



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 10:05 AM UTC

PDB ID : 8IXP / pdb_00008ixp
Title : Apo structure of glycosyltransferase LmbT wild type
Authors : Mori, T.; Sun, X.; Abe, I.
Deposited on : 2023-04-02
Resolution : 2.45 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

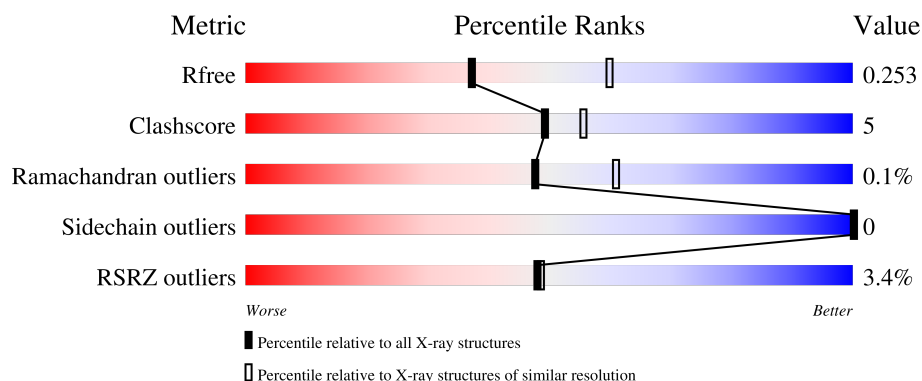
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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	1190 (2.46-2.46)
Clashscore	190562	1229 (2.46-2.46)
Ramachandran outliers	187476	1218 (2.46-2.46)
Sidechain outliers	187428	1218 (2.46-2.46)
RSRZ outliers	180081	1190 (2.46-2.46)

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	451	3% 82% 13% 5%
1	B	451	3% 81% 14% 5%
1	C	451	6% 82% 12% 7%
1	D	451	% 82% 12% 5%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12992 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 Glycosyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	429	Total	C	N	O	S	0	0	0
			3205	2012	590	596	7			
1	B	429	Total	C	N	O	S	0	0	0
			3213	2014	596	596	7			
1	C	421	Total	C	N	O	S	0	0	0
			3091	1944	563	577	7			
1	D	428	Total	C	N	O	S	0	0	0
			3206	2010	594	595	7			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	437	LYS	-	expression tag	UNP A9Y8T1
A	438	LEU	-	expression tag	UNP A9Y8T1
A	439	ALA	-	expression tag	UNP A9Y8T1
A	440	ALA	-	expression tag	UNP A9Y8T1
A	441	ALA	-	expression tag	UNP A9Y8T1
A	442	LEU	-	expression tag	UNP A9Y8T1
A	443	GLU	-	expression tag	UNP A9Y8T1
A	444	HIS	-	expression tag	UNP A9Y8T1
A	445	HIS	-	expression tag	UNP A9Y8T1
A	446	HIS	-	expression tag	UNP A9Y8T1
A	447	HIS	-	expression tag	UNP A9Y8T1
A	448	HIS	-	expression tag	UNP A9Y8T1
A	449	HIS	-	expression tag	UNP A9Y8T1
A	450	HIS	-	expression tag	UNP A9Y8T1
A	451	HIS	-	expression tag	UNP A9Y8T1
B	437	LYS	-	expression tag	UNP A9Y8T1
B	438	LEU	-	expression tag	UNP A9Y8T1
B	439	ALA	-	expression tag	UNP A9Y8T1
B	440	ALA	-	expression tag	UNP A9Y8T1
B	441	ALA	-	expression tag	UNP A9Y8T1
B	442	LEU	-	expression tag	UNP A9Y8T1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	443	GLU	-	expression tag	UNP A9Y8T1
B	444	HIS	-	expression tag	UNP A9Y8T1
B	445	HIS	-	expression tag	UNP A9Y8T1
B	446	HIS	-	expression tag	UNP A9Y8T1
B	447	HIS	-	expression tag	UNP A9Y8T1
B	448	HIS	-	expression tag	UNP A9Y8T1
B	449	HIS	-	expression tag	UNP A9Y8T1
B	450	HIS	-	expression tag	UNP A9Y8T1
B	451	HIS	-	expression tag	UNP A9Y8T1
C	437	LYS	-	expression tag	UNP A9Y8T1
C	438	LEU	-	expression tag	UNP A9Y8T1
C	439	ALA	-	expression tag	UNP A9Y8T1
C	440	ALA	-	expression tag	UNP A9Y8T1
C	441	ALA	-	expression tag	UNP A9Y8T1
C	442	LEU	-	expression tag	UNP A9Y8T1
C	443	GLU	-	expression tag	UNP A9Y8T1
C	444	HIS	-	expression tag	UNP A9Y8T1
C	445	HIS	-	expression tag	UNP A9Y8T1
C	446	HIS	-	expression tag	UNP A9Y8T1
C	447	HIS	-	expression tag	UNP A9Y8T1
C	448	HIS	-	expression tag	UNP A9Y8T1
C	449	HIS	-	expression tag	UNP A9Y8T1
C	450	HIS	-	expression tag	UNP A9Y8T1
C	451	HIS	-	expression tag	UNP A9Y8T1
D	437	LYS	-	expression tag	UNP A9Y8T1
D	438	LEU	-	expression tag	UNP A9Y8T1
D	439	ALA	-	expression tag	UNP A9Y8T1
D	440	ALA	-	expression tag	UNP A9Y8T1
D	441	ALA	-	expression tag	UNP A9Y8T1
D	442	LEU	-	expression tag	UNP A9Y8T1
D	443	GLU	-	expression tag	UNP A9Y8T1
D	444	HIS	-	expression tag	UNP A9Y8T1
D	445	HIS	-	expression tag	UNP A9Y8T1
D	446	HIS	-	expression tag	UNP A9Y8T1
D	447	HIS	-	expression tag	UNP A9Y8T1
D	448	HIS	-	expression tag	UNP A9Y8T1
D	449	HIS	-	expression tag	UNP A9Y8T1
D	450	HIS	-	expression tag	UNP A9Y8T1
D	451	HIS	-	expression tag	UNP A9Y8T1

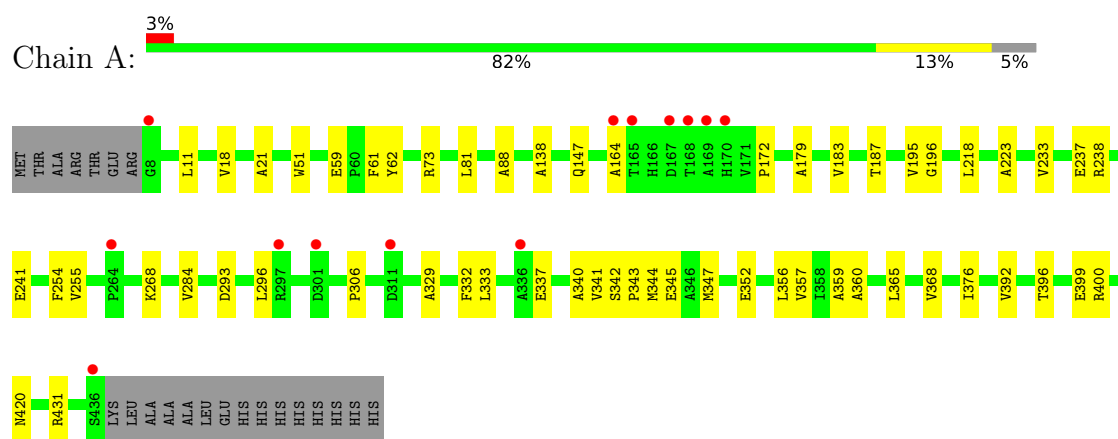
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	73	Total 73	O 73	0	0
2	B	61	Total 61	O 61	0	0
2	C	50	Total 50	O 50	0	0
2	D	93	Total 93	O 93	0	0

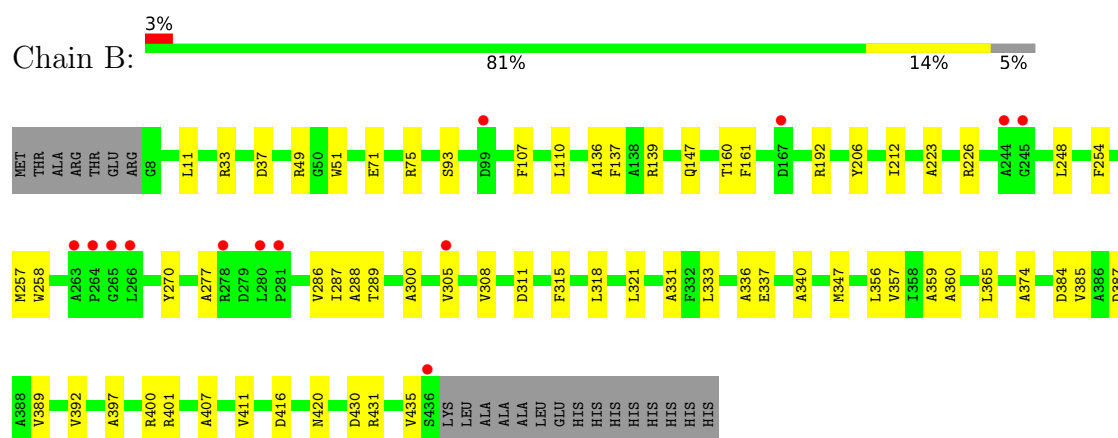
3 Residue-property plots [i](#)

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.

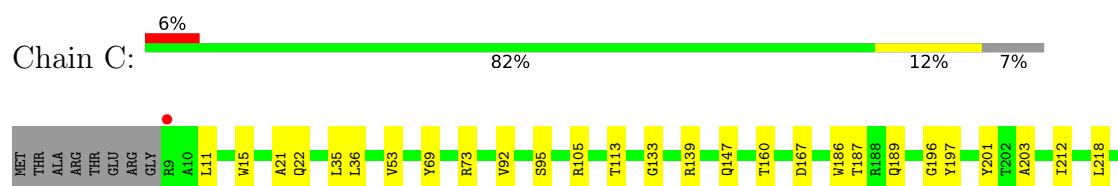
• Molecule 1: Glycosyltransferase

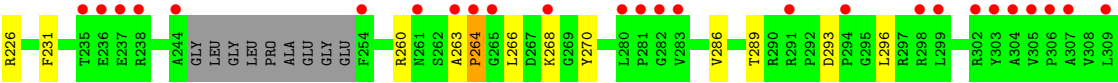


• Molecule 1: Glycosyltransferase

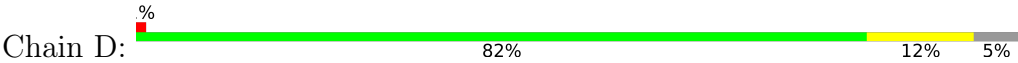


• Molecule 1: Glycosyltransferase





● Molecule 1: Glycosyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	97.54Å 142.01Å 158.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.77 – 2.45 48.77 – 2.45	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.77-2.45) 100.0 (48.77-2.45)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.48 (at 2.45Å)	Xtriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.203 , 0.254 0.203 , 0.253	Depositor DCC
R_{free} test set	2000 reflections (2.45%)	wwPDB-VP
Wilson B-factor (Å ²)	38.9	Xtriage
Anisotropy	0.915	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 30.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12992	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 4.24% 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	0.32	0/3273	0.51	0/4464
1	B	0.32	0/3281	0.49	0/4472
1	C	0.32	0/3156	0.53	0/4313
1	D	0.35	0/3274	0.52	0/4465
All	All	0.33	0/12984	0.51	0/17714

There are no bond length outliers.

There are no bond angle outliers.

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	3205	0	3124	36	0
1	B	3213	0	3132	39	0
1	C	3091	0	2957	32	0
1	D	3206	0	3123	34	0
2	A	73	0	0	1	0
2	B	61	0	0	1	0
2	C	50	0	0	1	0
2	D	93	0	0	4	0
All	All	12992	0	12336	135	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 5.

All (135) 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:263:ALA:HB1	1:C:264:PRO:HD2	1.64	0.79
1:C:286:VAL:HG11	1:C:321:LEU:HD21	1.74	0.67
1:B:49:ARG:NH2	1:B:430:ASP:OD1	2.30	0.65
1:D:46:LEU:HD13	1:D:53:VAL:HG21	1.80	0.63
1:B:147:GLN:HG3	1:D:95:SER:O	1.99	0.63
1:C:359:ALA:HB1	1:C:365:LEU:HB3	1.81	0.62
1:B:400:ARG:NH1	2:B:504:HOH:O	2.32	0.62
1:C:347:MET:HG2	1:C:407:ALA:HB1	1.81	0.62
1:B:347:MET:HG3	1:B:357:VAL:HG21	1.81	0.61
1:A:164:ALA:HB1	1:A:172:PRO:HG2	1.82	0.61
1:D:11:LEU:HB2	1:D:51:TRP:CE3	2.36	0.60
1:D:356:LEU:HD11	1:D:400:ARG:HG3	1.84	0.59
1:D:271:HIS:NE2	2:D:501:HOH:O	2.32	0.58
1:A:187:THR:HG21	1:A:195:VAL:HG23	1.85	0.58
1:B:315:PHE:HA	1:B:318:LEU:HD12	1.86	0.58
1:A:284:VAL:HG12	1:A:306:PRO:HG2	1.85	0.57
1:B:270:TYR:HB3	1:B:287:ILE:HD13	1.86	0.57
1:B:359:ALA:HB1	1:B:365:LEU:HB3	1.86	0.57
1:B:226:ARG:HD3	1:B:411:VAL:HG12	1.87	0.56
1:A:340:ALA:O	1:A:344:MET:HE3	2.06	0.56
1:A:431:ARG:NH2	2:A:503:HOH:O	2.38	0.56
1:D:376:ILE:HG13	1:D:392:VAL:HG22	1.86	0.56
1:A:343:PRO:HB2	1:A:368:VAL:HG11	1.88	0.55
1:C:21:ALA:O	1:C:73:ARG:HD2	2.07	0.54
1:D:39:GLN:HG3	1:D:55:PHE:CD2	2.43	0.53
1:B:286:VAL:HG11	1:B:321:LEU:HD21	1.91	0.53
1:C:268:LYS:HB2	1:C:270:TYR:CE2	2.44	0.53
1:B:160:THR:HG23	1:B:161:PHE:CG	2.44	0.53
1:B:257:MET:HG2	1:B:331:ALA:O	2.08	0.53
1:C:260:ARG:NH2	1:C:266:LEU:HD11	2.26	0.51
1:C:332:PHE:HE2	1:C:342:SER:HB3	1.74	0.51
1:C:332:PHE:CE2	1:C:342:SER:HB3	2.46	0.51
1:D:398:ASP:O	1:D:402:ARG:HG3	2.10	0.51
1:B:347:MET:HE3	1:B:407:ALA:HA	1.92	0.51
1:B:392:VAL:O	1:B:400:ARG:NH2	2.44	0.50
1:D:289:THR:O	1:D:311:ASP:HA	2.11	0.50
1:D:260:ARG:HB2	2:D:582:HOH:O	2.10	0.50
1:C:187:THR:HG21	1:C:212:ILE:HG23	1.94	0.50
1:C:289:THR:O	1:C:311:ASP:HA	2.12	0.50
1:D:94:ASP:O	1:D:105:ARG:HD2	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:248:LEU:HD23	1:B:308:VAL:HG21	1.95	0.49
1:D:347:MET:HG2	1:D:407:ALA:HB1	1.93	0.49
1:B:277:ALA:HB3	1:B:305:VAL:HG21	1.94	0.49
1:D:81:LEU:HD12	1:D:88:ALA:HB2	1.95	0.49
1:A:81:LEU:HD12	1:A:88:ALA:HB2	1.95	0.48
1:A:18:VAL:O	1:A:62:TYR:OH	2.31	0.48
1:A:359:ALA:HB1	1:A:365:LEU:HB3	1.95	0.48
1:D:260:ARG:HG3	1:D:266:LEU:HD21	1.94	0.48
1:D:297:ARG:NH2	2:D:508:HOH:O	2.46	0.48
1:A:233:VAL:HG11	1:A:352:GLU:OE1	2.14	0.48
1:B:93:SER:OG	1:D:147:GLN:NE2	2.47	0.48
1:A:396:THR:OG1	1:A:399:GLU:HG3	2.13	0.47
1:B:110:LEU:HG	1:B:137:PHE:CE1	2.48	0.47
1:B:11:LEU:HB2	1:B:51:TRP:CE3	2.49	0.47
1:B:206:TYR:HB3	1:B:212:ILE:HD12	1.97	0.47
1:A:183:VAL:O	1:A:187:THR:HG23	2.15	0.47
1:B:139:ARG:NH2	1:D:94:ASP:OD1	2.48	0.47
1:C:376:ILE:HG23	1:C:391:ARG:NH2	2.30	0.47
1:C:92:VAL:HB	1:C:113:THR:HG21	1.96	0.46
1:B:337:GLU:HG2	1:B:340:ALA:HB2	1.97	0.46
1:B:401:ARG:HH11	1:B:401:ARG:HG3	1.80	0.46
1:D:110:LEU:HG	1:D:137:PHE:CE1	2.51	0.46
1:A:293:ASP:HB3	1:A:296:LEU:HB2	1.98	0.46
1:A:333:LEU:HA	1:A:360:ALA:HB2	1.97	0.46
1:A:254:PHE:CD1	1:A:284:VAL:HG23	2.51	0.46
1:C:15:TRP:CE2	1:C:35:LEU:HD21	2.51	0.46
1:B:107:PHE:CD1	1:B:136:ALA:HA	2.51	0.46
1:C:11:LEU:HD23	1:C:53:VAL:HG22	1.98	0.46
1:C:186:TRP:HA	1:C:189:GLN:HB3	1.97	0.46
1:D:359:ALA:HB1	1:D:365:LEU:HB3	1.98	0.45
1:A:138:ALA:HB3	1:A:179:ALA:HB1	1.98	0.45
1:B:384:ASP:HA	1:B:387:ASP:HB2	1.99	0.45
1:A:332:PHE:HE2	1:A:342:SER:HB3	1.81	0.45
1:A:11:LEU:HB2	1:A:51:TRP:CE3	2.51	0.45
1:A:268:LYS:HE2	1:A:337:GLU:OE2	2.17	0.45
1:B:226:ARG:NE	1:B:416:ASP:OD1	2.43	0.45
1:C:187:THR:CG2	1:C:212:ILE:HG23	2.47	0.45
1:C:167:ASP:OD2	1:C:201:TYR:OH	2.28	0.44
1:A:347:MET:HG3	1:A:357:VAL:HG21	2.00	0.44
1:D:372:GLY:HA2	1:D:375:GLY:O	2.18	0.44
1:C:231:PHE:O	1:C:351:ARG:NH2	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:347:MET:HG3	1:D:357:VAL:HG21	1.99	0.44
1:A:341:VAL:O	1:A:345:GLU:HG3	2.18	0.44
1:D:275:GLU:HG3	1:D:303:TYR:CE2	2.53	0.44
1:A:356:LEU:HD11	1:A:400:ARG:HG3	1.98	0.44
1:B:385:VAL:O	1:B:389:VAL:HG23	2.18	0.44
1:D:412:ARG:NH1	2:D:509:HOH:O	2.49	0.44
1:A:21:ALA:HB3	1:A:59:GLU:OE1	2.18	0.44
1:A:21:ALA:O	1:A:73:ARG:HD2	2.17	0.44
1:C:196:GLY:HA2	1:C:218:LEU:O	2.18	0.43
1:D:332:PHE:HE2	1:D:342:SER:HB3	1.82	0.43
1:A:376:ILE:HG13	1:A:392:VAL:HG22	1.99	0.43
1:D:286:VAL:HG11	1:D:321:LEU:HD11	2.01	0.43
1:A:61:PHE:HB2	1:C:147:GLN:NE2	2.33	0.43
1:A:147:GLN:HG3	1:C:95:SER:O	2.17	0.43
1:A:238:ARG:HD3	1:A:238:ARG:HA	1.90	0.43
1:B:192:ARG:HG2	1:B:435:VAL:HG11	2.01	0.43
1:C:105:ARG:HD3	1:D:104:GLU:OE2	2.18	0.43
1:C:293:ASP:HB3	1:C:296:LEU:HB2	2.01	0.42
1:C:226:ARG:HB2	1:C:348:TRP:CE2	2.54	0.42
1:B:248:LEU:HB3	1:B:254:PHE:CZ	2.53	0.42
1:B:300:ALA:O	1:B:305:VAL:HG12	2.19	0.42
1:D:92:VAL:HB	1:D:113:THR:HG21	2.02	0.42
1:D:378:THR:HB	1:D:388:ALA:HB2	2.01	0.42
1:A:396:THR:HG23	1:A:399:GLU:OE1	2.19	0.42
1:D:107:PHE:CD1	1:D:136:ALA:HA	2.55	0.42
1:D:138:ALA:O	1:D:141:PRO:HD2	2.19	0.42
1:A:254:PHE:HD1	1:A:284:VAL:HG23	1.83	0.42
1:B:258:TRP:HA	1:B:288:ALA:O	2.19	0.42
1:D:238:ARG:HA	1:D:238:ARG:HE	1.83	0.42
1:D:263:ALA:HB1	1:D:264:PRO:HD3	2.02	0.42
1:B:71:GLU:O	1:B:75:ARG:HG3	2.19	0.41
1:B:289:THR:O	1:B:311:ASP:HA	2.19	0.41
1:C:420:ASN:HD22	1:C:420:ASN:HA	1.66	0.41
1:C:347:MET:HG3	1:C:357:VAL:HG21	2.02	0.41
1:A:223:ALA:HB2	1:A:420:ASN:HD22	1.86	0.41
1:C:197:TYR:CD1	1:C:203:ALA:HB2	2.55	0.41
1:D:32:VAL:O	1:D:36:LEU:HG	2.20	0.41
1:B:33:ARG:NH1	1:B:37:ASP:OD2	2.53	0.41
1:B:397:ALA:O	1:B:401:ARG:HG2	2.20	0.41
1:C:36:LEU:HD23	1:C:36:LEU:HA	1.70	0.41
1:C:139:ARG:HD2	2:C:521:HOH:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:332:PHE:CE2	1:A:342:SER:HB3	2.55	0.41
1:A:196:GLY:HA2	1:A:218:LEU:O	2.21	0.41
1:C:22:GLN:HB3	1:C:69:TYR:CE1	2.55	0.41
1:B:356:LEU:HD11	1:B:400:ARG:HG3	2.03	0.41
1:B:374:ALA:HB1	1:B:407:ALA:HA	2.02	0.41
1:B:333:LEU:HA	1:B:360:ALA:HB2	2.03	0.41
1:C:133:GLY:HA2	1:C:160:THR:O	2.21	0.41
1:D:93:SER:HB2	1:D:106:PHE:CD1	2.55	0.41
1:A:223:ALA:HB2	1:A:420:ASN:ND2	2.36	0.41
1:A:255:VAL:HA	1:A:329:ALA:O	2.20	0.41
1:A:237:GLU:O	1:A:241:GLU:HG3	2.21	0.40
1:B:431:ARG:O	1:B:435:VAL:HG23	2.22	0.40
1:B:223:ALA:HB2	1:B:420:ASN:HD22	1.86	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	427/451 (95%)	413 (97%)	14 (3%)	0	100	100
1	B	427/451 (95%)	409 (96%)	17 (4%)	1 (0%)	43	54
1	C	417/451 (92%)	399 (96%)	17 (4%)	1 (0%)	43	54
1	D	426/451 (94%)	412 (97%)	14 (3%)	0	100	100
All	All	1697/1804 (94%)	1633 (96%)	62 (4%)	2 (0%)	48	61

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	336	ALA
1	C	264	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	307/335 (92%)	307 (100%)	0	100	100
1	B	307/335 (92%)	307 (100%)	0	100	100
1	C	288/335 (86%)	288 (100%)	0	100	100
1	D	307/335 (92%)	307 (100%)	0	100	100
All	All	1209/1340 (90%)	1209 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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	166	HIS
1	A	240	ASN
1	B	39	GLN
1	B	80	HIS
1	B	145	GLN
1	D	145	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 oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	429/451 (95%)	0.16	13 (3%) 52 53	30, 45, 70, 86	0
1	B	429/451 (95%)	0.30	13 (3%) 52 53	32, 47, 73, 82	0
1	C	421/451 (93%)	0.45	29 (6%) 23 20	29, 48, 83, 94	0
1	D	428/451 (94%)	-0.09	3 (0%) 84 86	30, 41, 56, 72	0
All	All	1707/1804 (94%)	0.20	58 (3%) 48 48	29, 45, 74, 94	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	438	LEU	5.8
1	C	261	ASN	4.0
1	A	169	ALA	3.7
1	B	436	SER	3.6
1	D	436	SER	3.6
1	C	264	PRO	3.5
1	D	264	PRO	3.5
1	A	311	ASP	3.4
1	A	167	ASP	3.3
1	C	283	VAL	3.3
1	C	302	ARG	3.2
1	C	254	PHE	3.2
1	C	299	LEU	3.2
1	A	168	THR	3.2
1	A	436	SER	3.1
1	C	312	ASP	3.1
1	B	167	ASP	3.0
1	C	305	VAL	2.9
1	B	264	PRO	2.8
1	B	99	ASP	2.7
1	B	280	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	236	GLU	2.7
1	C	244	ALA	2.6
1	C	281	PRO	2.6
1	C	237	GLU	2.6
1	C	306	PRO	2.5
1	C	291	ARG	2.5
1	A	8	GLY	2.5
1	B	266	LEU	2.5
1	C	304	ALA	2.5
1	C	303	TYR	2.5
1	B	263	ALA	2.5
1	B	245	GLY	2.4
1	C	309	LEU	2.4
1	C	9	ARG	2.4
1	A	164	ALA	2.4
1	C	263	ALA	2.4
1	A	336	ALA	2.4
1	C	235	THR	2.3
1	A	170	HIS	2.3
1	C	294	PRO	2.3
1	C	307	ALA	2.3
1	A	264	PRO	2.2
1	A	297	ARG	2.2
1	C	238	ARG	2.2
1	B	281	PRO	2.2
1	D	25	ALA	2.2
1	C	280	LEU	2.2
1	C	282	GLY	2.1
1	C	298	ARG	2.1
1	B	265	GLY	2.1
1	B	278	ARG	2.1
1	C	268	LYS	2.1
1	C	265	GLY	2.1
1	A	301	ASP	2.0
1	B	305	VAL	2.0
1	B	244	ALA	2.0
1	A	165	THR	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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.