



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 06:13 AM UTC

PDB ID : 3ZGJ / pdb_00003zgj
Title : S221M V223F Y359A mutant of 4-Hydroxymandelate synthase from *Streptomyces coelicolor*
Authors : Pratter, S.; Straganz, G.; Grogan, G.
Deposited on : 2012-12-18
Resolution : 1.95 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

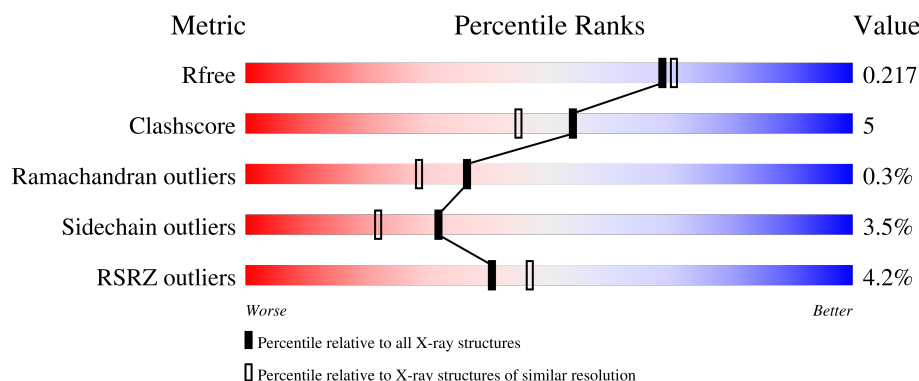
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	371	5% 75% 12% • 12%
1	B	371	2% 80% 11% •• 8%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5614 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 4-HYDROXYPHENYLPYRUVIC ACID DIOXYGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	327	Total	C	N	O	S	0	1	0
			2457	1559	419	473	6			
1	B	343	Total	C	N	O	S	0	0	0
			2602	1641	455	500	6			

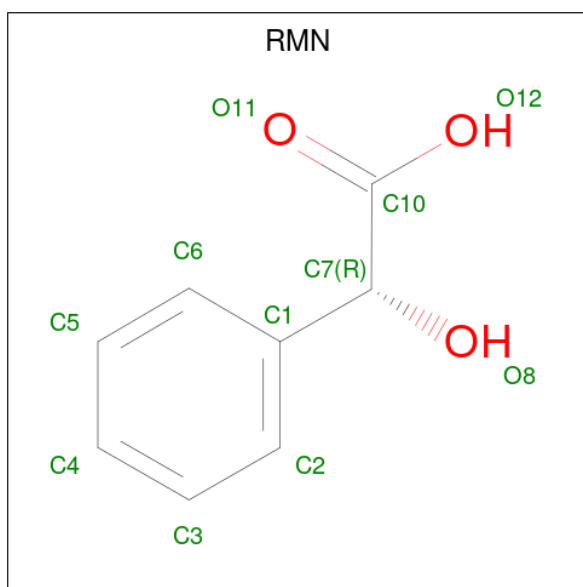
There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	221	MET	SER	engineered mutation	UNP Q9Z4X7
A	223	PHE	VAL	engineered mutation	UNP Q9Z4X7
A	359	ALA	TYR	engineered mutation	UNP Q9Z4X7
B	221	MET	SER	engineered mutation	UNP Q9Z4X7
B	223	PHE	VAL	engineered mutation	UNP Q9Z4X7
B	359	ALA	TYR	engineered mutation	UNP Q9Z4X7

- Molecule 2 is COBALT (II) ION (CCD ID: CO) (formula: Co).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Co	0	0
			1	1		
2	B	1	Total	Co	0	0
			1	1		

- Molecule 3 is (R)-MANDELIC ACID (CCD ID: RMN) (formula: C₈H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			11	8	3		
3	B	1	Total	C	O	0	0
			11	8	3		

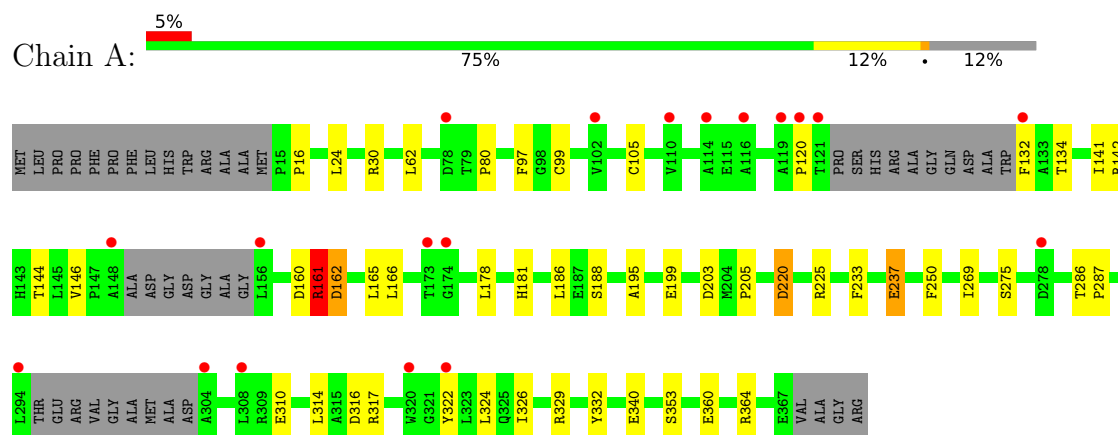
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	220	Total	O	0	0
			220	220		
4	B	311	Total	O	0	0
			311	311		

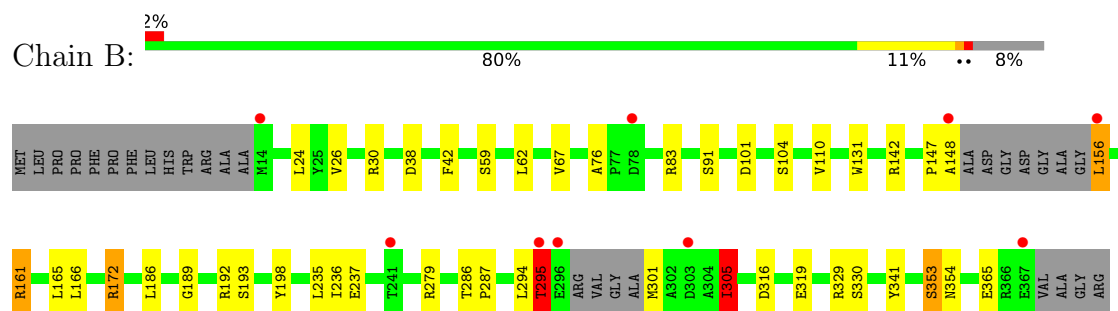
3 Residue-property plots [i](#)

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: 4-HYDROXYPHENYLPYRUVIC ACID DIOXYGENASE



• Molecule 1: 4-HYDROXYPHENYLPYRUVIC ACID DIOXYGENASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 4	Depositor
Cell constants a, b, c, α , β , γ	122.87Å 122.87Å 54.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	54.95 – 1.95 54.95 – 1.95	Depositor EDS
% Data completeness (in resolution range)	100.0 (54.95-1.95) 100.0 (54.95-1.95)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.86 (at 1.88Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.175 , 0.215 (Not available) , 0.217	Depositor DCC
R_{free} test set	3389 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	28.2	Xtriage
Anisotropy	0.421	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 35.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.034 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5614	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.00% 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: RMN, CO

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	1.29	8/2515 (0.3%)	1.24	8/3432 (0.2%)
1	B	1.44	14/2661 (0.5%)	1.24	8/3629 (0.2%)
All	All	1.37	22/5176 (0.4%)	1.24	16/7061 (0.2%)

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	59	SER	N-CA	6.58	1.54	1.46
1	B	76	ALA	N-CA	6.57	1.52	1.46
1	B	161	ARG	CD-NE	-6.39	1.37	1.46
1	A	233	PHE	C-O	6.23	1.31	1.24
1	B	353	SER	CA-C	5.92	1.60	1.52
1	B	192	ARG	C-O	-5.91	1.17	1.24
1	B	67	VAL	N-CA	5.89	1.53	1.46
1	B	186	LEU	CA-C	5.81	1.59	1.52
1	B	341	TYR	C-O	5.74	1.31	1.24
1	B	26	VAL	CA-C	5.50	1.59	1.52
1	A	203	ASP	C-O	5.47	1.30	1.23
1	B	295	THR	N-CA	5.46	1.53	1.46
1	A	181	HIS	C-O	5.41	1.30	1.23
1	A	237	GLU	CA-C	5.32	1.59	1.52
1	B	91	SER	C-O	5.31	1.30	1.23
1	B	236	ILE	N-CA	5.27	1.52	1.46
1	A	286	THR	CA-C	5.23	1.58	1.52
1	B	110	VAL	CA-C	5.23	1.59	1.52
1	A	186	LEU	CA-C	5.22	1.58	1.52
1	A	340	GLU	CA-C	-5.14	1.46	1.52
1	A	62	LEU	CA-C	-5.05	1.46	1.52
1	B	235	LEU	N-CA	5.01	1.52	1.46

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	162	ASP	N-CA-CB	-13.12	89.86	110.85
1	B	161	ARG	NE-CZ-NH2	-5.95	113.85	119.20
1	B	198	TYR	CA-CB-CG	-5.71	103.63	113.90
1	B	76	ALA	CA-C-N	5.70	125.65	119.78
1	B	76	ALA	C-N-CA	5.70	125.65	119.78
1	B	330	SER	CA-C-N	-5.42	114.71	121.00
1	B	330	SER	C-N-CA	-5.42	114.71	121.00
1	A	195	ALA	N-CA-C	5.42	117.19	111.28
1	A	237	GLU	CA-C-N	-5.33	114.49	120.14
1	A	237	GLU	C-N-CA	-5.33	114.49	120.14
1	A	161	ARG	N-CA-C	-5.32	101.04	108.96
1	A	134	THR	N-CA-C	5.24	116.93	108.34
1	B	193	SER	N-CA-C	-5.12	105.88	111.82
1	A	332	TYR	CA-C-N	5.07	124.51	119.24
1	A	332	TYR	C-N-CA	5.07	124.51	119.24
1	B	305	ILE	CB-CA-C	-5.00	105.49	112.04

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	2457	0	2341	25	0
1	B	2602	0	2488	24	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	11	0	6	0	0
3	B	11	0	6	0	0
4	A	220	0	0	7	0
4	B	311	0	0	11	0
All	All	5614	0	4841	48	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 5.

All (48) 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:319:GLU:HG3	4:B:2281:HOH:O	1.82	0.80
1:B:294:LEU:O	1:B:295:THR:OG1	2.01	0.79
1:B:30:ARG:NH2	4:B:2023:HOH:O	2.09	0.78
1:B:83:ARG:NH2	4:B:2089:HOH:O	2.20	0.73
1:A:30[B]:ARG:HD2	4:A:2022:HOH:O	1.89	0.72
1:B:301:MET:O	1:B:305:ILE:HG12	1.92	0.69
1:B:38:ASP:OD1	4:B:2043:HOH:O	2.13	0.67
1:A:80:PRO:HD2	4:A:2053:HOH:O	1.99	0.62
1:A:220:ASP:OD2	1:B:172:ARG:NH1	2.34	0.60
1:A:199:GLU:HG2	1:A:205:PRO:HA	1.83	0.60
1:A:310:GLU:OE2	4:A:2194:HOH:O	2.16	0.60
1:A:99:CYS:HG	1:A:105:CYS:HG	1.51	0.59
1:A:16:PRO:HB3	1:A:97:PHE:HB3	1.85	0.59
1:B:279:ARG:NH1	4:B:2258:HOH:O	2.35	0.57
1:B:101:ASP:CG	1:B:104:SER:HB3	2.30	0.57
1:A:178:LEU:C	1:A:178:LEU:HD12	2.31	0.55
1:A:269:ILE:HD11	1:A:326:ILE:HG22	1.90	0.53
1:B:131:TRP:O	1:B:147:PRO:HG3	2.10	0.52
1:B:294:LEU:O	1:B:295:THR:CB	2.59	0.51
1:B:30:ARG:NE	4:B:2023:HOH:O	2.44	0.50
1:B:142:ARG:HD2	4:B:2052:HOH:O	2.10	0.49
1:B:156:LEU:CB	4:B:2167:HOH:O	2.60	0.48
1:B:329:ARG:HD3	1:B:365:GLU:OE2	2.13	0.48
1:A:316:ASP:OD2	1:A:353:SER:HB3	2.14	0.47
1:B:30:ARG:CZ	4:B:2023:HOH:O	2.56	0.47
1:B:148:ALA:C	4:B:2163:HOH:O	2.57	0.46
1:B:156:LEU:C	1:B:156:LEU:HD12	2.41	0.46
1:B:42:PHE:HB3	1:B:62:LEU:HB3	1.98	0.46
1:A:188:SER:HA	1:A:237:GLU:HG3	1.98	0.46
1:A:99:CYS:CB	1:A:105:CYS:HG	2.29	0.45
1:A:142:ARG:NE	4:A:2096:HOH:O	2.44	0.45
1:B:156:LEU:HB3	4:B:2167:HOH:O	2.15	0.44
1:A:30[B]:ARG:NH1	4:A:2022:HOH:O	2.24	0.44
1:A:99:CYS:SG	1:A:105:CYS:SG	3.11	0.44
1:A:250:PHE:C	1:A:250:PHE:CD1	2.95	0.44
1:A:205:PRO:HD2	1:A:225:ARG:O	2.18	0.44
1:B:295:THR:O	1:B:295:THR:HG22	2.17	0.43
1:A:160:ASP:OD1	1:A:161:ARG:HD3	2.18	0.43
1:B:316:ASP:HB2	1:B:354:ASN:CG	2.43	0.43
1:A:317:ARG:HA	1:A:322:TYR:HA	2.01	0.42
1:A:144:THR:HG22	1:A:146:VAL:HG13	2.02	0.42
1:B:286:THR:HA	1:B:287:PRO:HD3	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:314:LEU:O	1:A:324:LEU:HA	2.20	0.41
1:B:189:GLY:N	1:B:237:GLU:OE2	2.49	0.41
1:A:99:CYS:HB3	1:A:105:CYS:HG	1.86	0.41
1:A:287:PRO:HD3	1:A:364:ARG:CZ	2.51	0.41
1:A:142:ARG:NH2	4:A:2096:HOH:O	2.46	0.40
1:A:360:GLU:OE1	4:A:2217:HOH:O	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	320/371 (86%)	314 (98%)	5 (2%)	1 (0%)	36	28
1	B	337/371 (91%)	331 (98%)	5 (2%)	1 (0%)	36	28
All	All	657/742 (88%)	645 (98%)	10 (2%)	2 (0%)	36	28

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	295	THR
1	A	120	PRO

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	248/289 (86%)	238 (96%)	10 (4%)	28	17
1	B	264/289 (91%)	256 (97%)	8 (3%)	36	27
All	All	512/578 (89%)	494 (96%)	18 (4%)	32	22

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	LEU
1	A	132	PHE
1	A	141	ILE
1	A	161	ARG
1	A	162	ASP
1	A	165	LEU
1	A	166	LEU
1	A	220	ASP
1	A	275	SER
1	A	329	ARG
1	B	24	LEU
1	B	156	LEU
1	B	161	ARG
1	B	165	LEU
1	B	166	LEU
1	B	172	ARG
1	B	305	ILE
1	B	353	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	HIS
1	A	246	GLN

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](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	RMN	B	1369	2	11,11,11	1.84	4 (36%)	14,14,14	1.09	0
3	RMN	A	1369	2	11,11,11	1.56	3 (27%)	14,14,14	1.18	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
3	RMN	B	1369	2	-	4/8/8/8	0/1/1/1
3	RMN	A	1369	2	-	4/8/8/8	0/1/1/1

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1369	RMN	C1-C7	-3.22	1.42	1.52
3	B	1369	RMN	O11-C10	3.09	1.31	1.22
3	A	1369	RMN	C1-C7	-2.89	1.43	1.52
3	B	1369	RMN	O8-C7	2.81	1.48	1.42
3	B	1369	RMN	O12-C10	-2.61	1.22	1.30
3	A	1369	RMN	O8-C7	2.22	1.47	1.42
3	A	1369	RMN	O12-C10	-2.10	1.24	1.30

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1369	RMN	O12-C10-C7	2.18	118.11	113.00
3	A	1369	RMN	O11-C10-C7	-2.02	117.68	122.52

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1369	RMN	O11-C10-C7-O8
3	A	1369	RMN	O12-C10-C7-O8
3	A	1369	RMN	C2-C1-C7-C10
3	A	1369	RMN	C6-C1-C7-C10
3	B	1369	RMN	C2-C1-C7-C10
3	B	1369	RMN	O11-C10-C7-O8
3	B	1369	RMN	C6-C1-C7-C10
3	B	1369	RMN	O12-C10-C7-O8

There are no ring outliers.

No monomer is involved in short contacts.

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	327/371 (88%)	0.22	19 (5%)	29 33	15, 35, 61, 75	1 (0%)
1	B	343/371 (92%)	-0.20	9 (2%)	57 64	16, 28, 55, 74	0
All	All	670/742 (90%)	0.00	28 (4%)	40 47	15, 32, 58, 75	1 (0%)

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	294	LEU	4.3
1	B	156	LEU	4.1
1	B	14	MET	3.8
1	B	295	THR	3.5
1	A	304	ALA	3.4
1	A	121	THR	3.2
1	A	132	PHE	3.1
1	A	173	THR	3.0
1	A	119	ALA	3.0
1	A	120	PRO	3.0
1	B	296	GLU	3.0
1	B	367	GLU	2.9
1	A	116	ALA	2.9
1	A	156	LEU	2.9
1	B	78	ASP	2.5
1	A	322	TYR	2.5
1	B	241	THR	2.4
1	A	148	ALA	2.2
1	A	78	ASP	2.2
1	B	303	ASP	2.2
1	A	320	TRP	2.1
1	A	102	VAL	2.1
1	A	114	ALA	2.1
1	B	148	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	278	ASP	2.1
1	A	110	VAL	2.0
1	A	308	LEU	2.0
1	A	174	GLY	2.0

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	RMN	A	1369	11/11	0.92	0.10	34,41,45,54	0
3	RMN	B	1369	11/11	0.93	0.12	33,46,50,51	0
2	CO	A	1368	1/1	0.99	0.02	27,27,27,27	0
2	CO	B	1368	1/1	0.99	0.02	21,21,21,21	0

6.5 Other polymers [i](#)

There are no such residues in this entry.