



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 02:42 PM UTC

PDB ID : 5Z5J / pdb_00005z5j
Title : Crystal structure of a lactonase double mutant
Authors : Zheng, Y.Y.; Liu, W.D.; Chen, C.C.; Guo, R.T.
Deposited on : 2018-01-18
Resolution : 2.15 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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
Mogul : 2022.3.0, CSD as543be (2022)
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

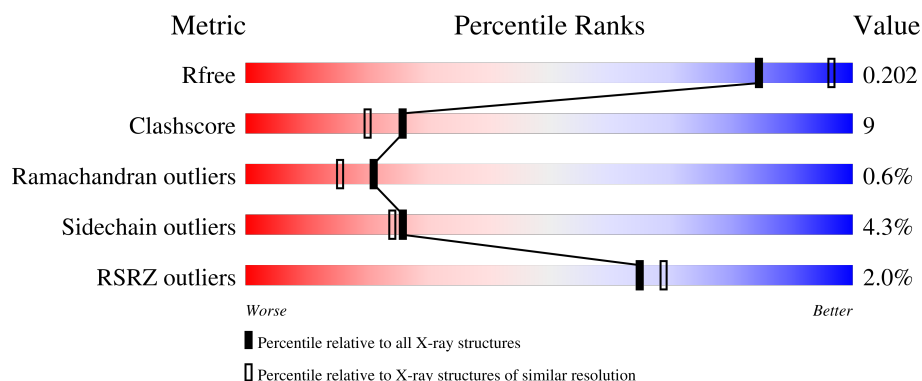
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (2.16-2.16)

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	264	0% 77% 21% .
1	B	264	77% 21% .
1	C	264	2% 75% 23% .
1	D	264	2% 80% 19% .
1	E	264	3% 75% 21% ..

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Mol	Chain	Length	Quality of chain
1	F	264	
1	G	264	
1	H	264	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	PEG	B	301	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 17760 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 Lactonase for protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	263	Total	C	N	O	S	0	0	0
			2048	1300	347	392	9			
1	B	263	Total	C	N	O	S	0	0	0
			2048	1300	347	392	9			
1	C	263	Total	C	N	O	S	0	0	0
			2048	1300	347	392	9			
1	D	264	Total	C	N	O	S	0	0	0
			2053	1303	348	393	9			
1	E	262	Total	C	N	O	S	0	0	0
			2038	1294	345	390	9			
1	F	263	Total	C	N	O	S	0	0	0
			2048	1300	347	392	9			
1	G	262	Total	C	N	O	S	0	0	0
			2038	1294	345	390	9			
1	H	262	Total	C	N	O	S	0	0	0
			2038	1294	345	390	9			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	105	ALA	SER	engineered mutation	UNP A0A0D2ILK1
A	160	ALA	TYR	engineered mutation	UNP A0A0D2ILK1
B	105	ALA	SER	engineered mutation	UNP A0A0D2ILK1
B	160	ALA	TYR	engineered mutation	UNP A0A0D2ILK1
C	105	ALA	SER	engineered mutation	UNP A0A0D2ILK1
C	160	ALA	TYR	engineered mutation	UNP A0A0D2ILK1
D	105	ALA	SER	engineered mutation	UNP A0A0D2ILK1
D	160	ALA	TYR	engineered mutation	UNP A0A0D2ILK1
E	105	ALA	SER	engineered mutation	UNP A0A0D2ILK1
E	160	ALA	TYR	engineered mutation	UNP A0A0D2ILK1
F	105	ALA	SER	engineered mutation	UNP A0A0D2ILK1
F	160	ALA	TYR	engineered mutation	UNP A0A0D2ILK1
G	105	ALA	SER	engineered mutation	UNP A0A0D2ILK1

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Chain	Residue	Modelled	Actual	Comment	Reference
G	160	ALA	TYR	engineered mutation	UNP A0A0D2ILK1
H	105	ALA	SER	engineered mutation	UNP A0A0D2ILK1
H	160	ALA	TYR	engineered mutation	UNP A0A0D2ILK1

- Molecule 2 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			7	4	3		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	245	Total	O	0	0
			245	245		
3	B	231	Total	O	0	0
			231	231		
3	C	180	Total	O	0	0
			180	180		
3	D	151	Total	O	0	0
			151	151		
3	E	162	Total	O	0	0
			162	162		
3	F	101	Total	O	0	0
			101	101		
3	G	206	Total	O	0	0
			206	206		

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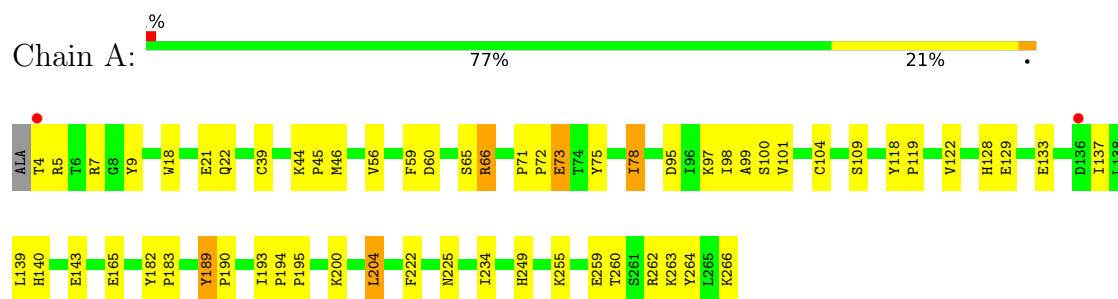
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	H	118	Total 118	O 118	0	0

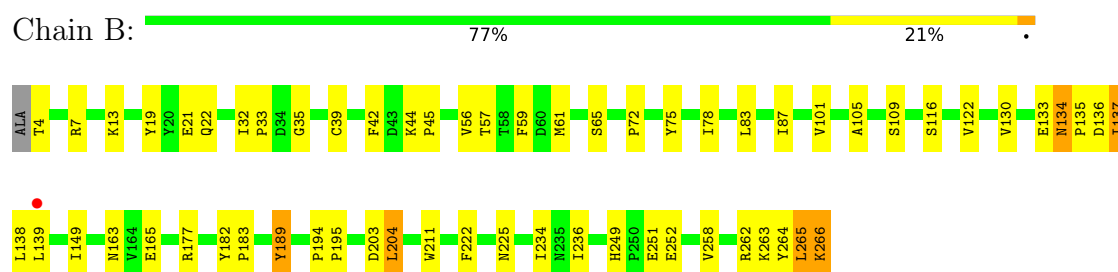
3 Residue-property plots [i](#)

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.

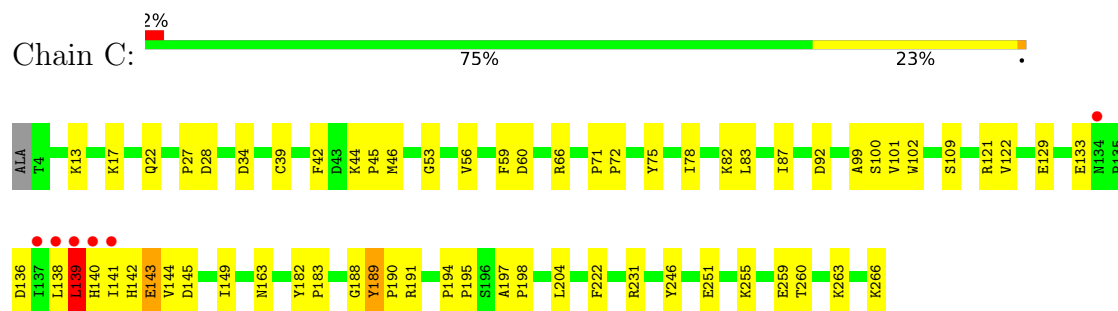
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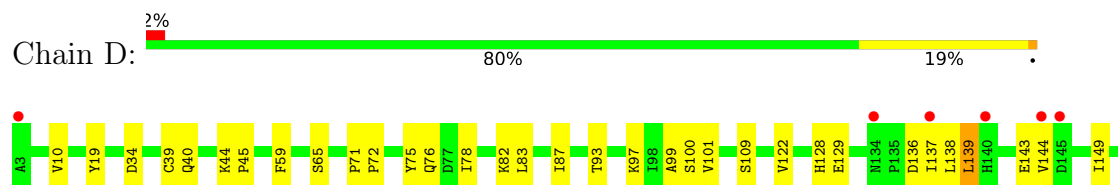
• Molecule 1: Lactonase for protein



• Molecule 1: Lactonase for protein

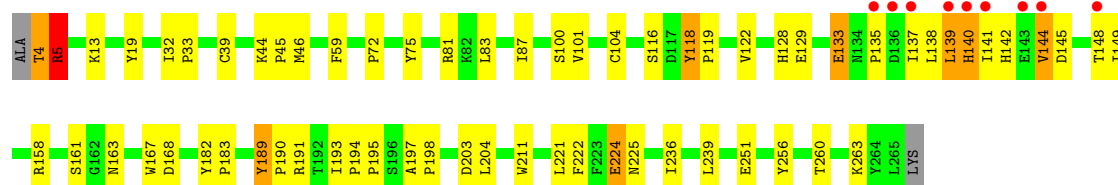
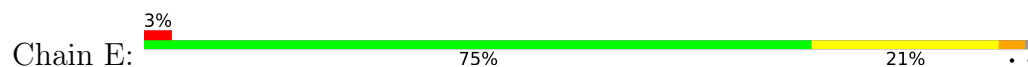


• Molecule 1: Lactonase for protein

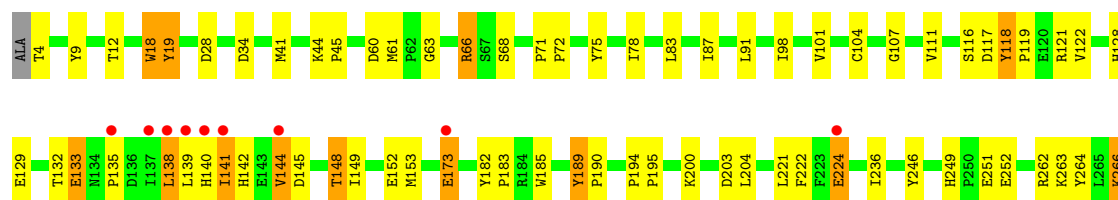




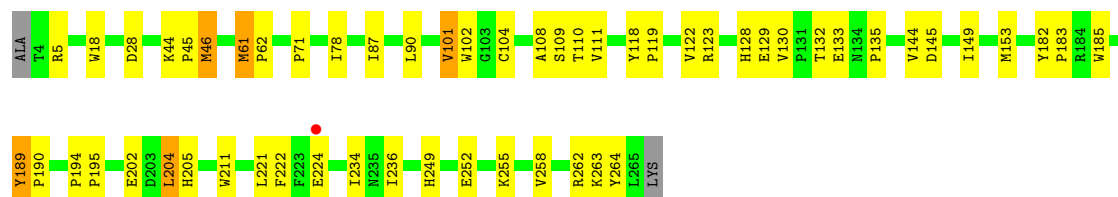
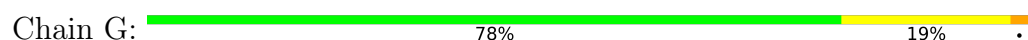
- Molecule 1: Lactonase for protein



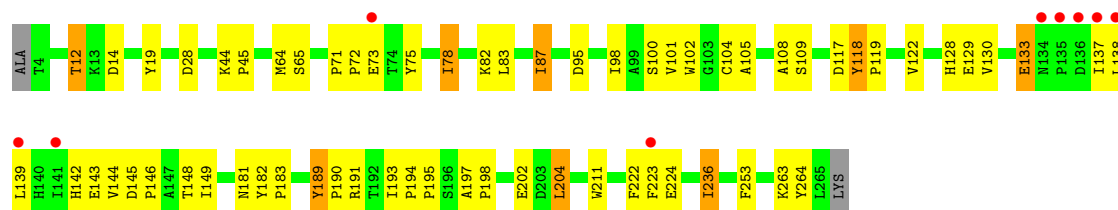
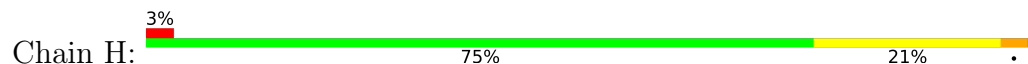
- Molecule 1: Lactonase for protein



- Molecule 1: Lactonase for protein



- Molecule 1: Lactonase for protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	75.38Å 94.97Å 100.50Å 90.71° 92.11° 91.91°	Depositor
Resolution (Å)	24.70 – 2.15 24.70 – 2.15	Depositor EDS
% Data completeness (in resolution range)	94.7 (24.70-2.15) 87.6 (24.70-2.15)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.31 (at 2.15Å)	Xtriage
Refinement program	PHENIX (1.12_2829: ???)	Depositor
R, R_{free}	0.171 , 0.211 0.183 , 0.202	Depositor DCC
R_{free} test set	2024 reflections (1.41%)	wwPDB-VP
Wilson B-factor (Å ²)	27.4	Xtriage
Anisotropy	0.251	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 40.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.044 for h,-k,-l 0.016 for -h,k,-l 0.015 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	17760	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.45% 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: PEG

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	0.84	0/2106	0.99	11/2875 (0.4%)
1	B	0.88	0/2106	1.03	12/2875 (0.4%)
1	C	0.81	0/2106	0.98	11/2875 (0.4%)
1	D	0.80	0/2111	0.97	10/2882 (0.3%)
1	E	0.84	2/2096 (0.1%)	0.98	9/2864 (0.3%)
1	F	0.75	0/2106	0.97	15/2875 (0.5%)
1	G	0.81	0/2096	0.97	12/2864 (0.4%)
1	H	0.80	0/2096	1.04	13/2864 (0.5%)
All	All	0.82	2/16823 (0.0%)	0.99	93/22974 (0.4%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	158	ARG	C-O	-5.49	1.17	1.24
1	E	168	ASP	C-O	-5.11	1.17	1.24

The worst 5 of 93 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	71	PRO	CA-C-N	8.61	128.75	119.28
1	H	71	PRO	C-N-CA	8.61	128.75	119.28
1	B	204	LEU	N-CA-C	8.33	123.67	113.17
1	B	265	LEU	N-CA-C	8.15	119.85	110.97
1	A	204	LEU	N-CA-C	8.15	124.22	113.30

There are no chirality outliers.

There are no planarity outliers.

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	2048	0	1989	29	0
1	B	2048	0	1989	39	0
1	C	2048	0	1989	36	0
1	D	2053	0	1994	31	0
1	E	2038	0	1976	42	0
1	F	2048	0	1989	55	0
1	G	2038	0	1976	32	0
1	H	2038	0	1976	45	0
2	B	7	0	10	4	0
3	A	245	0	0	4	0
3	B	231	0	0	2	0
3	C	180	0	0	4	0
3	D	151	0	0	0	0
3	E	162	0	0	3	0
3	F	101	0	0	2	0
3	G	206	0	0	0	0
3	H	118	0	0	1	0
All	All	17760	0	15888	305	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 9.

The worst 5 of 305 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:35:GLY:HA3	2:B:301:PEG:H11	1.39	1.01
1:D:255:LYS:HE2	1:D:259:GLU:CG	2.01	0.90
3:A:430:HOH:O	1:C:231:ARG:HG2	1.71	0.89
1:D:136:ASP:HA	1:D:139:LEU:HD23	1.54	0.89
1:E:4:THR:HA	3:E:363:HOH:O	1.72	0.88

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	261/264 (99%)	254 (97%)	6 (2%)	1 (0%)	30	26
1	B	261/264 (99%)	253 (97%)	6 (2%)	2 (1%)	16	10
1	C	261/264 (99%)	252 (97%)	6 (2%)	3 (1%)	11	7
1	D	262/264 (99%)	254 (97%)	7 (3%)	1 (0%)	30	26
1	E	260/264 (98%)	251 (96%)	7 (3%)	2 (1%)	16	10
1	F	261/264 (99%)	247 (95%)	13 (5%)	1 (0%)	30	26
1	G	260/264 (98%)	253 (97%)	6 (2%)	1 (0%)	30	26
1	H	260/264 (98%)	248 (95%)	11 (4%)	1 (0%)	30	26
All	All	2086/2112 (99%)	2012 (96%)	62 (3%)	12 (1%)	21	15

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	189	TYR
1	C	139	LEU
1	E	163	ASN
1	A	189	TYR
1	B	163	ASN

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	222/222 (100%)	213 (96%)	9 (4%)	27	26

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	222/222 (100%)	214 (96%)	8 (4%)	31	31
1	C	222/222 (100%)	214 (96%)	8 (4%)	31	31
1	D	222/222 (100%)	214 (96%)	8 (4%)	31	31
1	E	221/222 (100%)	210 (95%)	11 (5%)	22	18
1	F	222/222 (100%)	208 (94%)	14 (6%)	16	11
1	G	221/222 (100%)	217 (98%)	4 (2%)	51	58
1	H	221/222 (100%)	207 (94%)	14 (6%)	16	11
All	All	1773/1776 (100%)	1697 (96%)	76 (4%)	26	24

5 of 76 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	266	LYS
1	H	143	GLU
1	G	109	SER
1	H	95	ASP
1	H	236	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	GLN
1	A	179	HIS
1	B	52	ASN
1	F	140	HIS
1	H	142	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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	PEG	B	301	-	6,6,6	0.32	0	5,5,5	0.61	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	PEG	B	301	-	-	0/4/4/4	-

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.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	301	PEG	4	0

5.7 Other polymers [i](#)

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	263/264 (99%)	-0.28	2 (0%) 82 84	22, 29, 43, 62	0
1	B	263/264 (99%)	-0.29	1 (0%) 88 90	20, 28, 42, 68	0
1	C	263/264 (99%)	-0.12	6 (2%) 61 64	21, 32, 58, 78	0
1	D	264/264 (100%)	-0.01	6 (2%) 61 64	23, 34, 62, 83	0
1	E	262/264 (99%)	-0.01	9 (3%) 48 52	24, 35, 52, 89	0
1	F	263/264 (99%)	0.25	9 (3%) 48 52	28, 41, 67, 94	0
1	G	262/264 (99%)	-0.15	1 (0%) 88 90	24, 33, 47, 58	0
1	H	262/264 (99%)	0.18	9 (3%) 48 52	25, 39, 65, 93	0
All	All	2102/2112 (99%)	-0.05	43 (2%) 65 69	20, 34, 56, 94	0

The worst 5 of 43 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	140	HIS	4.1
1	E	135	PRO	3.8
1	D	3	ALA	3.8
1	F	141	ILE	3.7
1	H	135	PRO	3.5

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

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($\text{\AA}^2$)	Q<0.9
2	PEG	B	301	7/7	0.92	0.11	22,42,48,51	0

6.5 Other polymers

There are no such residues in this entry.