



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 03:13 AM UTC

PDB ID : 3VSV / pdb_00003vsv
Title : The complex structure of XylC with xylose
Authors : Huang, C.H.; Sun, Y.; Ko, T.P.; Ma, Y.; Chen, C.C.; Zheng, Y.; Chan, H.C.;
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Deposited on : 2012-05-09
Resolution : 1.48 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

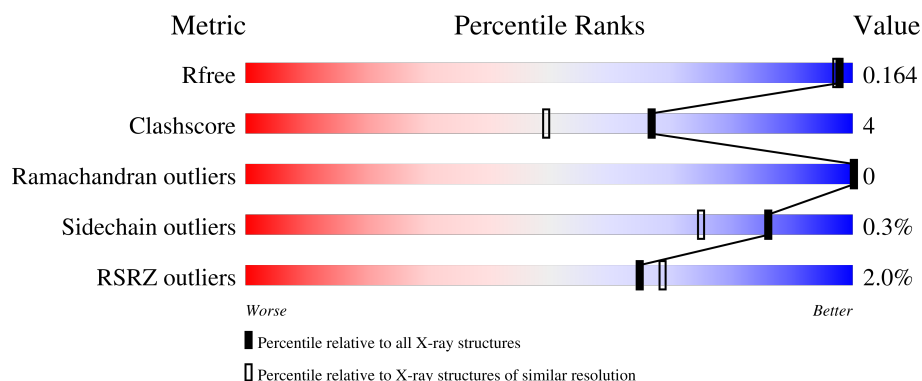
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.48 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	6779 (1.50-1.46)
Clashscore	190562	7025 (1.50-1.46)
Ramachandran outliers	187476	6917 (1.50-1.46)
Sidechain outliers	187428	6914 (1.50-1.46)
RSRZ outliers	180081	6781 (1.50-1.46)

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	638	<div> <div>0%</div> <div>92%</div> <div>8%</div> </div>
1	B	638	<div> <div>2%</div> <div>92%</div> <div>7%</div> </div>
1	C	638	<div> <div>2%</div> <div>93%</div> <div>7%</div> </div>
1	D	638	<div> <div>2%</div> <div>92%</div> <div>8%</div> </div>

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	XYP	A	707	-	-	X	-
2	XYP	D	701	-	-	X	-

2 Entry composition [i](#)

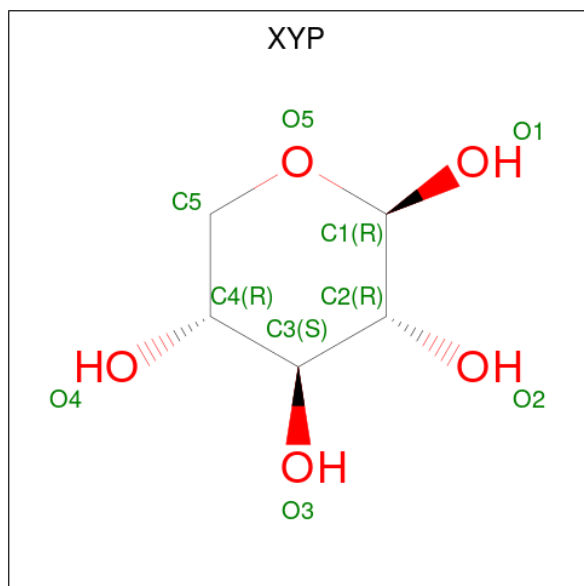
There are 4 unique types of molecules in this entry. The entry contains 24551 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Xylosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	638	Total	C	N	O	S	0	0	0
			5147	3275	877	983	12			
1	B	638	Total	C	N	O	S	0	0	0
			5147	3275	877	983	12			
1	C	638	Total	C	N	O	S	0	0	0
			5147	3275	877	983	12			
1	D	638	Total	C	N	O	S	0	0	0
			5147	3275	877	983	12			

- Molecule 2 is beta-D-xylopyranose (CCD ID: XYP) (formula: C₅H₁₀O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			10	5	5		
2	A	1	Total	C	O	0	0
			10	5	5		

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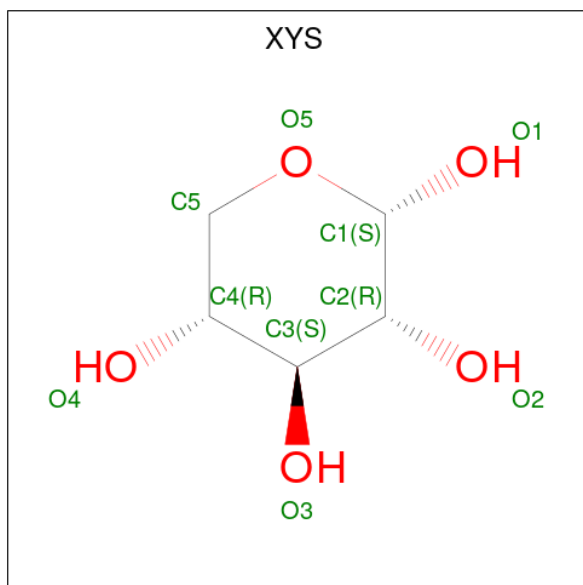
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			10	5	5		
2	A	1	Total	C	O	0	0
			10	5	5		
2	A	1	Total	C	O	0	0
			10	5	5		
2	A	1	Total	C	O	0	0
			10	5	5		
2	A	1	Total	C	O	0	0
			10	5	5		
2	B	1	Total	C	O	0	0
			10	5	5		
2	B	1	Total	C	O	0	0
			10	5	5		
2	B	1	Total	C	O	0	0
			10	5	5		
2	B	1	Total	C	O	0	0
			10	5	5		
2	B	1	Total	C	O	0	0
			10	5	5		
2	B	1	Total	C	O	0	0
			10	5	5		
2	C	1	Total	C	O	0	0
			10	5	5		
2	C	1	Total	C	O	0	0
			10	5	5		
2	C	1	Total	C	O	0	0
			10	5	5		
2	C	1	Total	C	O	0	0
			10	5	5		
2	C	1	Total	C	O	0	0
			10	5	5		
2	D	1	Total	C	O	0	0
			10	5	5		
2	D	1	Total	C	O	0	0
			10	5	5		
2	D	1	Total	C	O	0	0
			10	5	5		
2	D	1	Total	C	O	0	0
			10	5	5		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	D	1	Total	C	O	0	0
			10	5	5		
2	D	1	Total	C	O	0	0
			10	5	5		
2	D	1	Total	C	O	0	0
			10	5	5		

- Molecule 3 is alpha-D-xylopyranose (CCD ID: YYS) (formula: C₅H₁₀O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			10	5	5		
3	A	1	Total	C	O	0	0
			10	5	5		
3	B	1	Total	C	O	0	0
			10	5	5		
3	B	1	Total	C	O	0	0
			10	5	5		
3	C	1	Total	C	O	0	0
			10	5	5		
3	C	1	Total	C	O	0	0
			10	5	5		
3	C	1	Total	C	O	0	0
			10	5	5		
3	D	1	Total	C	O	0	0
			10	5	5		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	D	1	Total	C	O	0	0
			10	5	5		

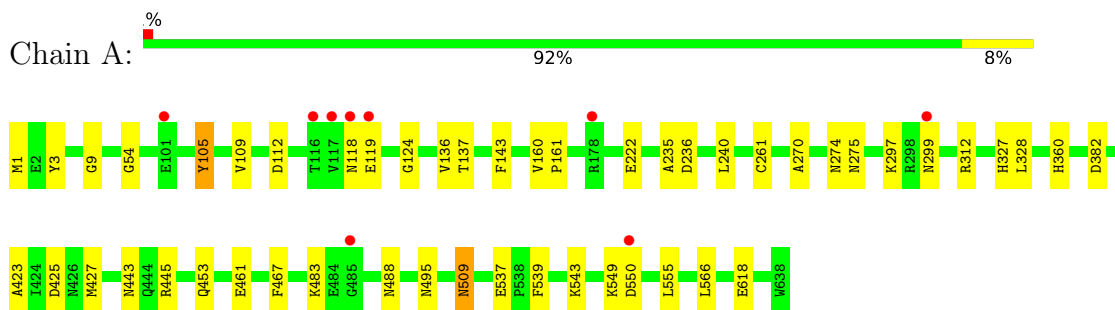
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	912	Total	O	0	0
			912	912		
4	B	942	Total	O	0	0
			942	942		
4	C	842	Total	O	0	0
			842	842		
4	D	917	Total	O	0	0
			917	917		

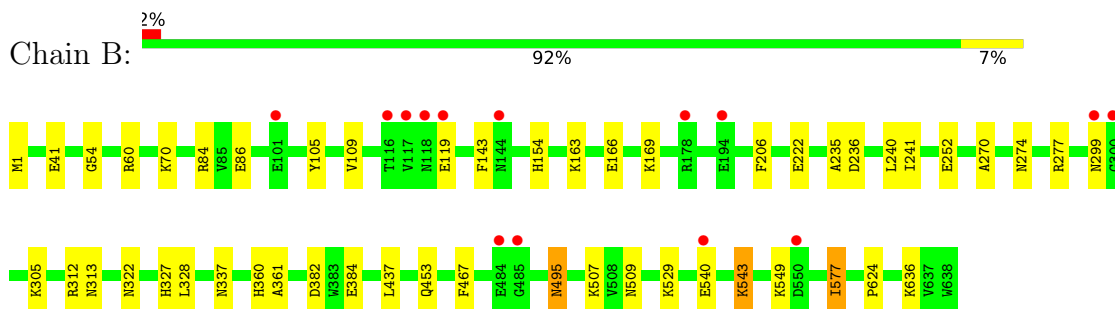
3 Residue-property plots [i](#)

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.

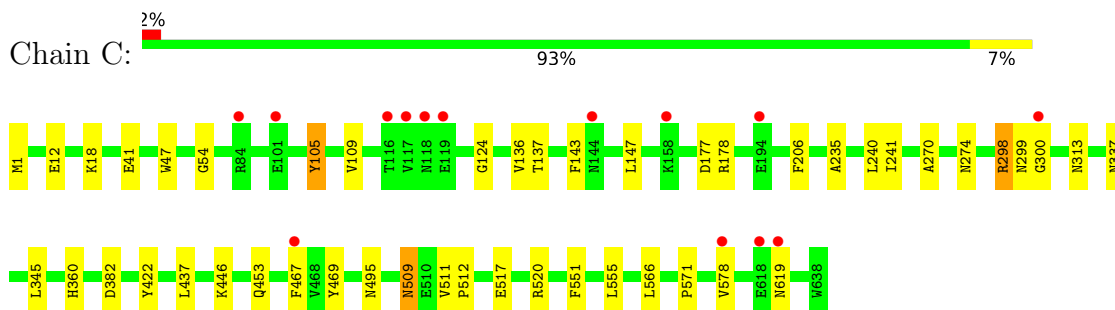
- Molecule 1: Xylosidase



- Molecule 1: Xylosidase

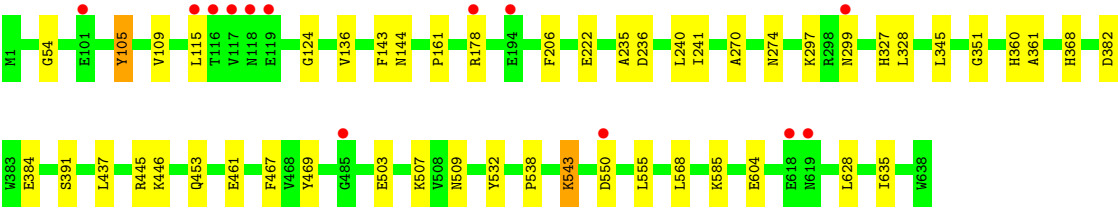


- Molecule 1: Xylosidase



- Molecule 1: Xylosidase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	88.78Å 201.95Å 100.11Å 90.00° 99.18° 90.00°	Depositor
Resolution (Å)	25.00 – 1.48 25.00 – 1.48	Depositor EDS
% Data completeness (in resolution range)	(Not available) (25.00-1.48) 95.2 (25.00-1.48)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.50 (at 1.48Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.150 , 0.168 0.146 , 0.164	Depositor DCC
R_{free} test set	27272 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	10.9	Xtriage
Anisotropy	0.254	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 50.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	24551	wwPDB-VP
Average B, all atoms (Å ²)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.16% 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: XYS, XYP

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	0.79	1/5276 (0.0%)	1.06	16/7151 (0.2%)
1	B	0.82	1/5276 (0.0%)	1.06	15/7151 (0.2%)
1	C	0.80	1/5276 (0.0%)	1.06	14/7151 (0.2%)
1	D	0.79	0/5276	1.06	10/7151 (0.1%)
All	All	0.80	3/21104 (0.0%)	1.06	55/28604 (0.2%)

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
1	C	0	1
1	D	0	1
All	All	0	4

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	1	MET	SD-CE	6.38	1.95	1.79
1	C	1	MET	SD-CE	5.92	1.94	1.79
1	A	261	CYS	CA-C	5.26	1.55	1.52

The worst 5 of 55 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	143	PHE	N-CA-C	10.46	122.77	111.36
1	A	143	PHE	N-CA-C	9.74	123.67	111.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	143	PHE	N-CA-C	9.27	123.09	111.69
1	C	109	VAL	N-CA-C	-9.20	96.70	108.84
1	D	143	PHE	N-CA-C	8.71	122.41	111.69

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	105	TYR	Sidechain
1	B	105	TYR	Sidechain
1	C	105	TYR	Sidechain
1	D	105	TYR	Sidechain

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	5147	0	4962	38	0
1	B	5147	0	4962	37	0
1	C	5147	0	4962	43	0
1	D	5147	0	4962	41	0
2	A	70	0	0	9	0
2	B	60	0	0	0	0
2	C	50	0	0	2	0
2	D	80	0	0	11	0
3	A	20	0	20	4	0
3	B	20	0	20	0	0
3	C	30	0	30	2	0
3	D	20	0	20	3	0
4	A	912	0	0	7	0
4	B	942	0	0	16	0
4	C	842	0	0	6	0
4	D	917	0	0	15	0
All	All	24551	0	19938	151	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 4.

The worst 5 of 151 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:A:509:ASN:HB3	4:A:1676:HOH:O	1.34	1.27
1:C:509:ASN:HB3	4:C:1589:HOH:O	1.32	1.23
2:D:701:XYP:C4	4:D:1665:HOH:O	1.86	1.20
1:C:337:ASN:HB2	4:C:1599:HOH:O	1.47	1.15
1:A:427:MET:CE	1:A:445:ARG:HH21	1.58	1.15

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	636/638 (100%)	612 (96%)	24 (4%)	0	100	100
1	B	636/638 (100%)	612 (96%)	24 (4%)	0	100	100
1	C	636/638 (100%)	610 (96%)	26 (4%)	0	100	100
1	D	636/638 (100%)	614 (96%)	22 (4%)	0	100	100
All	All	2544/2552 (100%)	2448 (96%)	96 (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	550/550 (100%)	548 (100%)	2 (0%)	84	70
1	B	550/550 (100%)	548 (100%)	2 (0%)	84	70
1	C	550/550 (100%)	548 (100%)	2 (0%)	84	70
1	D	550/550 (100%)	550 (100%)	0	100	100
All	All	2200/2200 (100%)	2194 (100%)	6 (0%)	86	75

5 of 6 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	577	ILE
1	C	18	LYS
1	C	147	LEU
1	A	618	GLU
1	A	119	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	477	ASN
1	D	477	ASN
1	C	93	GLN
1	C	632	ASN
1	B	632	ASN

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 oligosaccharides in this entry.

5.6 Ligand geometry

35 ligands are 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	XYP	D	705	-	10,10,10	1.01	0	14,14,14	0.51	0
3	XYS	C	707	-	10,10,10	1.61	2 (20%)	14,14,14	0.58	0
3	XYS	C	708	-	10,10,10	1.53	2 (20%)	14,14,14	1.31	1 (7%)
3	XYS	A	708	-	10,10,10	1.06	0	14,14,14	0.69	0
2	XYP	C	705	-	10,10,10	1.08	1 (10%)	14,14,14	1.01	1 (7%)
2	XYP	A	702	-	10,10,10	0.98	0	14,14,14	0.66	0
2	XYP	A	701	-	10,10,10	1.77	3 (30%)	14,14,14	1.01	1 (7%)
3	XYS	D	709	-	10,10,10	1.69	2 (20%)	14,14,14	0.71	0
2	XYP	D	702	-	10,10,10	2.11	3 (30%)	14,14,14	1.12	1 (7%)
2	XYP	D	708	-	10,10,10	1.27	2 (20%)	14,14,14	0.99	1 (7%)
3	XYS	C	706	-	10,10,10	1.13	0	14,14,14	0.75	0
2	XYP	D	706	-	10,10,10	0.92	0	14,14,14	1.03	1 (7%)
2	XYP	B	705	-	10,10,10	1.14	1 (10%)	14,14,14	0.82	0
2	XYP	B	703	-	10,10,10	0.87	0	14,14,14	0.67	0
2	XYP	D	707	-	10,10,10	1.07	0	14,14,14	0.64	0
2	XYP	C	701	-	10,10,10	2.28	5 (50%)	14,14,14	1.02	1 (7%)
2	XYP	B	701	-	10,10,10	1.96	4 (40%)	14,14,14	1.01	0
2	XYP	B	704	-	10,10,10	1.02	0	14,14,14	0.65	0
2	XYP	C	704	-	10,10,10	1.39	2 (20%)	14,14,14	1.03	1 (7%)
2	XYP	C	702	-	10,10,10	0.98	0	14,14,14	0.63	0
2	XYP	C	703	-	10,10,10	1.10	1 (10%)	14,14,14	0.71	0
2	XYP	A	703	-	10,10,10	1.10	1 (10%)	14,14,14	0.71	1 (7%)
3	XYS	B	707	-	10,10,10	1.54	1 (10%)	14,14,14	0.59	0
2	XYP	D	703	-	10,10,10	0.97	0	14,14,14	0.75	0
2	XYP	B	706	-	10,10,10	1.07	1 (10%)	14,14,14	0.64	0
2	XYP	B	702	-	10,10,10	1.04	1 (10%)	14,14,14	0.88	1 (7%)
2	XYP	D	701	-	10,10,10	0.95	0	14,14,14	0.90	0
2	XYP	A	704	-	10,10,10	0.92	0	14,14,14	0.60	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	XYP	A	707	-	10,10,10	0.95	0	14,14,14	1.23	1 (7%)
3	XYS	A	709	-	10,10,10	1.34	1 (10%)	14,14,14	0.74	0
2	XYP	D	704	-	10,10,10	0.89	0	14,14,14	0.89	1 (7%)
3	XYS	B	708	-	10,10,10	1.35	0	14,14,14	0.70	0
3	XYS	D	710	-	10,10,10	1.22	0	14,14,14	0.70	0
2	XYP	A	705	-	10,10,10	1.01	0	14,14,14	1.05	1 (7%)
2	XYP	A	706	-	10,10,10	1.20	0	14,14,14	1.12	2 (14%)

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	XYP	D	705	-	-	-	0/1/1/1
3	XYS	C	707	-	-	-	0/1/1/1
3	XYS	C	708	-	-	-	0/1/1/1
3	XYS	A	708	-	-	-	0/1/1/1
2	XYP	C	705	-	-	-	0/1/1/1
2	XYP	A	702	-	-	-	0/1/1/1
2	XYP	A	701	-	-	-	0/1/1/1
3	XYS	D	709	-	-	-	0/1/1/1
2	XYP	D	702	-	-	-	0/1/1/1
2	XYP	D	708	-	-	-	0/1/1/1
3	XYS	C	706	-	-	-	0/1/1/1
2	XYP	D	706	-	-	-	0/1/1/1
2	XYP	B	705	-	-	-	0/1/1/1
2	XYP	B	703	-	-	-	0/1/1/1
2	XYP	D	707	-	-	-	0/1/1/1
2	XYP	C	701	-	-	-	0/1/1/1
2	XYP	B	701	-	-	-	0/1/1/1
2	XYP	B	704	-	-	-	0/1/1/1
2	XYP	C	704	-	-	-	0/1/1/1
2	XYP	C	702	-	-	-	0/1/1/1
2	XYP	C	703	-	-	-	0/1/1/1
2	XYP	A	703	-	-	-	0/1/1/1
3	XYS	B	707	-	-	-	0/1/1/1
2	XYP	D	703	-	-	-	0/1/1/1
2	XYP	B	706	-	-	-	0/1/1/1
2	XYP	B	702	-	-	-	0/1/1/1
2	XYP	D	701	-	-	-	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	XYP	A	704	-	-	-	0/1/1/1
2	XYP	A	707	-	-	-	0/1/1/1
3	XYS	A	709	-	-	-	0/1/1/1
2	XYP	D	704	-	-	-	0/1/1/1
3	XYS	B	708	-	-	-	0/1/1/1
3	XYS	D	710	-	-	-	0/1/1/1
2	XYP	A	705	-	-	-	0/1/1/1
2	XYP	A	706	-	-	-	0/1/1/1

The worst 5 of 33 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	701	XYP	C4-C3	4.43	1.59	1.52
2	D	702	XYP	O1-C1	3.73	1.51	1.39
3	D	709	XYS	O5-C1	3.50	1.49	1.43
2	D	702	XYP	C3-C2	3.48	1.61	1.52
2	C	701	XYP	O1-C1	3.27	1.49	1.39

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	708	XYS	C1-C2-C3	3.32	117.12	110.36
2	A	705	XYP	C5-O5-C1	-2.77	106.69	112.46
2	A	706	XYP	C5-C4-C3	-2.71	105.70	109.64
2	C	704	XYP	C4-C3-C2	-2.42	106.61	110.86
2	D	706	XYP	C5-O5-C1	-2.40	107.47	112.46

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

11 monomers are involved in 31 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	707	XYS	2	0
2	C	705	XYP	2	0
3	D	709	XYS	3	0
2	D	706	XYP	1	0
2	D	703	XYP	1	0
2	D	701	XYP	7	0
2	A	704	XYP	1	0
2	A	707	XYP	7	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	709	XYS	4	0
2	D	704	XYP	2	0
2	A	705	XYP	1	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	638/638 (100%)	-0.45	9 (1%) 73 77	6, 12, 26, 44	0
1	B	638/638 (100%)	-0.49	14 (2%) 62 66	7, 11, 25, 42	0
1	C	638/638 (100%)	-0.36	14 (2%) 62 66	7, 13, 26, 43	0
1	D	638/638 (100%)	-0.47	13 (2%) 65 69	7, 12, 24, 44	0
All	All	2552/2552 (100%)	-0.44	50 (1%) 65 69	6, 12, 25, 44	0

The worst 5 of 50 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	117	VAL	6.1
1	C	117	VAL	4.6
1	A	117	VAL	4.0
1	B	117	VAL	3.8
1	B	116	THR	3.7

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(\AA^2)	Q<0.9
3	XYS	A	709	10/10	0.68	0.19	37,42,44,45	0
2	XYP	A	704	10/10	0.72	0.18	39,43,45,45	0
3	XYS	C	708	10/10	0.75	0.17	46,47,48,49	0
2	XYP	C	704	10/10	0.77	0.19	34,38,40,40	0
2	XYP	C	703	10/10	0.78	0.16	31,37,38,39	0
2	XYP	D	708	10/10	0.78	0.18	34,37,39,41	0
3	XYS	C	707	10/10	0.79	0.15	32,35,36,36	0
3	XYS	D	709	10/10	0.79	0.17	29,33,34,34	0
2	XYP	B	705	10/10	0.80	0.18	34,40,41,41	0
2	XYP	A	703	10/10	0.80	0.14	41,43,43,44	0
2	XYP	B	703	10/10	0.80	0.14	42,43,44,44	0
2	XYP	D	704	10/10	0.80	0.15	51,52,53,53	0
2	XYP	D	705	10/10	0.80	0.15	32,37,39,40	0
3	XYS	D	710	10/10	0.80	0.16	34,37,38,39	0
2	XYP	A	702	10/10	0.81	0.14	40,42,44,44	0
2	XYP	B	702	10/10	0.81	0.16	33,34,37,38	0
2	XYP	D	706	10/10	0.81	0.17	24,29,33,36	0
2	XYP	B	704	10/10	0.82	0.13	31,35,36,37	0
2	XYP	A	707	10/10	0.83	0.14	16,19,21,24	0
2	XYP	A	706	10/10	0.83	0.15	29,33,36,36	0
2	XYP	D	707	10/10	0.83	0.12	35,40,42,42	0
2	XYP	A	705	10/10	0.84	0.16	24,32,34,37	0
2	XYP	B	706	10/10	0.84	0.15	25,32,34,37	0
2	XYP	C	705	10/10	0.84	0.14	25,33,35,39	0
3	XYS	C	706	10/10	0.84	0.13	34,37,38,38	0
3	XYS	B	707	10/10	0.85	0.13	26,29,30,30	0
3	XYS	A	708	10/10	0.85	0.13	32,34,36,36	0
2	XYP	D	703	10/10	0.85	0.12	33,35,37,37	0
2	XYP	C	702	10/10	0.86	0.12	39,41,42,42	0
2	XYP	D	701	10/10	0.87	0.11	16,19,21,22	0
3	XYS	B	708	10/10	0.91	0.10	24,27,28,28	0
2	XYP	C	701	10/10	0.95	0.07	10,14,20,21	0
2	XYP	A	701	10/10	0.95	0.07	10,14,20,21	0
2	XYP	D	702	10/10	0.95	0.07	10,13,19,20	0
2	XYP	B	701	10/10	0.96	0.07	10,14,20,20	0

6.5 Other polymers ⓘ

There are no such residues in this entry.