



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 01:46 AM UTC

PDB ID : 2Y0B / pdb_00002y0b
Title : Caspase-3 in Complex with an Inhibitory DARPin-3.4_S76R
Authors : Barandun, J.; Schroeder, T.; Mittl, P.; Grutter, M.G.
Deposited on : 2010-12-01
Resolution : 2.10 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
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

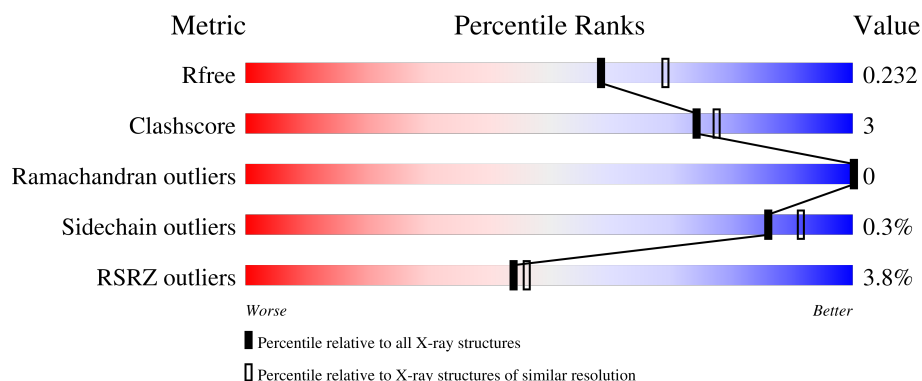
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	149	90% 5% 5%
1	C	149	84% 11% 5%
2	B	118	3% 76% 20%
2	D	118	3% 74% 5% 21%
3	G	136	6% 84% 12%

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Mol	Chain	Length	Quality of chain
3	H	136	7% 82% 6% 12%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6013 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 CASPASE-3 SUBUNIT P17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	141	Total	C	N	O	S	0	2	0
			1131	698	203	221	9			
1	C	141	Total	C	N	O	S	0	1	0
			1129	697	203	219	10			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	27	MET	-	expression tag	UNP P42574
A	28	SER	-	expression tag	UNP P42574
C	27	MET	-	expression tag	UNP P42574
C	28	SER	-	expression tag	UNP P42574

- Molecule 2 is a protein called CASPASE-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	94	Total	C	N	O	S	0	0	0
			783	514	126	137	6			
2	D	93	Total	C	N	O	S	0	0	0
			777	511	125	136	5			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	278	ALA	-	expression tag	UNP P42574
B	279	LEU	-	expression tag	UNP P42574
B	280	GLU	-	expression tag	UNP P42574
B	281	VAL	-	expression tag	UNP P42574
B	282	LEU	-	expression tag	UNP P42574
B	283	PHE	-	expression tag	UNP P42574
B	284	GLN	-	expression tag	UNP P42574
B	285	GLY	-	expression tag	UNP P42574

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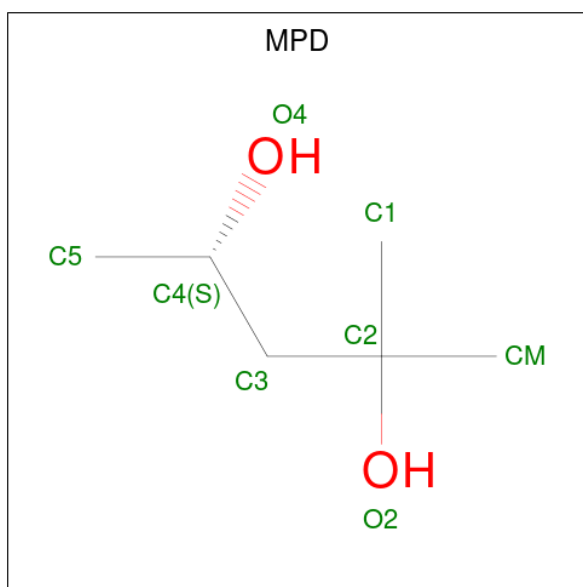
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Chain	Residue	Modelled	Actual	Comment	Reference
B	286	PRO	-	expression tag	UNP P42574
B	287	HIS	-	expression tag	UNP P42574
B	288	HIS	-	expression tag	UNP P42574
B	289	HIS	-	expression tag	UNP P42574
B	290	HIS	-	expression tag	UNP P42574
B	291	HIS	-	expression tag	UNP P42574
B	292	HIS	-	expression tag	UNP P42574
B	293	HIS	-	expression tag	UNP P42574
D	278	ALA	-	expression tag	UNP P42574
D	279	LEU	-	expression tag	UNP P42574
D	280	GLU	-	expression tag	UNP P42574
D	281	VAL	-	expression tag	UNP P42574
D	282	LEU	-	expression tag	UNP P42574
D	283	PHE	-	expression tag	UNP P42574
D	284	GLN	-	expression tag	UNP P42574
D	285	GLY	-	expression tag	UNP P42574
D	286	PRO	-	expression tag	UNP P42574
D	287	HIS	-	expression tag	UNP P42574
D	288	HIS	-	expression tag	UNP P42574
D	289	HIS	-	expression tag	UNP P42574
D	290	HIS	-	expression tag	UNP P42574
D	291	HIS	-	expression tag	UNP P42574
D	292	HIS	-	expression tag	UNP P42574
D	293	HIS	-	expression tag	UNP P42574

- Molecule 3 is a protein called DARPIN-3.4_S76R.

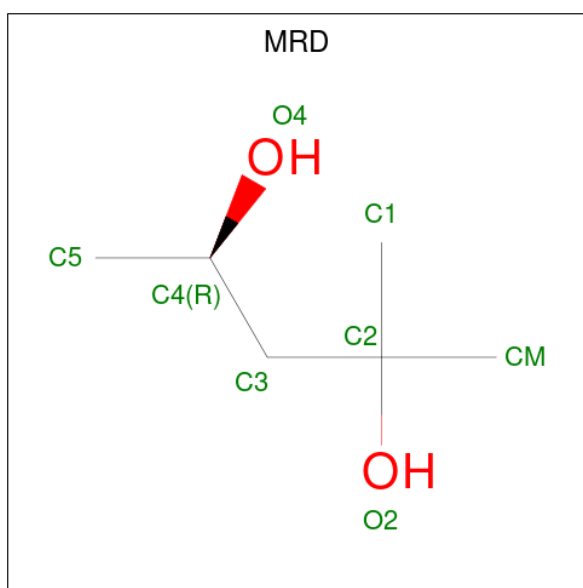
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	119	Total	C	N	O	S	0	1	0
			904	563	159	180	2			
3	H	120	Total	C	N	O	S	0	1	0
			912	569	160	181	2			

- Molecule 4 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: C₆H₁₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			8	6	2		
4	B	1	Total	C	O	0	0
			8	6	2		

- Molecule 5 is (4R)-2-METHYLPENTANE-2,4-DIOL (CCD ID: MRD) (formula: $C_6H_{14}O_2$).

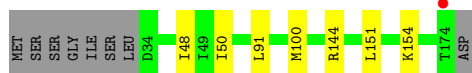


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			8	6	2		
5	C	1	Total	C	O	0	0
			8	6	2		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	90	Total 90	O 90	0	0
6	B	46	Total 46	O 46	0	0
6	C	101	Total 101	O 101	0	0
6	D	53	Total 53	O 53	0	0
6	G	35	Total 35	O 35	0	0
6	H	20	Total 20	O 20	0	0

• Molecule 1: CASPASE-3 SUBUNIT P17



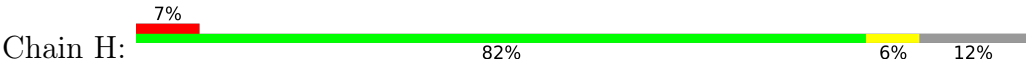
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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Ser | Gly | Ile | Ser | Leu | Asp | Met | Ser | Ser | Gly | Ile | Ser | Leu | Asp |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

- SER
GLY
VAL
ASP
ASP
ASP
MET
ALA
C184
L194
R207
S213
M233
Y276
H277
ALA
LEU
GLU
VAL
LEU
PHE
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- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| SER | GLY | VAL | ASP | ASP | ASP | MET | CYS | H185 | L194 | R207 | S213 | M233 | F252 | Y276 | H277 | ALA | LEU | GLU | GLU | LEU | PHE | GLN | GLY | PRO | HIS | HIS | HIS | HIS | HIS | HIS |
|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|-----|-----|-----|-----|-----|
| MET | ARG | GLY | SER | HTS | HTS | HTS | HTS | HTS | HTS | GLY | SER | D13 | T22 | E29 | P50 | L93 | V96 | F112 | G113 | F117 | G124 | N125 | L128 | T131 | LEU | GLN | LYS | LEU | ASN |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|-----|-----|-----|-----|-----|

- Molecule 3: DARPIN-3.4 S76R



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	98.00Å 98.00Å 192.90Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	84.87 – 2.10 84.87 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.2 (84.87-2.10) 98.9 (84.87-2.10)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.95 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.192 , 0.217 0.210 , 0.232	Depositor DCC
R_{free} test set	3178 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	43.9	Xtriage
Anisotropy	0.085	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 34.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.029 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6013	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 41.73 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.2605e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: MPD, MRD, CSO

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	0.42	0/1144	0.74	0/1531
1	C	0.43	0/1136	0.73	0/1519
2	B	0.42	0/808	0.71	0/1091
2	D	0.45	0/802	0.72	0/1083
3	G	0.43	0/918	0.76	0/1244
3	H	0.44	0/926	0.76	0/1255
All	All	0.43	0/5734	0.74	0/7723

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	1131	0	1124	5	0
1	C	1129	0	1122	11	0
2	B	783	0	759	7	0
2	D	777	0	754	8	0
3	G	904	0	893	2	0
3	H	912	0	904	4	0
4	A	8	0	14	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	8	0	14	0	0
5	A	8	0	14	0	0
5	C	8	0	14	0	0
6	A	90	0	0	0	0
6	B	46	0	0	1	0
6	C	101	0	0	0	0
6	D	53	0	0	0	0
6	G	35	0	0	0	0
6	H	20	0	0	0	0
All	All	6013	0	5612	35	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 3.

All (35) 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)
2:D:194:LEU:CD1	2:D:233:MET:HE1	2.09	0.82
2:B:194:LEU:CD1	2:B:233:MET:HE1	2.10	0.79
2:B:194:LEU:HD11	2:B:233:MET:HE1	1.72	0.72
2:D:194:LEU:HD11	2:D:233:MET:HE1	1.72	0.71
2:D:194:LEU:HD13	2:D:233:MET:HE1	1.75	0.67
2:D:252:PHE:HE1	3:H:20:GLU:HG3	1.60	0.67
3:H:53:LEU:O	3:H:57:ARG:HG2	1.96	0.66
2:B:194:LEU:HD13	2:B:233:MET:HE1	1.79	0.63
1:A:48:ILE:HG21	1:A:100:MET:HE1	1.80	0.63
1:C:48:ILE:HG21	1:C:100:MET:HE1	1.82	0.61
1:C:39:MET:HB2	2:D:277:HIS:HB3	1.85	0.59
3:G:96:VAL:HG21	3:G:128:LEU:HD11	1.83	0.59
1:C:52:ASN:HD21	1:C:91:LEU:H	1.51	0.58
2:B:207:ARG:HA	2:B:213:SER:HA	1.89	0.55
1:C:55:PHE:CD2	1:C:61[A]:MET:HE3	2.42	0.54
2:B:194:LEU:CD1	2:B:233:MET:CE	2.87	0.52
2:D:207:ARG:HA	2:D:213:SER:HA	1.91	0.52
3:H:96:VAL:HG21	3:H:128:LEU:HD11	1.92	0.52
3:H:79:TRP:O	3:H:110:ASP:HB2	2.13	0.49
1:C:100:MET:HG3	1:C:139:ILE:HG23	1.96	0.47
1:A:144:ARG:HD2	6:B:2006:HOH:O	2.15	0.46
2:D:194:LEU:HD13	2:D:233:MET:CE	2.43	0.45
1:C:151:LEU:HA	1:C:154:LYS:HD2	1.98	0.45
2:D:194:LEU:CD1	2:D:233:MET:CE	2.89	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:LEU:HA	1:A:154:LYS:HD2	1.99	0.44
1:C:52:ASN:ND2	1:C:91:LEU:H	2.14	0.44
1:C:74:LEU:HD13	1:C:117:VAL:HG11	2.01	0.43
2:B:194:LEU:HD13	2:B:233:MET:CE	2.45	0.43
1:C:50:ILE:HD11	1:C:100:MET:HE3	2.01	0.43
2:B:233:MET:HE2	2:B:233:MET:HA	2.01	0.43
1:C:173:GLU:H	1:C:173:GLU:CD	2.27	0.42
1:A:91:LEU:HD21	4:A:1175:MPD:HM1	2.01	0.41
3:G:22:THR:HG21	3:G:50:PRO:O	2.20	0.41
1:A:50:ILE:HD11	1:A:100:MET:HE3	2.02	0.40
1:C:51:ASN:HD22	1:C:89:ASN:ND2	2.18	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	140/149 (94%)	140 (100%)	0	0	100	100
1	C	139/149 (93%)	138 (99%)	1 (1%)	0	100	100
2	B	92/118 (78%)	92 (100%)	0	0	100	100
2	D	91/118 (77%)	91 (100%)	0	0	100	100
3	G	118/136 (87%)	117 (99%)	1 (1%)	0	100	100
3	H	119/136 (88%)	119 (100%)	0	0	100	100
All	All	699/806 (87%)	697 (100%)	2 (0%)	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	128/133 (96%)	128 (100%)	0	100	100
1	C	127/133 (96%)	127 (100%)	0	100	100
2	B	84/104 (81%)	84 (100%)	0	100	100
2	D	83/104 (80%)	83 (100%)	0	100	100
3	G	93/107 (87%)	92 (99%)	1 (1%)	65	74
3	H	94/107 (88%)	93 (99%)	1 (1%)	65	74
All	All	609/688 (88%)	607 (100%)	2 (0%)	86	91

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	G	29	GLU
3	H	132	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	80	ASN
1	A	89	ASN
1	A	141	ASN
1	C	52	ASN
1	C	56	HIS
1	C	73	ASN
1	C	80	ASN
1	C	87	ASN
1	C	89	ASN
1	C	141	ASN
1	C	161	GLN
2	D	240	ASN
3	G	36	ASN
3	H	36	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	CSO	A	163	1	3,6,7	0.65	0	1,6,8	0.66	0
1	CSO	C	163	1	3,6,7	0.67	0	1,6,8	0.45	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
1	CSO	A	163	1	-	1/1/5/7	-
1	CSO	C	163	1	-	1/1/5/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	163	CSO	N-CA-CB-SG
1	C	163	CSO	N-CA-CB-SG

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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	$\# Z > 2$
4	MPD	A	1175	-	7,7,7	0.28	0	9,10,10	0.38	0
5	MRD	C	1175	-	7,7,7	0.29	0	9,10,10	0.35	0
5	MRD	A	1176	-	7,7,7	0.30	0	9,10,10	0.39	0
4	MPD	B	1278	-	7,7,7	0.31	0	9,10,10	0.30	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
4	MPD	A	1175	-	-	4/5/5/5	-
5	MRD	C	1175	-	-	3/5/5/5	-
5	MRD	A	1176	-	-	4/5/5/5	-
4	MPD	B	1278	-	-	5/5/5/5	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1175	MPD	CM-C2-C3-C4
4	A	1175	MPD	C2-C3-C4-O4

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Mol	Chain	Res	Type	Atoms
4	B	1278	MPD	C2-C3-C4-O4
4	B	1278	MPD	C2-C3-C4-C5
5	A	1176	MRD	C2-C3-C4-C5
4	A	1175	MPD	C1-C2-C3-C4
4	B	1278	MPD	C1-C2-C3-C4
4	B	1278	MPD	CM-C2-C3-C4
4	A	1175	MPD	C2-C3-C4-C5
5	C	1175	MRD	C2-C3-C4-C5
4	B	1278	MPD	O2-C2-C3-C4
5	A	1176	MRD	O2-C2-C3-C4
5	A	1176	MRD	C2-C3-C4-O4
5	C	1175	MRD	C2-C3-C4-O4
5	A	1176	MRD	C1-C2-C3-C4
5	C	1175	MRD	CM-C2-C3-C4

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1175	MPD	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 ⓘ

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	140/149 (93%)	0.05	1 (0%) 84 86	28, 49, 64, 80	2 (1%)
1	C	140/149 (93%)	0.03	2 (1%) 73 75	27, 47, 62, 68	1 (0%)
2	B	94/118 (79%)	-0.16	3 (3%) 50 53	33, 42, 60, 66	0
2	D	93/118 (78%)	-0.11	3 (3%) 50 53	32, 41, 59, 70	0
3	G	119/136 (87%)	0.69	8 (6%) 24 25	35, 67, 120, 150	1 (0%)
3	H	120/136 (88%)	0.90	10 (8%) 17 18	33, 71, 140, 170	1 (0%)
All	All	706/806 (87%)	0.25	27 (3%) 44 46	27, 51, 104, 170	5 (0%)

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	H	112	PHE	5.6
2	D	277	HIS	4.2
1	A	174	THR	4.0
3	G	112	PHE	3.6
3	H	121	ILE	3.3
1	C	174	THR	3.1
1	C	58	SER	3.0
2	D	185	HIS	2.8
2	B	184	CYS	2.7
2	B	276	TYR	2.6
3	H	132	LEU	2.4
3	H	14	LEU	2.4
2	B	277	HIS	2.3
3	H	111	LYS	2.3
3	H	106	VAL	2.3
3	G	125	ASN	2.3
3	G	117	PHE	2.2
3	G	131	ILE	2.2
2	D	276	TYR	2.2

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Mol	Chain	Res	Type	RSRZ
3	G	113	GLY	2.2
3	H	69	HIS	2.2
3	G	124	GLY	2.2
3	H	108	ALA	2.2
3	G	128	LEU	2.1
3	H	117	PHE	2.1
3	H	129	ALA	2.0
3	G	93	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
1	CSO	C	163	7/8	0.96	0.07	35,36,42,43	0
1	CSO	A	163	7/8	0.97	0.07	39,40,46,48	0

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(Å ²)	Q<0.9
4	MPD	A	1175	8/8	0.83	0.22	76,76,76,76	0
5	MRD	A	1176	8/8	0.86	0.22	85,86,86,86	0
4	MPD	B	1278	8/8	0.87	0.20	92,92,92,93	0
5	MRD	C	1175	8/8	0.89	0.25	90,91,91,91	0

6.5 Other polymers [i](#)

There are no such residues in this entry.