



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 12, 2026 – 04:36 PM UTC

PDB ID : 4RHH / pdb_00004rhh
Title : Crystal structure of the catalytic mutant Xyn52B2-E335G, a GH52 Beta-D-xylosidase from *Geobacillus stearothermophilus* T6
Authors : Dann, R.; Lansky, S.; Lavid, N.; Zehavi, A.; Belakhov, V.; Baasov, T.; Manjasetty, B.; Belrhali, H.; Shoham, Y.; Shoham, G.
Deposited on : 2014-10-02
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

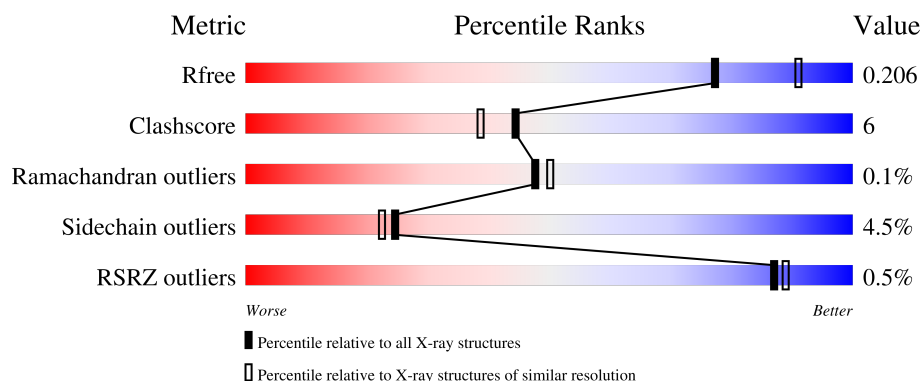
1 Overall quality at a glance

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	705	84% 12% ..
1	B	705	85% 11% ..
1	C	705	85% 12% ..
1	D	705	85% 11% ..

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
3	TRS	A	802	-	X	-	-
3	TRS	C	802	-	X	-	-
3	TRS	C	803	-	X	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 24010 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-xylosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	694	Total	C	N	O	S	0	0	0
			5543	3534	942	1041	26			
1	B	694	Total	C	N	O	S	0	2	0
			5565	3546	950	1043	26			
1	C	696	Total	C	N	O	S	0	0	0
			5550	3538	944	1042	26			
1	D	693	Total	C	N	O	S	0	0	0
			5534	3528	941	1039	26			

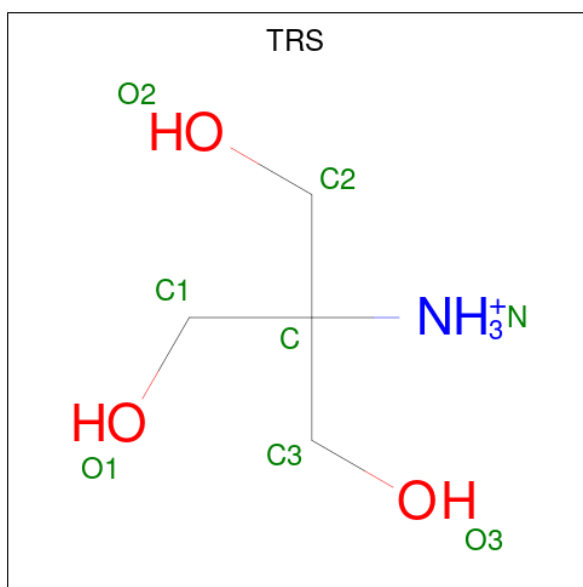
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	335	GLY	GLU	engineered mutation	UNP Q09LZ0
B	335	GLY	GLU	engineered mutation	UNP Q09LZ0
C	335	GLY	GLU	engineered mutation	UNP Q09LZ0
D	335	GLY	GLU	engineered mutation	UNP Q09LZ0

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		
2	B	1	Total	Ca	0	0
			1	1		
2	C	2	Total	Ca	0	0
			2	2		
2	D	1	Total	Ca	0	0
			1	1		

- Molecule 3 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: C₄H₁₂NO₃).



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

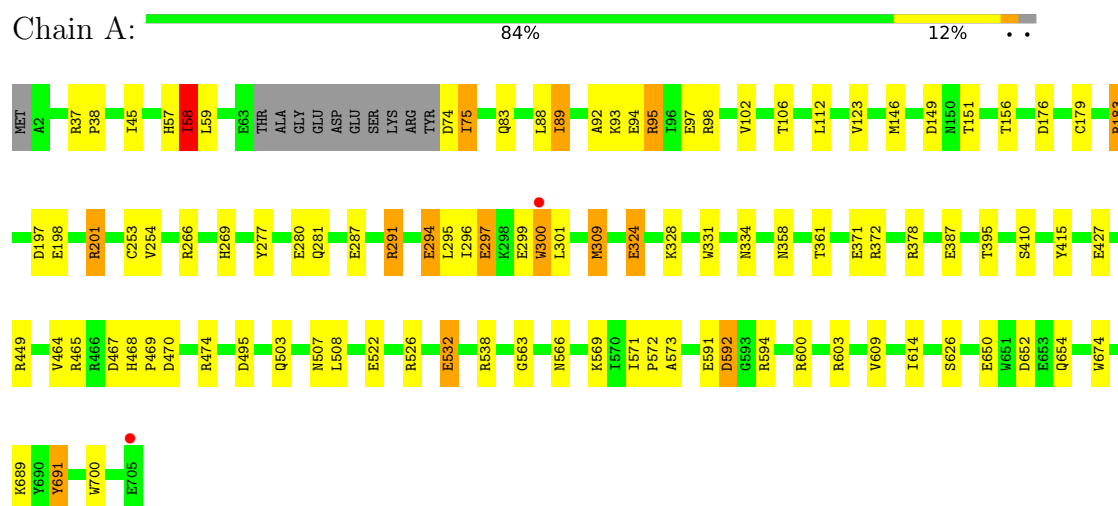
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	434	Total	O	0	0
			434	434		
4	B	439	Total	O	0	0
			439	439		
4	C	454	Total	O	0	0
			454	454		
4	D	430	Total	O	0	0
			430	430		

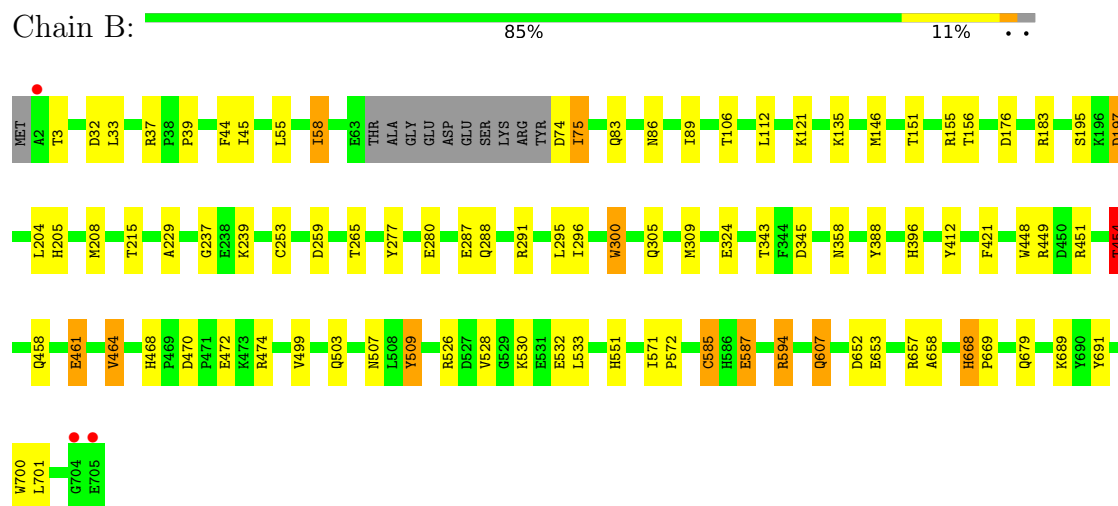
3 Residue-property plots

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.

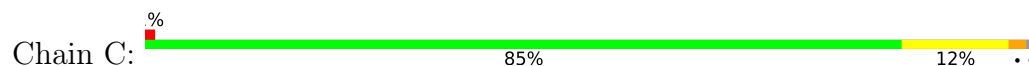
• Molecule 1: Beta-xylosidase

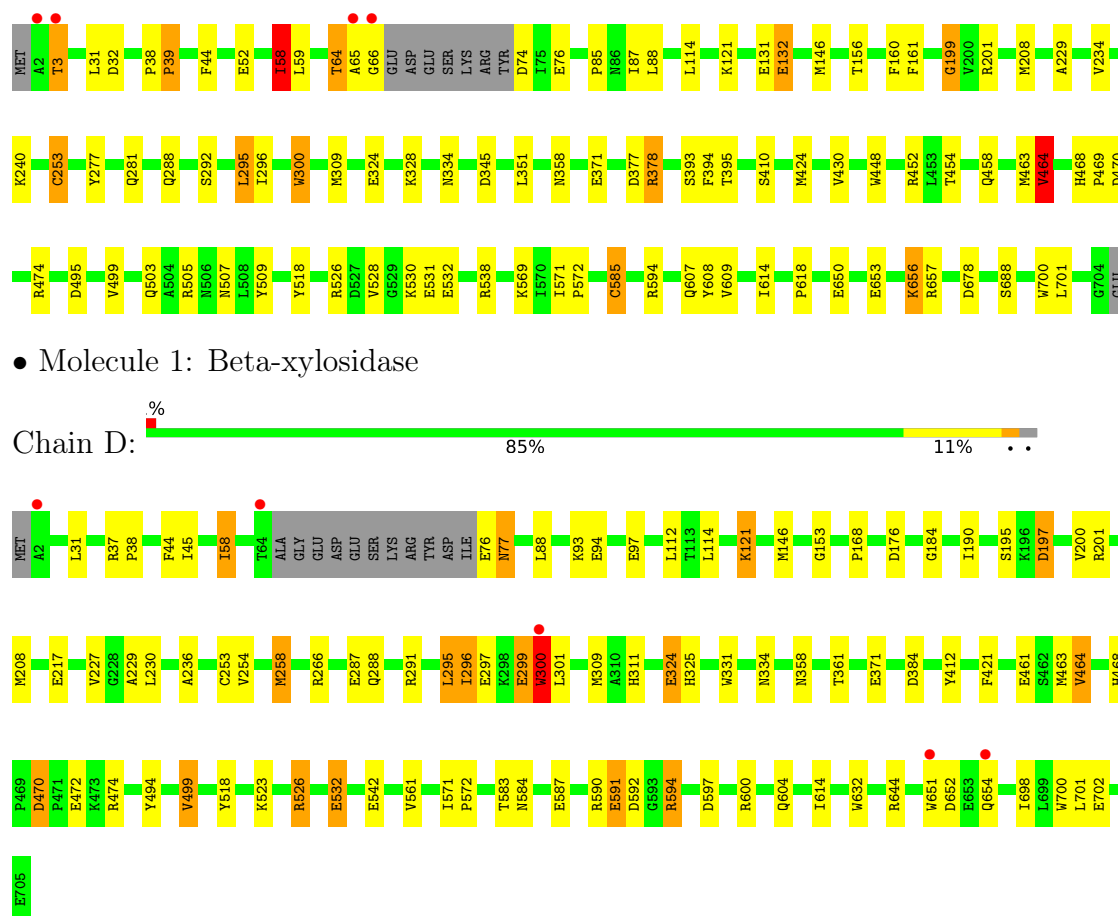


• Molecule 1: Beta-xylosidase



• Molecule 1: Beta-xylosidase





• Molecule 1: Beta-xylosidase

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	97.45Å 119.08Å 243.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.43 – 2.15 39.43 – 2.15	Depositor EDS
% Data completeness (in resolution range)	98.5 (39.43-2.15) 98.5 (39.43-2.15)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.91 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.150 , 0.203 0.159 , 0.206	Depositor DCC
R_{free} test set	7592 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	21.4	Xtriage
Anisotropy	0.042	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 39.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	24010	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.08% 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: CA, 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	1.16	6/5689 (0.1%)	1.09	5/7721 (0.1%)
1	B	1.19	6/5711 (0.1%)	1.11	12/7749 (0.2%)
1	C	1.16	5/5696 (0.1%)	1.09	11/7731 (0.1%)
1	D	1.17	4/5680 (0.1%)	1.09	7/7709 (0.1%)
All	All	1.17	21/22776 (0.1%)	1.09	35/30910 (0.1%)

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	626	SER	C-O	-7.73	1.14	1.24
1	A	372	ARG	C-O	-6.75	1.16	1.24
1	B	658	ALA	N-CA	6.65	1.54	1.46
1	D	300	TRP	NE1-CE2	-6.60	1.30	1.37
1	A	183	ARG	N-CA	-6.11	1.38	1.46

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	454	THR	CB-CA-C	-8.04	98.25	110.88
1	A	495	ASP	N-CA-C	6.87	118.77	111.28
1	D	470	ASP	CA-C-N	6.84	127.12	119.32
1	D	470	ASP	C-N-CA	6.84	127.12	119.32
1	C	58	ILE	CA-CB-CG2	6.68	121.85	110.50

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	5543	0	5337	76	0
1	B	5565	0	5361	54	0
1	C	5550	0	5346	61	0
1	D	5534	0	5329	68	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	2	0	0	0	0
2	D	1	0	0	0	0
3	A	16	0	24	6	0
3	B	8	0	12	0	0
3	C	16	0	24	8	0
3	D	16	0	24	2	0
4	A	434	0	0	27	0
4	B	439	0	0	15	0
4	C	454	0	0	12	0
4	D	430	0	0	18	0
All	All	24010	0	21457	264	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 6.

The worst 5 of 264 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:607:GLN:HG3	4:B:1317:HOH:O	1.50	1.12
1:B:208:MET:HE1	1:B:229:ALA:HB2	1.40	1.00
1:A:468:HIS:HD2	1:A:470:ASP:H	1.16	0.92
1:D:208:MET:HE1	1:D:229:ALA:HB2	1.52	0.90
1:B:296:ILE:HG21	4:B:1326:HOH:O	1.71	0.89

There are no symmetry-related clashes.

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	690/705 (98%)	664 (96%)	25 (4%)	1 (0%)	48	50
1	B	692/705 (98%)	675 (98%)	17 (2%)	0	100	100
1	C	692/705 (98%)	675 (98%)	16 (2%)	1 (0%)	48	50
1	D	689/705 (98%)	662 (96%)	25 (4%)	2 (0%)	36	34
All	All	2763/2820 (98%)	2676 (97%)	83 (3%)	4 (0%)	48	50

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	77	ASN
1	D	614	ILE
1	C	614	ILE
1	A	614	ILE

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	584/593 (98%)	558 (96%)	26 (4%)	24	22
1	B	586/593 (99%)	558 (95%)	28 (5%)	23	20
1	C	584/593 (98%)	560 (96%)	24 (4%)	27	26
1	D	583/593 (98%)	556 (95%)	27 (5%)	24	22
All	All	2337/2372 (98%)	2232 (96%)	105 (4%)	24	22

5 of 105 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	114	LEU
1	C	499	VAL
1	D	499	VAL
1	C	132	GLU
1	C	324	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	288	GLN
1	C	468	HIS
1	C	350	GLN
1	C	551	HIS
1	B	458	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 [i](#)

Of 12 ligands modelled in this entry, 5 are monoatomic - leaving 7 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
3	TRS	A	802	-	7,7,7	1.25	0	9,9,9	1.60	3 (33%)
3	TRS	B	802	-	7,7,7	0.64	0	9,9,9	1.86	3 (33%)
3	TRS	C	802	-	7,7,7	0.84	0	9,9,9	1.97	3 (33%)
3	TRS	D	803	-	7,7,7	0.61	0	9,9,9	2.02	2 (22%)
3	TRS	D	802	-	7,7,7	0.64	0	9,9,9	1.16	1 (11%)
3	TRS	A	803	-	7,7,7	1.24	1 (14%)	9,9,9	1.91	2 (22%)
3	TRS	C	803	-	7,7,7	0.96	0	9,9,9	2.38	5 (55%)

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
3	TRS	A	802	-	-	8/9/9/9	-
3	TRS	B	802	-	-	5/9/9/9	-
3	TRS	C	802	-	-	9/9/9/9	-
3	TRS	D	803	-	-	6/9/9/9	-
3	TRS	D	802	-	-	2/9/9/9	-
3	TRS	A	803	-	-	5/9/9/9	-
3	TRS	C	803	-	-	6/9/9/9	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	803	TRS	C1-C	-2.01	1.47	1.53

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	803	TRS	O2-C2-C	-4.94	97.10	110.88
3	A	803	TRS	C2-C-C1	-4.04	99.89	110.66
3	C	803	TRS	O1-C1-C	-3.96	99.82	110.88
3	C	802	TRS	C3-C-C1	3.75	120.63	110.66
3	B	802	TRS	C3-C-C1	3.71	120.53	110.66

There are no chirality outliers.

5 of 41 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	802	TRS	N-C-C1-O1
3	A	802	TRS	C3-C-C2-O2
3	A	802	TRS	N-C-C2-O2
3	A	802	TRS	N-C-C3-O3
3	A	803	TRS	C1-C-C2-O2

There are no ring outliers.

5 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	802	TRS	5	0
3	C	802	TRS	5	0
3	D	802	TRS	2	0
3	A	803	TRS	1	0
3	C	803	TRS	3	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	694/705 (98%)	-0.48	2 (0%) 90 91	10, 21, 41, 73	0
1	B	694/705 (98%)	-0.51	3 (0%) 88 90	10, 19, 42, 79	2 (0%)
1	C	696/705 (98%)	-0.57	4 (0%) 85 87	11, 20, 37, 87	0
1	D	693/705 (98%)	-0.50	5 (0%) 84 85	12, 20, 43, 79	0
All	All	2777/2820 (98%)	-0.52	14 (0%) 87 89	10, 20, 41, 87	2 (0%)

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	65	ALA	3.9
1	C	2	ALA	3.6
1	D	651	TRP	3.4
1	B	705	GLU	2.8
1	D	64	THR	2.5

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](#)

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
3	TRS	D	802	8/8	0.78	0.20	54,65,70,76	0
3	TRS	C	802	8/8	0.79	0.17	28,31,46,55	0
3	TRS	A	802	8/8	0.80	0.15	33,36,41,50	0
3	TRS	C	803	8/8	0.89	0.12	20,25,28,30	0
3	TRS	A	803	8/8	0.89	0.11	21,25,27,34	0
3	TRS	D	803	8/8	0.92	0.07	18,20,21,23	0
2	CA	C	804	1/1	0.95	0.06	53,53,53,53	0
3	TRS	B	802	8/8	0.95	0.07	18,23,26,26	0
2	CA	A	801	1/1	0.99	0.03	22,22,22,22	0
2	CA	D	801	1/1	0.99	0.03	17,17,17,17	0
2	CA	C	801	1/1	0.99	0.01	19,19,19,19	0
2	CA	B	801	1/1	1.00	0.01	13,13,13,13	0

6.5 Other polymers ⓘ

There are no such residues in this entry.