



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 09:29 PM UTC

PDB ID : 2XZT / pdb_00002xzt
Title : Caspase-3 in Complex with DARPin-3.4_I78S
Authors : Barandun, J.; Schroeder, T.; Mittl, P.; Grutter, M.G.
Deposited on : 2010-11-29
Resolution : 2.70 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

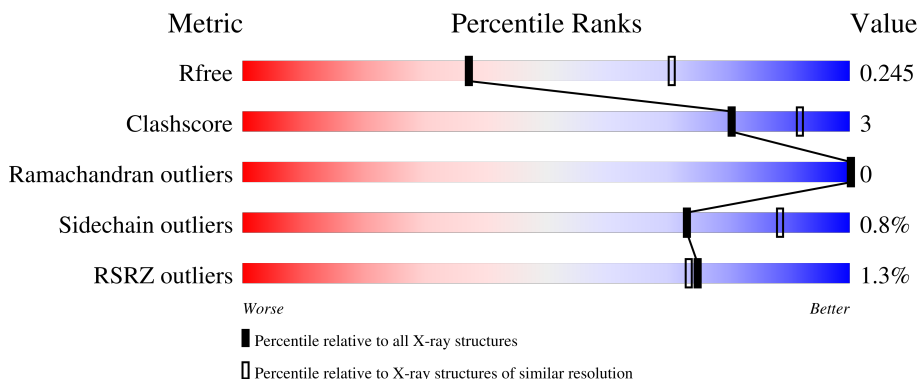
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

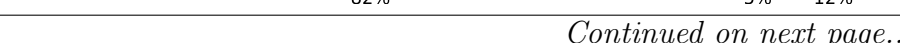
The reported resolution of this entry is 2.70 Å.

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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	 87% 8% 5%
1	C	149	 87% 8% 5%
2	B	118	 2% 74% 6% 20%
2	D	118	 2% 75% 1% 21%
3	G	136	 0% 82% 5% 12%

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Mol	Chain	Length	Quality of chain
3	H	136	2% 82% 6% 12%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5800 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	141	Total	C	N	O	S	0	1	0
			1126	695	202	220	9			
1	C	142	Total	C	N	O	S	0	0	0
			1129	696	203	221	9			

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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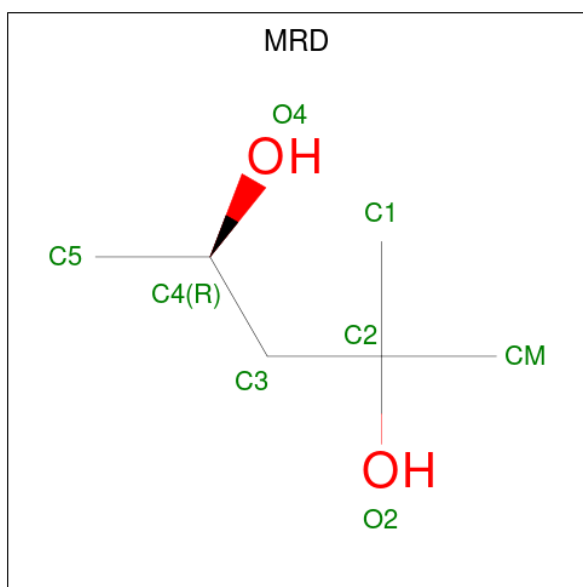
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Chain	Residue	Modelled	Actual	Comment	Reference
B	286	PRO	-	expression tag	UNP P42574
B	287	HIS	-	expression tag	UNP P42574
B	288	HIS	-	expression tag	UNP P42574
B	289	HIS	-	expression tag	UNP P42574
B	290	HIS	-	expression tag	UNP P42574
B	291	HIS	-	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_I78S.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	119	Total	C	N	O	S	0	1	0
			897	557	156	182	2			
3	H	120	Total	C	N	O	S	0	0	0
			900	560	157	181	2			

- Molecule 4 is (4R)-2-METHYLPENTANE-2,4-DIOL (CCD ID: MRD) (formula: C₆H₁₄O₂).



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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	37	Total	O	0	0
			37	37		
5	B	24	Total	O	0	0
			24	24		
5	C	45	Total	O	0	0
			45	45		
5	D	27	Total	O	0	0
			27	27		
5	G	14	Total	O	0	0
			14	14		
5	H	17	Total	O	0	0
			17	17		

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.

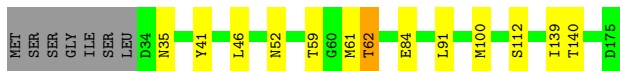
- Molecule 1: CASPASE-3

Chain A: 



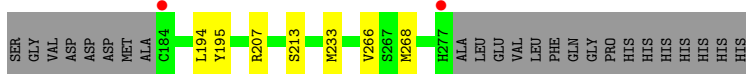
- Molecule 1: CASPASE-3

Chain C: 



- Molecule 2: CASPASE-3

Chain B: 



- Molecule 2: CASPASE-3

Chain D: 

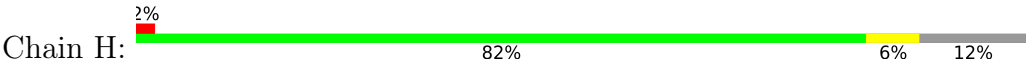


- Molecule 3: DARPIN-3.4_I78S

Chain G: 



- Molecule 3: DARPIN-3.4_I78S



MET	ARG	GLY	SER	HIS	HIS	HIS	HIS	HIS	GLY	SER	D13	D27	K56	R81	Y90	G91	H92	I95	D105	A108	A129	E130	I131	L132	GLN	LYS	LEU	ASN
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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 193.60Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.00 – 2.70 49.00 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.8 (49.00-2.70) 99.8 (49.00-2.70)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.27 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.197 , 0.231 0.207 , 0.245	Depositor DCC
R_{free} test set	1530 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	55.9	Xtriage
Anisotropy	0.025	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 50.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.031 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5800	wwPDB-VP
Average B, all atoms (Å ²)	58.0	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 38.69 % 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 3.5506e-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: 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	0.41	0/1136	0.73	0/1520
1	C	0.41	0/1136	0.75	0/1520
2	B	0.42	0/808	0.70	0/1091
2	D	0.44	0/802	0.72	0/1083
3	G	0.41	0/911	0.75	0/1235
3	H	0.43	0/911	0.78	0/1235
All	All	0.42	0/5704	0.74	0/7684

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	1126	0	1118	7	0
1	C	1129	0	1118	7	0
2	B	783	0	759	7	0
2	D	777	0	754	3	0
3	G	897	0	879	3	0
3	H	900	0	886	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	C	16	0	28	0	0
5	A	37	0	0	0	0
5	B	24	0	0	1	0
5	C	45	0	0	0	0
5	D	27	0	0	0	0
5	G	14	0	0	0	0
5	H	17	0	0	2	0
All	All	5800	0	5556	29	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 (29) 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:C:62:THR:HG22	5:H:2011:HOH:O	1.81	0.80
2:B:194:LEU:HD11	2:B:233:MET:HE1	1.78	0.65
1:A:75:ARG:O	1:A:79:ARG:HB2	2.00	0.61
2:D:207:ARG:HA	2:D:213:SER:HA	1.82	0.60
2:B:207:ARG:HA	2:B:213:SER:HA	1.86	0.58
2:B:194:LEU:CD1	2:B:233:MET:HE1	2.34	0.56
1:C:100:MET:HG3	1:C:139:ILE:HG23	1.94	0.48
3:H:92:HIS:HD2	3:H:95:ILE:H	1.60	0.48
3:G:26:GLN:HB3	3:G:29:GLU:HB2	1.95	0.48
1:A:170:CYS:HB3	5:B:2018:HOH:O	2.14	0.47
1:A:140:THR:HG21	2:B:195:TYR:HE2	1.80	0.47
1:A:100:MET:HG3	1:A:139:ILE:HG23	1.97	0.47
2:B:233:MET:HE2	2:B:233:MET:HA	1.98	0.46
2:B:266:VAL:HG12	2:B:268:MET:CE	2.45	0.46
1:C:52:ASN:HD21	1:C:91:LEU:H	1.63	0.46
1:A:93:ARG:HB2	1:A:134:VAL:HG22	1.98	0.45
1:A:41:TYR:HB2	1:A:112:SER:OG	2.19	0.43
3:H:81:ARG:HD3	5:H:2015:HOH:O	2.19	0.42
3:G:105:ASP:HB3	3:G:108:ALA:HB2	2.01	0.41
3:H:105:ASP:HB3	3:H:108:ALA:HB2	2.02	0.41
1:C:59:THR:HB	1:C:61:MET:HE2	2.02	0.41
2:D:240:ASN:ND2	2:D:263:PRO:HB2	2.36	0.41
2:B:207:ARG:HG2	2:B:213:SER:HB3	2.03	0.41
1:C:41:TYR:HB2	1:C:112:SER:OG	2.21	0.41
1:C:46:LEU:HD23	1:C:84:GLU:HB3	2.03	0.40
1:A:89:ASN:HD21	4:A:1175:MRD:HMC1	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:140:THR:HG21	2:D:195:TYR:HE2	1.86	0.40
3:G:42:ALA:O	3:G:50:PRO:HD3	2.22	0.40
3:H:56:LYS:O	3:H:90:VAL:HG21	2.22	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	139/149 (93%)	137 (99%)	2 (1%)	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%)	118 (100%)	0	0	100	100
3	H	118/136 (87%)	116 (98%)	2 (2%)	0	100	100
All	All	697/806 (86%)	692 (99%)	5 (1%)	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	127/133 (96%)	126 (99%)	1 (1%)	73	88
1	C	127/133 (96%)	125 (98%)	2 (2%)	55	80
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	85
3	H	93/107 (87%)	92 (99%)	1 (1%)	65	85
All	All	607/688 (88%)	602 (99%)	5 (1%)	73	88

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	35	ASN
1	C	35	ASN
1	C	62	THR
3	G	81	ARG
3	H	27	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	89	ASN
1	A	141	ASN
1	A	161	GLN
2	B	217	GLN
1	C	52	ASN
1	C	80	ASN
1	C	87	ASN
1	C	89	ASN
1	C	141	ASN
1	C	161	GLN
2	D	217	GLN
2	D	240	ASN
3	G	26	GLN
3	G	36	ASN
3	H	36	ASN
3	H	92	HIS
3	H	125	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	0.61	0	1,6,8	0.19	0
1	CSO	C	163	1	3,6,7	0.60	0	1,6,8	0.13	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	-	0/1/5/7	-
1	CSO	C	163	1	-	0/1/5/7	-

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.

No monomer is involved in short contacts.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

3 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	MRD	C	1177	-	7,7,7	0.33	0	9,10,10	0.53	0
4	MRD	C	1176	-	7,7,7	0.31	0	9,10,10	0.34	0
4	MRD	A	1175	-	7,7,7	0.30	0	9,10,10	0.35	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	MRD	C	1177	-	-	3/5/5/5	-
4	MRD	C	1176	-	-	4/5/5/5	-
4	MRD	A	1175	-	-	4/5/5/5	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1175	MRD	C2-C3-C4-C5
4	C	1176	MRD	C2-C3-C4-C5
4	C	1177	MRD	O2-C2-C3-C4
4	C	1176	MRD	C1-C2-C3-C4
4	C	1176	MRD	CM-C2-C3-C4
4	C	1177	MRD	C2-C3-C4-C5
4	C	1176	MRD	O2-C2-C3-C4
4	A	1175	MRD	C2-C3-C4-O4
4	C	1177	MRD	C2-C3-C4-O4

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Mol	Chain	Res	Type	Atoms
4	A	1175	MRD	C1-C2-C3-C4
4	A	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	MRD	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	140/149 (93%)	-0.23	0	100 100	30, 56, 75, 94	1 (0%)
1	C	141/149 (94%)	-0.29	0	100 100	35, 51, 66, 78	0
2	B	94/118 (79%)	-0.38	2 (2%)	63 61	36, 48, 69, 80	0
2	D	93/118 (78%)	-0.42	2 (2%)	62 59	33, 43, 65, 76	0
3	G	119/136 (87%)	0.30	2 (1%)	69 67	48, 76, 132, 168	1 (0%)
3	H	120/136 (88%)	0.13	3 (2%)	58 55	43, 62, 127, 155	0
All	All	707/806 (87%)	-0.14	9 (1%)	75 73	30, 55, 98, 168	2 (0%)

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	277	HIS	2.9
2	B	184	CYS	2.7
3	H	132	LEU	2.7
2	B	277	HIS	2.4
3	G	13	ASP	2.4
3	G	131	ILE	2.2
3	H	129	ALA	2.2
2	D	185	HIS	2.2
3	H	131	ILE	2.1

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($\text{\AA}^2$)	Q<0.9
1	CSO	A	163	7/8	0.96	0.07	45,46,49,51	0
1	CSO	C	163	7/8	0.97	0.06	36,37,39,39	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($\text{\AA}^2$)	Q<0.9
4	MRD	A	1175	8/8	0.85	0.23	99,99,99,99	0
4	MRD	C	1177	8/8	0.87	0.28	116,116,116,116	0
4	MRD	C	1176	8/8	0.90	0.27	102,102,102,102	0

6.5 Other polymers [i](#)

There are no such residues in this entry.