



Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 08:54 am BST

PDB ID : 3PTK
Title : The crystal structure of rice (*Oryza sativa* L.) Os4BGlu12
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Deposited on : 2010-12-03
Resolution : 2.49 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

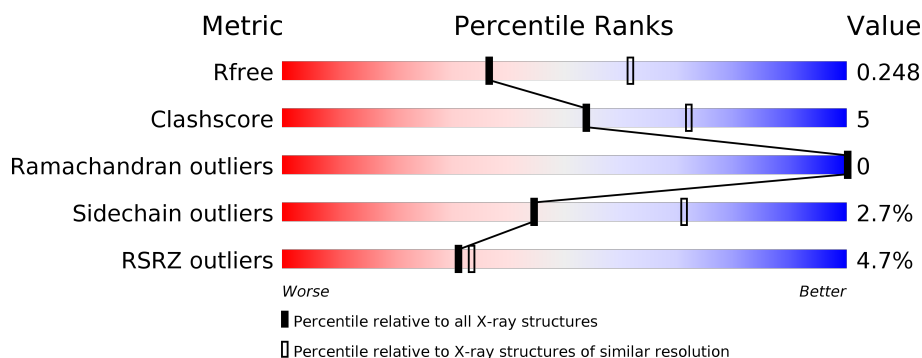
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.49 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}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (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 on 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	505	<div> <div>2%</div> <div> <div></div> <div>87%</div> <div>8%</div> <div>5%</div> </div> </div>
1	B	505	<div> <div>7%</div> <div> <div></div> <div>79%</div> <div>14%</div> <div>• 5%</div> </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7970 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-glucosidase Os4BGlu12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	478	Total	C	N	O	S	0	0	0
			3861	2481	665	704	11			
1	B	478	Total	C	N	O	S	0	0	0
			3861	2481	665	704	11			

There are 38 discrepancies between the modelled and reference sequences:

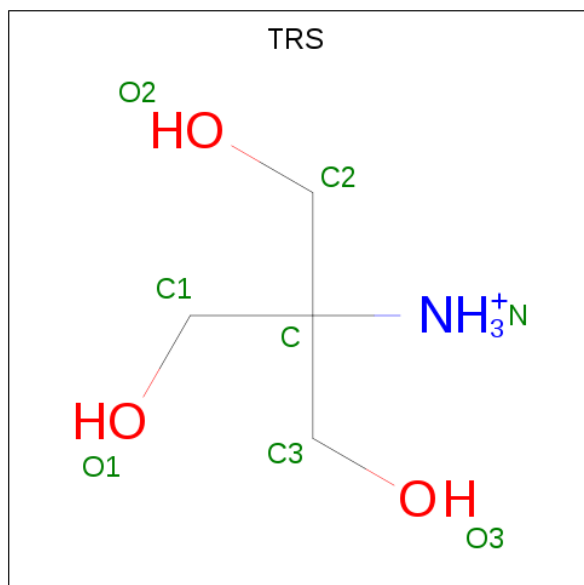
Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	ALA	-	EXPRESSION TAG	UNP Q01KB2
A	-17	MET	-	EXPRESSION TAG	UNP Q01KB2
A	-16	ALA	-	EXPRESSION TAG	UNP Q01KB2
A	-15	ASP	-	EXPRESSION TAG	UNP Q01KB2
A	-14	ILE	-	EXPRESSION TAG	UNP Q01KB2
A	-13	THR	-	EXPRESSION TAG	UNP Q01KB2
A	-12	SER	-	EXPRESSION TAG	UNP Q01KB2
A	-11	LEU	-	EXPRESSION TAG	UNP Q01KB2
A	-10	TYR	-	EXPRESSION TAG	UNP Q01KB2
A	-9	LYS	-	EXPRESSION TAG	UNP Q01KB2
A	-8	LYS	-	EXPRESSION TAG	UNP Q01KB2
A	-7	ALA	-	EXPRESSION TAG	UNP Q01KB2
A	-6	GLY	-	EXPRESSION TAG	UNP Q01KB2
A	-5	SER	-	EXPRESSION TAG	UNP Q01KB2
A	-4	ALA	-	EXPRESSION TAG	UNP Q01KB2
A	-3	ALA	-	EXPRESSION TAG	UNP Q01KB2
A	-2	ALA	-	EXPRESSION TAG	UNP Q01KB2
A	-1	PRO	-	EXPRESSION TAG	UNP Q01KB2
A	0	PHE	-	EXPRESSION TAG	UNP Q01KB2
B	-18	ALA	-	EXPRESSION TAG	UNP Q01KB2
B	-17	MET	-	EXPRESSION TAG	UNP Q01KB2
B	-16	ALA	-	EXPRESSION TAG	UNP Q01KB2
B	-15	ASP	-	EXPRESSION TAG	UNP Q01KB2
B	-14	ILE	-	EXPRESSION TAG	UNP Q01KB2
B	-13	THR	-	EXPRESSION TAG	UNP Q01KB2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-12	SER	-	EXPRESSION TAG	UNP Q01KB2
B	-11	LEU	-	EXPRESSION TAG	UNP Q01KB2
B	-10	TYR	-	EXPRESSION TAG	UNP Q01KB2
B	-9	LYS	-	EXPRESSION TAG	UNP Q01KB2
B	-8	LYS	-	EXPRESSION TAG	UNP Q01KB2
B	-7	ALA	-	EXPRESSION TAG	UNP Q01KB2
B	-6	GLY	-	EXPRESSION TAG	UNP Q01KB2
B	-5	SER	-	EXPRESSION TAG	UNP Q01KB2
B	-4	ALA	-	EXPRESSION TAG	UNP Q01KB2
B	-3	ALA	-	EXPRESSION TAG	UNP Q01KB2
B	-2	ALA	-	EXPRESSION TAG	UNP Q01KB2
B	-1	PRO	-	EXPRESSION TAG	UNP Q01KB2
B	0	PHE	-	EXPRESSION TAG	UNP Q01KB2

- Molecule 2 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: $C_4H_{12}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			8	4	1	3		
2	B	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

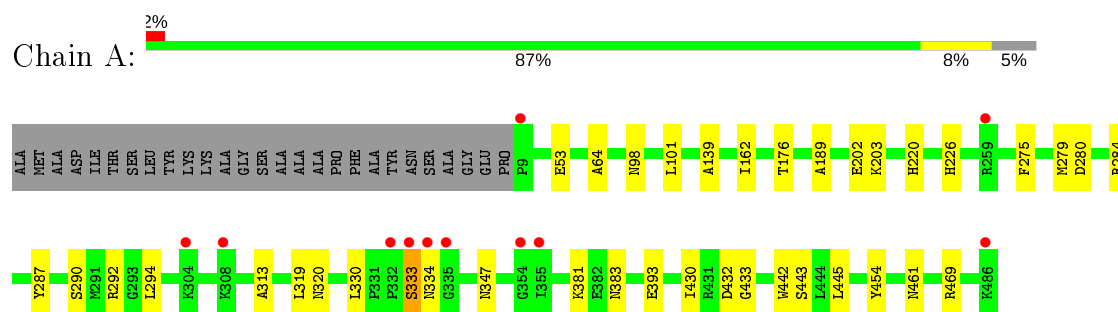
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	136	Total 136	O 136	0	0
4	B	95	Total 95	O 95	0	0

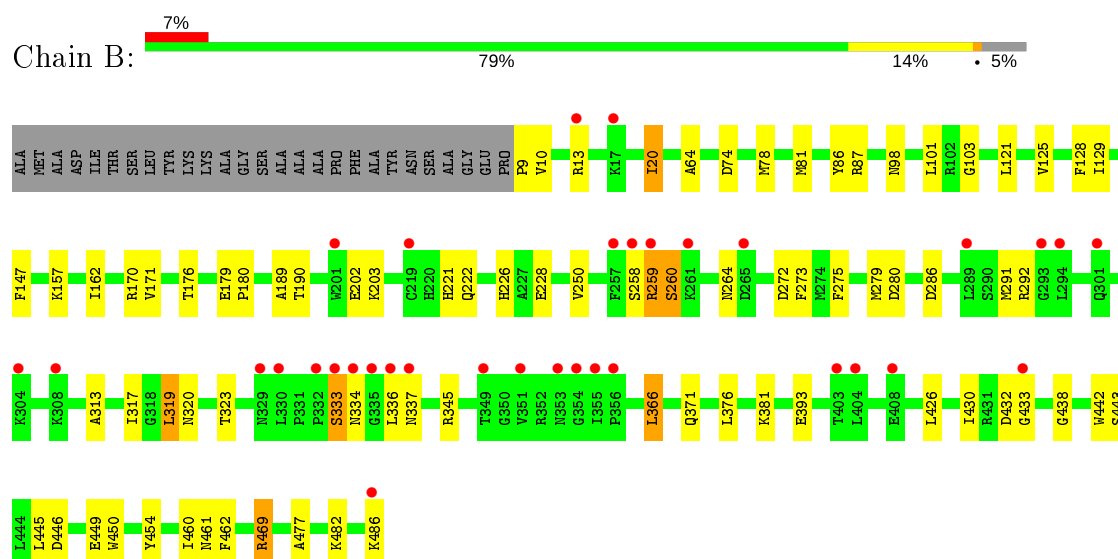
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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-glucosidase Os4BGlu12



• Molecule 1: Beta-glucosidase Os4BGlu12



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	112.66 Å 112.66 Å 182.77 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.49 26.19 – 2.49	Depositor EDS
% Data completeness (in resolution range)	99.8 (30.00-2.49) 99.9 (26.19-2.49)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.57 (at 2.50 Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.202 , 0.248 0.202 , 0.248	Depositor DCC
R_{free} test set	2097 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	33.0	Xtriage
Anisotropy	0.054	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 36.4	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	7970	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.19% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, TRS

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	0.46	0/3979	0.59	0/5392
1	B	0.49	0/3979	0.58	0/5392
All	All	0.48	0/7958	0.59	0/10784

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.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	333	SER	Peptide
1	B	333	SER	Peptide

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	3861	0	3703	23	0
1	B	3861	0	3703	57	0
2	A	8	0	12	0	0
2	B	8	0	12	2	0
3	A	1	0	0	0	0
4	A	136	0	0	0	0
4	B	95	0	0	10	0
All	All	7970	0	7430	80	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 (80) 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:259:ARG:HH11	1:B:259:ARG:HG3	1.11	1.06
1:B:323:THR:HG21	1:B:366:LEU:HA	1.51	0.92
1:B:78:MET:HE1	1:B:125:VAL:HG11	1.59	0.84
1:B:259:ARG:NH1	1:B:259:ARG:HG3	1.83	0.82
1:B:259:ARG:HH11	1:B:259:ARG:CG	1.94	0.80
1:B:291:MET:SD	4:B:569:HOH:O	2.40	0.80
1:A:333:SER:H	1:A:334:ASN:HB3	1.51	0.76
1:B:381:LYS:HE3	1:B:433:GLY:HA3	1.68	0.76
1:B:78:MET:CE	1:B:125:VAL:HG11	2.15	0.75
1:A:101:LEU:HD13	1:A:162:ILE:HD11	1.69	0.72
1:B:176:THR:OG1	1:B:226:HIS:HD2	1.73	0.72
1:B:345:ARG:HD3	4:B:576:HOH:O	1.90	0.71
1:B:78:MET:HE1	1:B:86:TYR:HB2	1.74	0.69
1:B:20:ILE:HD13	1:B:438:GLY:HA3	1.75	0.69
1:B:78:MET:HE3	4:B:496:HOH:O	1.91	0.68
1:B:273:PHE:HA	4:B:569:HOH:O	1.94	0.66
1:B:202:GLU:HG3	1:B:203:LYS:H	1.63	0.62
1:A:442:TRP:CD2	1:A:443:SER:HB3	2.34	0.62
1:B:101:LEU:CD1	1:B:162:ILE:HD11	2.30	0.61
1:B:129:ILE:HD12	1:B:171:VAL:HG21	1.83	0.61
1:B:189:ALA:O	1:B:202:GLU:HG2	2.03	0.59
1:B:226:HIS:HE1	1:B:313:ALA:O	1.86	0.58
1:A:189:ALA:O	1:A:202:GLU:HG2	2.04	0.58
1:A:445:LEU:HD23	1:A:461:ASN:HB2	1.87	0.57
1:A:202:GLU:HG3	1:A:203:LYS:H	1.70	0.56
1:B:393:GLU:OE1	2:B:1165:TRS:H12	2.06	0.56
1:A:98:ASN:HB2	1:A:139:ALA:CB	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:179:GLU:HG2	1:B:250:VAL:HB	1.87	0.55
1:A:64:ALA:HA	1:A:454:TYR:OH	2.06	0.54
1:B:98:ASN:OD1	1:B:103:GLY:HA3	2.07	0.54
1:B:272:ASP:O	4:B:569:HOH:O	2.18	0.54
1:B:430:ILE:O	1:B:432:ASP:O	2.27	0.53
1:A:430:ILE:O	1:A:432:ASP:O	2.27	0.52
1:B:202:GLU:HG3	1:B:203:LYS:N	2.24	0.52
1:A:381:LYS:CE	1:A:433:GLY:HA3	2.39	0.52
1:B:129:ILE:CD1	1:B:171:VAL:HG21	2.40	0.52
1:A:220:HIS:HD2	1:A:287:TYR:OH	1.93	0.52
1:B:101:LEU:HD12	1:B:162:ILE:HD11	1.91	0.51
1:A:320:ASN:CG	1:A:393:GLU:HB2	2.31	0.51
1:B:449:GLU:HG3	1:B:449:GLU:O	2.10	0.51
1:A:280:ASP:OD2	1:A:284:ARG:NH1	2.44	0.50
1:A:290:SER:O	1:A:294:LEU:HG	2.12	0.49
1:B:258:SER:HB2	4:B:573:HOH:O	2.11	0.49
1:A:176:THR:OG1	1:A:226:HIS:HD2	1.95	0.49
1:B:81:MET:HE3	1:B:477:ALA:HA	1.95	0.48
1:B:64:ALA:O	1:B:469:ARG:HD3	2.12	0.48
1:B:442:TRP:CD2	1:B:443:SER:HB3	2.49	0.47
1:B:190:THR:HA	1:B:202:GLU:HG2	1.96	0.47
1:B:446:ASP:OD2	1:B:462:PHE:HA	2.14	0.47
1:B:78:MET:HE2	1:B:125:VAL:HG11	1.97	0.47
1:A:381:LYS:HE3	1:A:433:GLY:HA3	1.97	0.47
1:B:445:LEU:HD23	1:B:461:ASN:HB2	1.96	0.46
1:A:333:SER:N	1:A:334:ASN:HB3	2.26	0.46
1:A:275:PHE:CE2	1:A:279:MET:HG3	2.52	0.45
1:B:320:ASN:CG	1:B:393:GLU:HB2	2.36	0.45
1:B:9:PRO:N	4:B:501:HOH:O	2.49	0.45
1:B:147:PHE:O	1:B:221:HIS:HD2	2.00	0.44
1:A:284:ARG:NH2	1:A:383:ASN:O	2.49	0.44
1:B:291:MET:CG	4:B:569:HOH:O	2.66	0.44
1:A:275:PHE:CZ	1:A:279:MET:HG3	2.52	0.44
1:A:330:LEU:HG	1:A:347:ASN:HB2	2.00	0.44
1:B:64:ALA:HA	1:B:454:TYR:OH	2.18	0.44
1:B:226:HIS:CE1	1:B:313:ALA:O	2.68	0.43
1:B:317:ILE:HG22	1:B:319:LEU:HD13	2.00	0.43
1:B:9:PRO:HB2	1:B:10:VAL:H	1.58	0.43
1:B:291:MET:HG3	4:B:569:HOH:O	2.18	0.43
1:B:260:SER:O	1:B:264:ASN:ND2	2.36	0.42
1:B:121:LEU:HD11	1:B:170:ARG:HB3	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:157:LYS:HD2	1:B:228:GLU:HG2	2.02	0.42
1:B:334:ASN:HB2	4:B:571:HOH:O	2.19	0.42
1:B:87:ARG:HA	1:B:128:PHE:O	2.20	0.41
1:B:157:LYS:NZ	1:B:228:GLU:HG2	2.36	0.41
1:B:275:PHE:CE2	1:B:279:MET:HG3	2.55	0.41
1:B:319:LEU:HA	1:B:319:LEU:HD12	1.90	0.41
1:B:450:TRP:HE1	2:B:1165:TRS:H22	1.85	0.41
1:B:180:PRO:HB3	1:B:222:GLN:OE1	2.20	0.41
1:B:74:ASP:O	1:B:78:MET:HG3	2.21	0.41
1:A:226:HIS:HE1	1:A:313:ALA:O	2.04	0.41
1:A:176:THR:OG1	1:A:226:HIS:CD2	2.74	0.40
1:B:81:MET:HE1	1:B:460:ILE:HG21	2.03	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	476/505 (94%)	461 (97%)	15 (3%)	0	100	100
1	B	476/505 (94%)	458 (96%)	18 (4%)	0	100	100
All	All	952/1010 (94%)	919 (96%)	33 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	406/423 (96%)	402 (99%)	4 (1%)	76	90
1	B	406/423 (96%)	388 (96%)	18 (4%)	28	52
All	All	812/846 (96%)	790 (97%)	22 (3%)	44	71

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53	GLU
1	A	292	ARG
1	A	319	LEU
1	A	469	ARG
1	B	13	ARG
1	B	20	ILE
1	B	259	ARG
1	B	260	SER
1	B	280	ASP
1	B	286	ASP
1	B	292	ARG
1	B	319	LEU
1	B	333	SER
1	B	336	LEU
1	B	337	ASN
1	B	366	LEU
1	B	371	GLN
1	B	376	LEU
1	B	426	LEU
1	B	469	ARG
1	B	482	LYS
1	B	486	LYS

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

Mol	Chain	Res	Type
1	A	220	HIS
1	A	221	HIS
1	A	226	HIS
1	A	263	ASN
1	A	360	GLN
1	A	420	HIS

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Mol	Chain	Res	Type
1	A	422	HIS
1	B	220	HIS
1	B	221	HIS
1	B	226	HIS
1	B	263	ASN
1	B	337	ASN
1	B	371	GLN
1	B	383	ASN
1	B	420	HIS
1	B	422	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	TRS	A	1164	-	7,7,7	0.29	0	9,9,9	0.37	0
2	TRS	B	1165	-	7,7,7	0.28	0	9,9,9	0.62	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	TRS	A	1164	-	-	3/9/9/9	-
2	TRS	B	1165	-	-	9/9/9/9	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1165	TRS	C2-C-C1-O1
2	B	1165	TRS	C3-C-C1-O1
2	B	1165	TRS	C1-C-C2-O2
2	B	1165	TRS	C3-C-C2-O2
2	B	1165	TRS	N-C-C2-O2
2	A	1164	TRS	C3-C-C2-O2
2	B	1165	TRS	N-C-C1-O1
2	B	1165	TRS	N-C-C3-O3
2	A	1164	TRS	C1-C-C2-O2
2	B	1165	TRS	C1-C-C3-O3
2	B	1165	TRS	C2-C-C3-O3
2	A	1164	TRS	N-C-C2-O2

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1165	TRS	2	0

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	478/505 (94%)	0.02	11 (2%) 60 63	17, 32, 48, 59	0
1	B	478/505 (94%)	0.19	34 (7%) 16 16	17, 32, 49, 59	0
All	All	956/1010 (94%)	0.10	45 (4%) 31 33	17, 32, 49, 59	0

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	336	LEU	5.1
1	A	354	GLY	4.8
1	B	486	LYS	4.8
1	A	9	PRO	4.8
1	B	333	SER	4.7
1	A	333	SER	4.7
1	B	257	PHE	4.4
1	B	351	VAL	4.3
1	B	355	ILE	4.1
1	B	334	ASN	3.8
1	B	289	LEU	3.6
1	B	353	ASN	3.5
1	B	293	GLY	3.3
1	B	261	LYS	3.1
1	A	486	LYS	3.0
1	B	329	ASN	3.0
1	B	337	ASN	2.9
1	B	201	TRP	2.9
1	B	259	ARG	2.8
1	B	308	LYS	2.7
1	B	403	THR	2.7
1	B	404	LEU	2.7
1	B	13	ARG	2.7
1	B	354	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	334	ASN	2.6
1	B	332	PRO	2.6
1	B	17	LYS	2.6
1	B	258	SER	2.5
1	A	332	PRO	2.5
1	A	304	LYS	2.4
1	B	330	LEU	2.4
1	B	408	GLU	2.4
1	B	335	GLY	2.3
1	B	301	GLN	2.3
1	B	433	GLY	2.3
1	B	294	LEU	2.3
1	B	304	LYS	2.2
1	B	349	THR	2.2
1	A	355	ILE	2.2
1	A	259	ARG	2.1
1	B	219	CYS	2.1
1	A	308	LYS	2.1
1	B	265	ASP	2.1
1	A	335	GLY	2.1
1	B	356	PRO	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 carbohydrates in this entry.

6.4 Ligands ⓘ

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(\AA^2)	Q<0.9
2	TRS	B	1165	8/8	0.86	0.22	48,48,49,49	0
2	TRS	A	1164	8/8	0.90	0.20	55,56,56,57	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	ZN	A	487	1/1	1.00	0.08	24,24,24,24	0

6.5 Other polymers [i](#)

There are no such residues in this entry.