



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:45 PM UTC

PDB ID : 9U77 / pdb_00009u77
Title : Crystal structure of Glycogen branching enzyme (VvGBE) from *Vibrio vulnificus* MO6-24/O
Authors : An, Y.; Lee, S.J.; Park, J.T.; Woo, E.J.
Deposited on : 2025-03-24
Resolution : 2.50 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

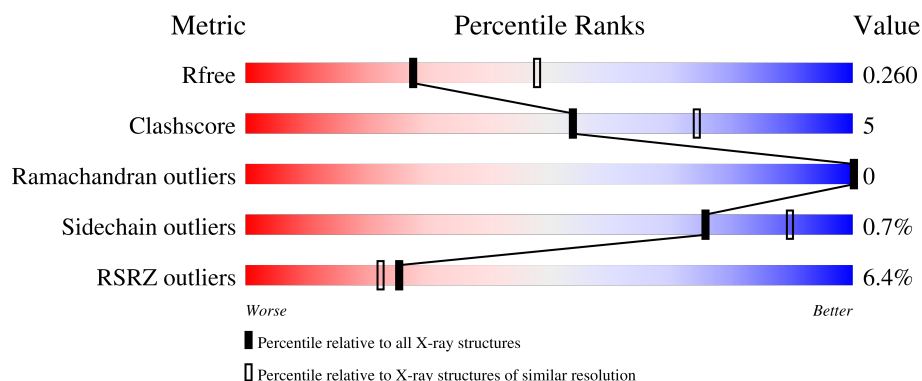
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	742	8% 81% 15%
1	B	742	4% 87% 10%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 11896 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 1,4-alpha-glucan branching enzyme GlgB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	717	Total	C	N	O	S	0	0	0
			5821	3745	986	1067	23			
1	B	717	Total	C	N	O	S	0	0	0
			5821	3745	986	1067	23			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP A0A2S3R8T2
A	2	ARG	-	expression tag	UNP A0A2S3R8T2
A	3	ILE	-	expression tag	UNP A0A2S3R8T2
A	4	VAL	MET	conflict	UNP A0A2S3R8T2
A	111	ILE	VAL	conflict	UNP A0A2S3R8T2
A	171	CYS	SER	conflict	UNP A0A2S3R8T2
B	1	MET	-	initiating methionine	UNP A0A2S3R8T2
B	2	ARG	-	expression tag	UNP A0A2S3R8T2
B	3	ILE	-	expression tag	UNP A0A2S3R8T2
B	4	VAL	MET	conflict	UNP A0A2S3R8T2
B	111	ILE	VAL	conflict	UNP A0A2S3R8T2
B	171	CYS	SER	conflict	UNP A0A2S3R8T2

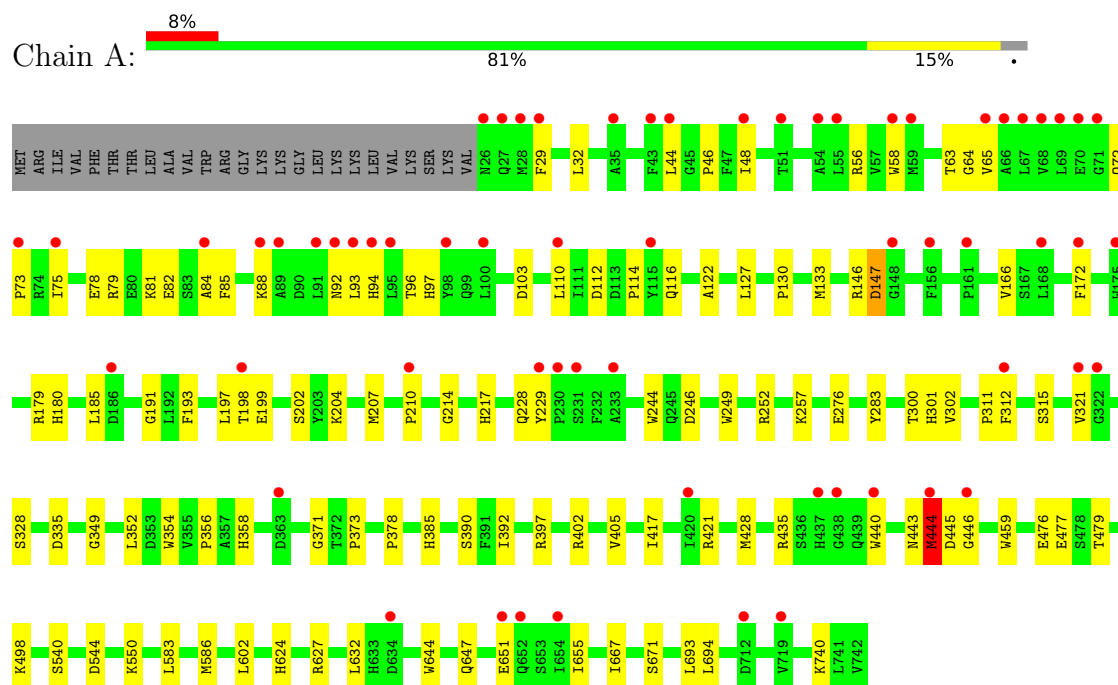
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	126	Total	O	0	0
			126	126		
2	B	128	Total	O	0	0
			128	128		

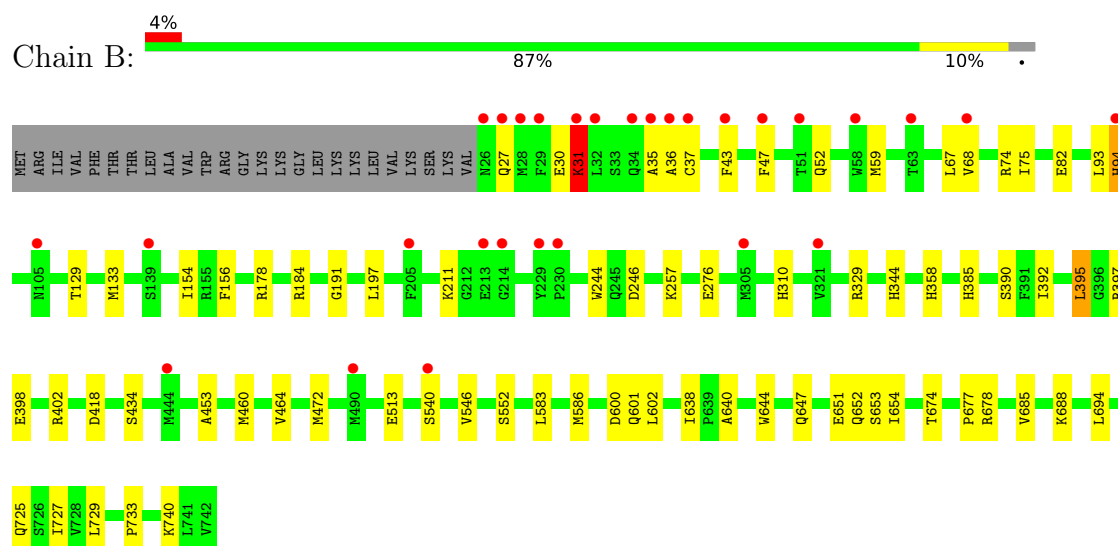
3 Residue-property plots [i](#)

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: 1,4-alpha-glucan branching enzyme GlgB



- Molecule 1: 1,4-alpha-glucan branching enzyme GlgB



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	166.80Å 106.06Å 141.13Å 90.00° 123.30° 90.00°	Depositor
Resolution (Å)	49.31 – 2.50 49.31 – 2.50	Depositor EDS
% Data completeness (in resolution range)	96.9 (49.31-2.50) 97.0 (49.31-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.19	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.40 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.216 , 0.257 0.217 , 0.260	Depositor DCC
R_{free} test set	1986 reflections (2.78%)	wwPDB-VP
Wilson B-factor (Å ²)	48.0	Xtriage
Anisotropy	0.795	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 30.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.009 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11896	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.78% 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	0.14	0/6014	0.37	9/8181 (0.1%)
1	B	0.10	0/6014	0.31	5/8181 (0.1%)
All	All	0.12	0/12028	0.34	14/16362 (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	1
1	B	0	1
All	All	0	2

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	31	LYS	CA-CB-CG	7.34	128.79	114.10
1	A	444	MET	CB-CG-SD	6.51	132.22	112.70
1	A	651	GLU	CB-CA-C	6.29	121.37	110.68
1	A	444	MET	CA-CB-CG	-5.50	103.11	114.10
1	A	651	GLU	N-CA-C	5.40	117.86	111.33
1	A	651	GLU	CG-CD-OE2	-5.34	106.11	118.40
1	B	30	GLU	CA-C-N	-5.33	111.80	121.14
1	B	30	GLU	C-N-CA	-5.33	111.80	121.14
1	A	443	ASN	CA-C-N	-5.27	111.47	121.54
1	A	443	ASN	C-N-CA	-5.27	111.47	121.54
1	A	651	GLU	CA-C-N	-5.23	112.34	122.06
1	A	651	GLU	C-N-CA	-5.23	112.34	122.06
1	B	93	LEU	CA-C-N	-5.16	115.48	123.17
1	B	93	LEU	C-N-CA	-5.16	115.48	123.17

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	444	MET	Peptide
1	B	94	HIS	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	5821	0	5476	69	1
1	B	5821	0	5476	44	1
2	A	126	0	0	3	0
2	B	128	0	0	3	0
All	All	11896	0	10952	111	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 (111) 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:31:LYS:HB3	1:B:36:ALA:HB3	1.58	0.85
1:A:133:MET:HE1	1:A:402:ARG:HB3	1.67	0.76
1:B:395:LEU:HD23	1:B:453:ALA:HA	1.70	0.72
1:A:32:LEU:HD21	1:A:44:LEU:HD11	1.75	0.69
1:B:677:PRO:HG3	1:B:733:PRO:HG3	1.75	0.68
1:B:651:GLU:OE2	2:B:801:HOH:O	2.11	0.68
1:A:92:ASN:HD22	1:A:93:LEU:N	1.94	0.66
1:A:300:THR:HG22	1:A:627:ARG:HD3	1.79	0.64
1:A:694:LEU:HD11	1:A:740:LYS:HB2	1.78	0.64
1:B:27:GLN:HB3	1:B:43:PHE:HZ	1.60	0.64
1:B:310:HIS:O	1:B:329:ARG:NH2	2.29	0.64
1:B:154:ILE:HD12	1:B:197:LEU:HB3	1.81	0.63
1:A:356:PRO:HG2	1:A:428:MET:HE1	1.81	0.63
1:B:397:ARG:NH1	2:B:804:HOH:O	2.31	0.62
1:A:373:PRO:HG2	1:A:378:PRO:HG3	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:276:GLU:H	1:A:276:GLU:CD	2.10	0.59
1:A:402:ARG:HG2	1:A:459:TRP:HH2	1.67	0.59
1:A:249:TRP:O	1:A:252:ARG:HG3	2.03	0.58
1:B:651:GLU:OE1	1:B:652:GLN:HG3	2.03	0.58
1:B:276:GLU:OE1	1:B:276:GLU:N	2.36	0.58
1:A:46:PRO:HB2	1:A:94:HIS:HB3	1.85	0.58
1:B:685:VAL:O	1:B:725:GLN:HB2	2.03	0.58
1:A:44:LEU:HD21	1:A:58:TRP:HB3	1.85	0.57
1:B:688:LYS:HG2	1:B:725:GLN:HG3	1.85	0.57
1:A:112:ASP:OD1	1:A:116:GLN:NE2	2.38	0.56
1:B:638:ILE:HG22	1:B:640:ALA:H	1.70	0.56
1:B:434:SER:O	1:B:434:SER:OG	2.21	0.55
1:B:68:VAL:HG12	1:B:74:ARG:HG2	1.89	0.55
1:A:78:GLU:OE1	1:A:88:LYS:HB2	2.07	0.54
1:A:46:PRO:HB2	1:A:94:HIS:CB	2.38	0.54
1:A:96:THR:HA	1:A:147:ASP:OD1	2.08	0.53
1:B:688:LYS:HZ3	1:B:725:GLN:HG3	1.72	0.53
1:A:498:LYS:NZ	2:A:802:HOH:O	2.41	0.53
1:B:694:LEU:HD11	1:B:740:LYS:HB2	1.91	0.53
1:A:228:GLN:NE2	1:A:328:SER:OG	2.38	0.53
1:B:47:PHE:CE1	1:B:94:HIS:HB2	2.44	0.52
1:A:544:ASP:O	1:A:550:LYS:HE2	2.09	0.52
1:B:586:MET:HB2	1:B:602:LEU:HD11	1.91	0.52
1:A:477:GLU:HB3	1:A:498:LYS:HE3	1.92	0.51
1:A:358:HIS:HB3	1:A:390:SER:HB2	1.93	0.51
1:A:444:MET:HA	1:A:446:GLY:H	1.74	0.51
1:A:92:ASN:ND2	1:A:93:LEU:O	2.44	0.51
1:A:48:ILE:HG12	1:A:56:ARG:HH21	1.77	0.50
1:A:540:SER:HA	1:A:583:LEU:HB3	1.93	0.50
1:B:257:LYS:HG3	1:B:472:MET:HG3	1.92	0.50
1:A:79:ARG:NH1	1:A:82:GLU:O	2.45	0.49
1:A:624:HIS:ND1	2:A:801:HOH:O	2.35	0.49
1:A:172:PHE:HD2	1:A:172:PHE:H	1.60	0.49
1:B:129:THR:O	1:B:133:MET:HG3	2.12	0.49
1:A:65:VAL:HG12	1:A:85:PHE:CD2	2.48	0.48
1:A:354:TRP:CE3	1:A:356:PRO:HG3	2.48	0.48
1:B:35:ALA:HB2	1:B:178:ARG:HG3	1.95	0.48
1:A:229:TYR:HB3	1:B:211:LYS:HE3	1.95	0.48
1:B:654:ILE:HD11	1:B:678:ARG:HG3	1.96	0.47
1:B:31:LYS:HD3	1:B:37:CYS:HA	1.96	0.47
1:A:204:LYS:HD2	1:A:217:HIS:HB3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:198:THR:OG1	1:A:199:GLU:N	2.49	0.46
1:A:373:PRO:O	1:A:397:ARG:NH1	2.46	0.46
1:A:352:LEU:HD22	1:A:417:ILE:HG21	1.97	0.46
1:B:67:LEU:HD23	1:B:75:ILE:HD12	1.97	0.46
1:A:72:GLN:HG3	1:A:73:PRO:HD2	1.98	0.45
1:A:435:ARG:HD2	1:A:440:TRP:HB3	1.98	0.45
1:A:477:GLU:OE2	1:A:479:THR:HB	2.15	0.45
1:A:166:VAL:HG13	1:A:207:MET:HG2	1.99	0.45
1:A:301:HIS:CD2	1:A:349:GLY:HA3	2.52	0.45
1:A:283:TYR:HB2	1:A:335:ASP:HB3	1.99	0.44
1:A:311:PRO:HD3	1:A:321:VAL:HG22	1.98	0.44
1:A:644:TRP:CE3	1:A:647:GLN:HB3	2.53	0.44
1:B:385:HIS:CG	1:B:392:ILE:HD11	2.53	0.44
1:B:644:TRP:CE3	1:B:647:GLN:HB3	2.53	0.44
1:A:130:PRO:HG2	1:A:459:TRP:CZ2	2.53	0.44
1:A:122:ALA:HB3	1:A:127:LEU:HD11	1.98	0.43
1:B:52:GLN:OE1	1:B:52:GLN:N	2.45	0.43
1:B:344:HIS:HE1	1:B:418:ASP:OD1	2.01	0.43
1:B:600:ASP:OD1	1:B:601:GLN:N	2.49	0.43
1:A:586:MET:HB2	1:A:602:LEU:HD11	2.00	0.43
1:B:546:VAL:HG12	1:B:552:SER:HA	2.01	0.43
1:A:96:THR:HA	1:A:147:ASP:CG	2.43	0.43
1:A:81:LYS:H	1:A:84:ALA:HB3	1.84	0.43
1:B:653:SER:HB2	1:B:674:THR:HG23	2.01	0.43
1:A:81:LYS:HB3	1:A:81:LYS:HE3	1.84	0.43
1:B:59:MET:HE2	1:B:59:MET:HB2	1.84	0.43
1:B:156:PHE:O	1:B:191:GLY:HA2	2.19	0.43
1:A:81:LYS:N	1:A:84:ALA:HB3	2.34	0.42
1:A:214:GLY:N	1:B:82:GLU:OE1	2.50	0.42
1:A:244:TRP:HB3	1:A:246:ASP:OD1	2.19	0.42
1:A:385:HIS:CG	1:A:392:ILE:HD11	2.53	0.42
1:A:97:HIS:HB2	1:A:146:ARG:HG2	2.00	0.42
1:B:244:TRP:HB3	1:B:246:ASP:OD1	2.18	0.42
1:A:63:THR:OG1	1:A:103:ASP:O	2.37	0.42
1:A:405:VAL:HG21	1:A:459:TRP:CE3	2.54	0.42
1:A:114:PRO:HB3	1:A:193:PHE:O	2.20	0.42
1:A:312:PHE:CD2	1:A:315:SER:HB3	2.55	0.42
1:B:358:HIS:HB3	1:B:390:SER:HB2	2.01	0.42
1:A:197:LEU:HD12	1:A:197:LEU:HA	1.88	0.41
1:A:257:LYS:NZ	2:A:812:HOH:O	2.48	0.41
1:A:632:LEU:HG	1:A:667:ILE:HD12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:179:ARG:HG2	1:A:180:HIS:ND1	2.36	0.41
1:A:210:PRO:HD3	1:A:371:GLY:HA3	2.01	0.41
1:B:688:LYS:HG2	1:B:725:GLN:CG	2.49	0.41
1:B:398:GLU:HG2	1:B:402:ARG:NH2	2.36	0.41
1:A:655:ILE:HG13	1:A:671:SER:HB2	2.03	0.41
1:B:460:MET:O	1:B:464:VAL:HG22	2.20	0.41
1:B:540:SER:HA	1:B:583:LEU:HB3	2.02	0.41
1:B:513:GLU:HG2	2:B:906:HOH:O	2.21	0.40
1:B:727:ILE:HD12	1:B:729:LEU:HD21	2.03	0.40
1:A:185:LEU:HD11	1:A:191:GLY:HA3	2.04	0.40
1:A:110:LEU:HD13	1:A:110:LEU:HA	1.94	0.40
1:A:64:GLY:HA2	1:A:85:PHE:HE2	1.87	0.40
1:A:421:ARG:HH11	1:A:476:GLU:HB2	1.86	0.40
1:A:445:ASP:OD1	1:A:445:ASP:N	2.54	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)
1:A:445:ASP:OD2	1:B:184:ARG:NH2[4_455]	2.17	0.03

5.3 Torsion angles

5.3.1 Protein backbone

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	715/742 (96%)	707 (99%)	8 (1%)	0	100	100
1	B	715/742 (96%)	708 (99%)	7 (1%)	0	100	100
All	All	1430/1484 (96%)	1415 (99%)	15 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	605/627 (96%)	599 (99%)	6 (1%)	68	86
1	B	605/627 (96%)	603 (100%)	2 (0%)	86	94
All	All	1210/1254 (96%)	1202 (99%)	8 (1%)	76	89

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	PHE
1	A	75	ILE
1	A	147	ASP
1	A	202	SER
1	A	302	VAL
1	A	693	LEU
1	B	31	LYS
1	B	395	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	92	ASN
1	A	94	HIS
1	A	97	HIS
1	A	228	GLN
1	A	245	GLN
1	A	563	GLN
1	A	564	GLN
1	A	601	GLN
1	A	616	GLN
1	A	624	HIS
1	B	92	ASN
1	B	245	GLN
1	B	250	GLN
1	B	277	GLN

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Mol	Chain	Res	Type
1	B	555	ASN
1	B	687	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	717/742 (96%)	0.83	63 (8%)	15 14	40, 55, 107, 144	0
1	B	717/742 (96%)	0.61	29 (4%)	42 38	38, 53, 78, 123	0
All	All	1434/1484 (96%)	0.72	92 (6%)	25 22	38, 54, 99, 144	0

All (92) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	36	ALA	6.0
1	B	94	HIS	6.0
1	A	95	LEU	5.4
1	A	321	VAL	5.2
1	A	229	TYR	5.0
1	A	91	LEU	4.9
1	A	89	ALA	4.6
1	A	67	LEU	4.6
1	A	230	PRO	4.4
1	B	31	LYS	4.4
1	B	214	GLY	4.3
1	B	321	VAL	4.1
1	A	93	LEU	4.0
1	A	75	ILE	3.7
1	A	446	GLY	3.6
1	B	230	PRO	3.6
1	A	651	GLU	3.5
1	A	437	HIS	3.5
1	B	28	MET	3.4
1	A	28	MET	3.3
1	A	444	MET	3.2
1	B	229	TYR	3.1
1	B	205	PHE	3.1
1	A	363	ASP	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	48	ILE	3.1
1	B	63	THR	3.0
1	A	233	ALA	3.0
1	B	27	GLN	3.0
1	B	305	MET	2.9
1	A	65	VAL	2.9
1	A	92	ASN	2.9
1	A	168	LEU	2.9
1	A	94	HIS	2.8
1	A	175	TRP	2.8
1	A	29	PHE	2.8
1	A	55	LEU	2.8
1	A	66	ALA	2.8
1	B	34	GLN	2.7
1	A	26	ASN	2.7
1	A	231	SER	2.7
1	A	84	ALA	2.7
1	A	71	GLY	2.7
1	B	490	MET	2.7
1	B	35	ALA	2.7
1	A	634	ASP	2.6
1	A	73	PRO	2.6
1	A	322	GLY	2.6
1	A	438	GLY	2.6
1	B	105	ASN	2.6
1	B	58	TRP	2.5
1	A	68	VAL	2.5
1	A	70	GLU	2.5
1	A	58	TRP	2.5
1	B	32	LEU	2.5
1	B	213	GLU	2.5
1	A	69	LEU	2.5
1	A	312	PHE	2.5
1	B	139	SER	2.4
1	A	88	LYS	2.4
1	B	29	PHE	2.4
1	B	51	THR	2.4
1	B	68	VAL	2.4
1	A	148	GLY	2.3
1	A	27	GLN	2.3
1	A	712	ASP	2.3
1	A	115	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	37	CYS	2.3
1	B	26	ASN	2.3
1	A	59	MET	2.3
1	A	98	TYR	2.3
1	A	44	LEU	2.2
1	B	444	MET	2.2
1	A	172	PHE	2.2
1	B	47	PHE	2.2
1	A	54	ALA	2.2
1	A	198	THR	2.2
1	A	420	ILE	2.2
1	A	654	ILE	2.2
1	A	110	LEU	2.2
1	A	652	GLN	2.1
1	A	100	LEU	2.1
1	A	161	PRO	2.1
1	B	43	PHE	2.1
1	A	719	VAL	2.1
1	A	35	ALA	2.1
1	A	43	PHE	2.1
1	A	186	ASP	2.1
1	A	440	TRP	2.0
1	A	210	PRO	2.0
1	A	156	PHE	2.0
1	A	51	THR	2.0
1	B	540	SER	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 ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.