR5
D	11	SER	-	expression tag	UNP A0A5M5BWR5
D	12	SER	-	expression tag	UNP A0A5M5BWR5
D	13	GLY	-	expression tag	UNP A0A5M5BWR5
D	14	LEU	-	expression tag	UNP A0A5M5BWR5
D	15	VAL	-	expression tag	UNP A0A5M5BWR5
D	16	PRO	-	expression tag	UNP A0A5M5BWR5
D	17	ARG	-	expression tag	UNP A0A5M5BWR5
D	18	GLY	-	expression tag	UNP A0A5M5BWR5
D	19	SER	-	expression tag	UNP A0A5M5BWR5
D	20	HIS	-	expression tag	UNP A0A5M5BWR5
D	21	MET	-	expression tag	UNP A0A5M5BWR5
D	22	ALA	-	expression tag	UNP A0A5M5BWR5
D	23	SER	-	expression tag	UNP A0A5M5BWR5
D	173	ASN	GLN	engineered mutation	UNP A0A5M5BWR5

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	83	Total O 83 83	0	0
2	B	76	Total O 76 76	0	0
2	C	56	Total O 56 56	0	0

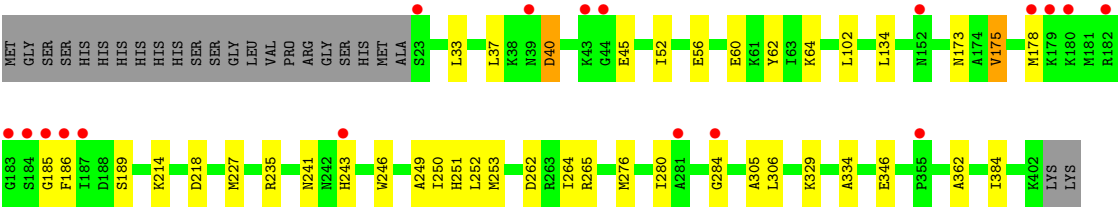
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	60	Total	O	0	0
			60	60		

- Molecule 1: Alginate lyase family protein





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	197.15Å 88.79Å 146.17Å 90.00° 120.25° 90.00°	Depositor
Resolution (Å)	48.72 – 2.47 48.72 – 2.47	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.72-2.47) 99.9 (48.72-2.47)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.86 (at 2.48Å)	Xtriage
Refinement program	PHENIX 1.21_5207	Depositor
R, R_{free}	0.205 , 0.250 0.206 , 0.250	Depositor DCC
R_{free} test set	3898 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	43.6	Xtriage
Anisotropy	0.055	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 39.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	12479	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.94% 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	0.42	0/3129	0.58	0/4241
1	B	0.39	0/3129	0.56	0/4241
1	C	0.40	1/3129 (0.0%)	0.58	1/4241 (0.0%)
1	D	0.34	0/3129	0.53	0/4241
All	All	0.39	1/12516 (0.0%)	0.56	1/16964 (0.0%)

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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	50	ARG	CD-NE	-5.82	1.38	1.46

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	50	ARG	CD-NE-CZ	-7.27	114.22	124.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	182	ARG	Sidechain

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	3051	0	3020	28	0
1	B	3051	0	3020	16	0
1	C	3051	0	3020	33	0
1	D	3051	0	3020	30	0
2	A	83	0	0	3	0
2	B	76	0	0	1	0
2	C	56	0	0	2	0
2	D	60	0	0	1	0
All	All	12479	0	12080	107	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 4.

All (107) 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:54:LEU:N	2:C:501:HOH:O	2.18	0.76
1:C:390:THR:HG22	1:C:392:ASP:H	1.50	0.75
1:B:336:ASP:OD1	1:B:377:TYR:OH	2.06	0.73
1:C:70:VAL:HG23	1:C:120:GLU:HG2	1.77	0.67
1:D:173:ASN:ND2	1:D:185:GLY:HA2	2.12	0.65
1:C:336:ASP:OD1	1:C:377:TYR:OH	2.14	0.64
1:B:252:LEU:HD22	1:B:264:ILE:HG23	1.79	0.64
1:A:252:LEU:HD22	1:A:264:ILE:HG23	1.80	0.62
1:C:265:ARG:HG3	1:C:318:ILE:HD11	1.82	0.61
1:C:173:ASN:OD1	1:C:185:GLY:HA2	2.02	0.59
1:A:336:ASP:OD1	1:A:377:TYR:OH	2.21	0.59
1:A:191:ARG:HD2	2:A:506:HOH:O	2.03	0.58
1:D:252:LEU:HD22	1:D:264:ILE:HG23	1.86	0.58
1:C:186:PHE:CZ	1:C:227:MET:HG2	2.41	0.55
1:C:54:LEU:HD21	1:C:389:SER:HA	1.89	0.54
1:A:228:GLU:OE2	1:A:251:HIS:NE2	2.38	0.54
1:A:186:PHE:HA	2:A:536:HOH:O	2.08	0.54
1:C:307:MET:HB2	1:C:321:TRP:HZ2	1.73	0.54
1:B:388:TYR:HA	1:B:402:LYS:HB3	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:89:SER:HG	1:C:92:TRP:CD1	2.26	0.53
1:A:70:VAL:HG23	1:A:120:GLU:HG2	1.89	0.53
1:A:187:ILE:HG22	1:A:190:ARG:NH1	2.23	0.53
1:D:214:LYS:HE2	1:D:218:ASP:OD2	2.09	0.53
1:C:386:LEU:HD13	1:C:395:THR:HB	1.92	0.52
1:D:276:MET:HE3	1:D:306:LEU:HD13	1.92	0.52
1:C:79:SER:O	1:C:80:LYS:HE3	2.10	0.51
1:A:51:TYR:CD1	1:A:399:LEU:HD13	2.46	0.50
1:D:186:PHE:HZ	1:D:227:MET:HE3	1.76	0.50
1:D:189:SER:HB2	1:D:250:ILE:HD13	1.94	0.50
1:C:173:ASN:HB2	1:C:185:GLY:HA2	1.94	0.50
1:A:265:ARG:HG3	1:A:318:ILE:HD11	1.95	0.49
1:B:190:ARG:O	1:B:194:ARG:HG3	2.11	0.49
1:D:173:ASN:HB2	1:D:185:GLY:HA2	1.94	0.49
1:D:40:ASP:OD1	1:D:40:ASP:N	2.46	0.49
1:A:180:LYS:O	1:A:181:MET:C	2.55	0.48
1:A:175:VAL:CG1	1:A:178:MET:HG2	2.44	0.48
1:C:186:PHE:CZ	1:C:227:MET:HE3	2.48	0.48
1:C:190:ARG:O	1:C:194:ARG:HG3	2.13	0.47
1:A:276:MET:HE2	1:A:276:MET:HB2	1.66	0.47
1:D:280:ILE:HG22	1:D:329:LYS:HD2	1.96	0.47
1:C:79:SER:C	1:C:80:LYS:HE3	2.38	0.47
1:B:38:LYS:HE2	1:B:139:TYR:O	2.13	0.47
1:A:255:LEU:HD13	1:A:263:ARG:HB3	1.97	0.47
1:D:60:GLU:HG3	1:D:64:LYS:HE3	1.96	0.47
1:D:250:ILE:HA	1:D:253:MET:HE3	1.96	0.47
1:D:173:ASN:HD22	1:D:185:GLY:HA2	1.80	0.46
1:C:186:PHE:CE2	1:C:227:MET:HG2	2.51	0.46
1:D:186:PHE:CZ	1:D:227:MET:HG2	2.51	0.46
1:D:62:TYR:HB3	1:D:134:LEU:HD11	1.97	0.46
1:D:175:VAL:CG2	1:D:178:MET:HG3	2.46	0.46
1:D:284:GLY:O	1:D:334:ALA:HA	2.15	0.46
1:C:200:LYS:HE2	1:C:257:TYR:O	2.16	0.46
1:D:186:PHE:CZ	1:D:227:MET:HE3	2.50	0.46
1:D:276:MET:HA	1:D:276:MET:HE2	1.97	0.46
1:A:175:VAL:HG12	1:A:178:MET:HG2	1.97	0.46
1:C:283:ASP:OD1	1:C:283:ASP:N	2.50	0.45
1:D:241:ASN:OD1	1:D:243:HIS:HB2	2.16	0.45
1:C:89:SER:HA	1:C:173:ASN:HD22	1.81	0.45
1:C:189:SER:HB2	1:C:250:ILE:HD13	1.98	0.45
1:D:265:ARG:HD3	2:D:529:HOH:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:188:ASP:OD1	1:B:188:ASP:N	2.50	0.45
1:A:182:ARG:NH2	1:A:231:THR:HG21	2.31	0.44
1:D:276:MET:CE	1:D:306:LEU:HD13	2.48	0.44
1:B:180:LYS:HE2	1:B:180:LYS:HB2	1.79	0.44
1:C:227:MET:HE2	1:C:227:MET:HB3	1.88	0.44
1:D:227:MET:HE1	1:D:251:HIS:HA	1.98	0.44
1:D:235:ARG:HH11	1:D:235:ARG:HG3	1.82	0.44
1:A:284:GLY:O	1:A:334:ALA:HA	2.18	0.44
1:C:60:GLU:O	1:C:64:LYS:HG3	2.16	0.44
1:C:50:ARG:HH11	1:C:50:ARG:HD3	1.48	0.44
1:A:73:LYS:HE3	1:A:77:PRO:HD3	2.00	0.44
1:C:173:ASN:HB2	1:C:185:GLY:CA	2.48	0.44
1:C:182:ARG:HA	1:C:182:ARG:HD2	1.83	0.44
1:C:248:GLU:HA	1:C:248:GLU:OE1	2.17	0.44
1:A:389:SER:HB2	2:B:501:HOH:O	2.17	0.43
1:A:149:ALA:O	1:A:153:HIS:HD2	2.00	0.43
1:B:181:MET:O	1:B:182:ARG:HD3	2.18	0.43
1:B:276:MET:SD	1:B:306:LEU:HD13	2.59	0.43
1:B:265:ARG:HG3	1:B:318:ILE:HD11	1.99	0.43
1:A:165:MET:HE1	1:A:192:PHE:CZ	2.54	0.43
1:A:85:TYR:CE2	1:A:120:GLU:HB3	2.54	0.42
1:B:52:ILE:O	1:B:56:GLU:HG3	2.19	0.42
1:C:262:ASP:HB2	2:C:553:HOH:O	2.18	0.42
1:A:188:ASP:CG	2:A:536:HOH:O	2.61	0.42
1:C:38:LYS:O	1:C:42:GLN:HG3	2.20	0.42
1:D:249:ALA:O	1:D:253:MET:HG3	2.20	0.42
1:A:178:MET:HG3	1:A:181:MET:SD	2.60	0.42
1:C:352:GLN:HG3	1:C:354:LYS:O	2.20	0.42
1:D:262:ASP:OD1	1:D:262:ASP:N	2.53	0.42
1:B:70:VAL:HG23	1:B:120:GLU:HG2	2.01	0.41
1:B:129:ASP:HA	1:B:393:VAL:HG21	2.02	0.41
1:A:231:THR:O	1:A:235:ARG:HG3	2.20	0.41
1:A:347:ASP:O	1:A:349:LYS:HG2	2.20	0.41
1:B:179:LYS:H	1:B:179:LYS:HG3	1.68	0.41
1:A:125:ASN:OD1	1:A:191:ARG:HD3	2.20	0.41
1:B:307:MET:HB2	1:B:321:TRP:HZ2	1.86	0.41
1:C:351:LYS:HB2	1:C:351:LYS:HE3	1.90	0.41
1:D:246:TRP:CE2	1:D:305:ALA:HB2	2.55	0.41
1:A:330:VAL:HG23	1:A:333:GLN:HG3	2.03	0.41
1:C:339:TYR:CE2	1:C:376:LYS:HE3	2.56	0.41
1:D:33:LEU:O	1:D:37:LEU:HD13	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:173:ASN:HB2	1:D:185:GLY:CA	2.50	0.41
1:D:52:ILE:O	1:D:56:GLU:HG3	2.21	0.40
1:A:118:TYR:CD1	1:A:118:TYR:N	2.90	0.40
1:C:186:PHE:HZ	1:C:227:MET:HG2	1.85	0.40
1:B:138:TYR:CD1	1:B:147:ALA:HB2	2.57	0.40
1:D:362:ALA:HB2	1:D:384:ILE:HG22	2.04	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	378/404 (94%)	364 (96%)	12 (3%)	2 (0%)	24	40
1	B	378/404 (94%)	364 (96%)	14 (4%)	0	100	100
1	C	378/404 (94%)	369 (98%)	9 (2%)	0	100	100
1	D	378/404 (94%)	367 (97%)	11 (3%)	0	100	100
All	All	1512/1616 (94%)	1464 (97%)	46 (3%)	2 (0%)	48	66

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	179	LYS
1	A	181	MET

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	324/344 (94%)	320 (99%)	4 (1%)	63	81
1	B	324/344 (94%)	318 (98%)	6 (2%)	50	73
1	C	324/344 (94%)	321 (99%)	3 (1%)	70	86
1	D	324/344 (94%)	319 (98%)	5 (2%)	57	78
All	All	1296/1376 (94%)	1278 (99%)	18 (1%)	59	79

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	SER
1	A	45	GLU
1	A	198	VAL
1	A	211	SER
1	B	39	ASN
1	B	70	VAL
1	B	98	LYS
1	B	180	LYS
1	B	188	ASP
1	B	265	ARG
1	C	49	THR
1	C	80	LYS
1	C	347	ASP
1	D	40	ASP
1	D	45	GLU
1	D	102	LEU
1	D	175	VAL
1	D	346	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	358	GLN
1	C	152	ASN
1	C	242	ASN
1	C	243	HIS
1	C	358	GLN
1	D	42	GLN
1	D	173	ASN

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Mol	Chain	Res	Type
1	D	229	ASN
1	D	344	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 ⓘ

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	380/404 (94%)	0.03	10 (2%) 57 53	30, 43, 65, 100	0
1	B	380/404 (94%)	0.05	10 (2%) 57 53	29, 44, 64, 115	0
1	C	380/404 (94%)	0.18	13 (3%) 48 44	30, 46, 70, 130	0
1	D	380/404 (94%)	0.40	18 (4%) 36 32	30, 53, 78, 114	0
All	All	1520/1616 (94%)	0.17	51 (3%) 48 44	29, 45, 72, 130	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	181	MET	5.1
1	D	187	ILE	4.5
1	B	183	GLY	4.4
1	B	180	LYS	4.2
1	D	179	LYS	4.2
1	C	179	LYS	4.1
1	A	181	MET	4.1
1	A	180	LYS	3.9
1	C	183	GLY	3.9
1	D	178	MET	3.7
1	C	185	GLY	3.7
1	B	179	LYS	3.6
1	D	182	ARG	3.5
1	B	182	ARG	3.4
1	C	182	ARG	3.4
1	B	186	PHE	3.3
1	D	180	LYS	3.3
1	C	184	SER	3.1
1	D	183	GLY	3.0
1	D	184	SER	2.9
1	D	43	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
1	D	185	GLY	2.8
1	A	182	ARG	2.8
1	C	74	LYS	2.8
1	D	186	PHE	2.8
1	A	23	SER	2.8
1	D	355	PRO	2.7
1	C	180	LYS	2.7
1	C	291	LYS	2.7
1	A	179	LYS	2.7
1	D	284	GLY	2.5
1	C	186	PHE	2.5
1	B	50	ARG	2.5
1	B	178	MET	2.5
1	C	50	ARG	2.4
1	A	276	MET	2.4
1	A	50	ARG	2.4
1	D	243	HIS	2.3
1	B	187	ILE	2.3
1	A	183	GLY	2.3
1	C	383	ARG	2.2
1	D	39	ASN	2.2
1	D	23	SER	2.1
1	D	281	ALA	2.1
1	B	46	LYS	2.1
1	C	99	ILE	2.1
1	C	259	ASP	2.1
1	D	152	ASN	2.1
1	A	346	GLU	2.0
1	A	43	LYS	2.0
1	D	44	GLY	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.