



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 03:19 pm GMT

PDB ID : 2XED
Title : NOCARDIA FARCINICA MALEATE CIS-TRANS ISOMERASE C194S
MUTANT WITH A COVALENTLY BOUND SUCCINYLCYSTEINE IN-
TERMEDIATE
Authors : Fisch, F.; Martinez-Fleites, C.; Baudendistel, N.; Hauer, B.; Turkenburg, J.P.;
Hart, S.; Bruce, N.C.; Grogan, G.
Deposited on : 2010-05-13
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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

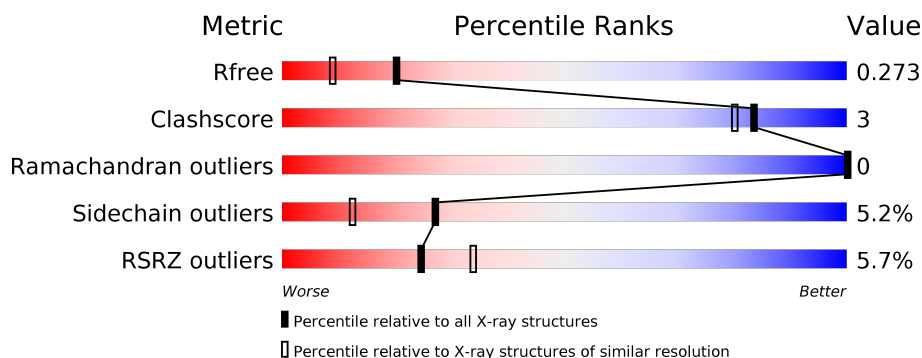
1 Overall quality at a glance

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}	100719	2004 (1.96-1.96)
Clashscore	112137	2136 (1.96-1.96)
Ramachandran outliers	110173	2117 (1.96-1.96)
Sidechain outliers	110143	2117 (1.96-1.96)
RSRZ outliers	101464	2018 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	273	<div> <div>4%</div> <div> <div></div> <div>85%</div> <div>6% • 8%</div> </div> </div>
1	B	273	<div> <div>4%</div> <div> <div></div> <div>83%</div> <div>6% • 10%</div> </div> </div>
1	C	273	<div> <div>8%</div> <div> <div></div> <div>78%</div> <div>11% • 10%</div> </div> </div>
1	D	273	<div> <div>5%</div> <div> <div></div> <div>81%</div> <div>8% • 10%</div> </div> </div>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 7976 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 PUTATIVE MALEATE ISOMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	252	Total	C	N	O	S	0	0	0
			1854	1158	329	354	13			
1	B	246	Total	C	N	O	S	0	2	0
			1829	1143	323	350	13			
1	C	245	Total	C	N	O	S	0	1	0
			1817	1135	324	346	12			
1	D	245	Total	C	N	O	S	0	0	0
			1809	1130	321	346	12			

There are 92 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	MET	-	EXPRESSION TAG	UNP Q5YXQ1
A	-20	GLY	-	EXPRESSION TAG	UNP Q5YXQ1
A	-19	SER	-	EXPRESSION TAG	UNP Q5YXQ1
A	-18	SER	-	EXPRESSION TAG	UNP Q5YXQ1
A	-17	HIS	-	EXPRESSION TAG	UNP Q5YXQ1
A	-16	HIS	-	EXPRESSION TAG	UNP Q5YXQ1
A	-15	HIS	-	EXPRESSION TAG	UNP Q5YXQ1
A	-14	HIS	-	EXPRESSION TAG	UNP Q5YXQ1
A	-13	HIS	-	EXPRESSION TAG	UNP Q5YXQ1
A	-12	HIS	-	EXPRESSION TAG	UNP Q5YXQ1
A	-11	SER	-	EXPRESSION TAG	UNP Q5YXQ1
A	-10	SER	-	EXPRESSION TAG	UNP Q5YXQ1
A	-9	GLY	-	EXPRESSION TAG	UNP Q5YXQ1
A	-8	LEU	-	EXPRESSION TAG	UNP Q5YXQ1
A	-7	GLU	-	EXPRESSION TAG	UNP Q5YXQ1
A	-6	VAL	-	EXPRESSION TAG	UNP Q5YXQ1
A	-5	LEU	-	EXPRESSION TAG	UNP Q5YXQ1
A	-4	PHE	-	EXPRESSION TAG	UNP Q5YXQ1
A	-3	GLN	-	EXPRESSION TAG	UNP Q5YXQ1
A	-2	GLY	-	EXPRESSION TAG	UNP Q5YXQ1
A	-1	PRO	-	EXPRESSION TAG	UNP Q5YXQ1

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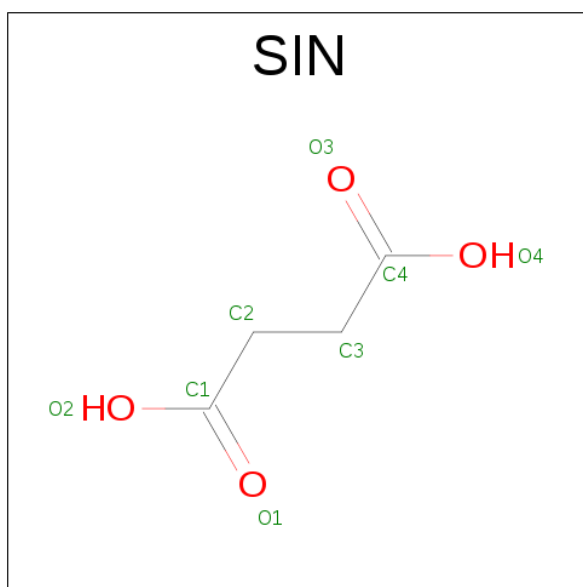
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	ALA	-	EXPRESSION TAG	UNP Q5YXQ1
B	-21	MET	-	EXPRESSION TAG	UNP Q5YXQ1
B	-20	GLY	-	EXPRESSION TAG	UNP Q5YXQ1
B	-19	SER	-	EXPRESSION TAG	UNP Q5YXQ1
B	-18	SER	-	EXPRESSION TAG	UNP Q5YXQ1
B	-17	HIS	-	EXPRESSION TAG	UNP Q5YXQ1
B	-16	HIS	-	EXPRESSION TAG	UNP Q5YXQ1
B	-15	HIS	-	EXPRESSION TAG	UNP Q5YXQ1
B	-14	HIS	-	EXPRESSION TAG	UNP Q5YXQ1
B	-13	HIS	-	EXPRESSION TAG	UNP Q5YXQ1
B	-12	HIS	-	EXPRESSION TAG	UNP Q5YXQ1
B	-11	SER	-	EXPRESSION TAG	UNP Q5YXQ1
B	-10	SER	-	EXPRESSION TAG	UNP Q5YXQ1
B	-9	GLY	-	EXPRESSION TAG	UNP Q5YXQ1
B	-8	LEU	-	EXPRESSION TAG	UNP Q5YXQ1
B	-7	GLU	-	EXPRESSION TAG	UNP Q5YXQ1
B	-6	VAL	-	EXPRESSION TAG	UNP Q5YXQ1
B	-5	LEU	-	EXPRESSION TAG	UNP Q5YXQ1
B	-4	PHE	-	EXPRESSION TAG	UNP Q5YXQ1
B	-3	GLN	-	EXPRESSION TAG	UNP Q5YXQ1
B	-2	GLY	-	EXPRESSION TAG	UNP Q5YXQ1
B	-1	PRO	-	EXPRESSION TAG	UNP Q5YXQ1
B	0	ALA	-	EXPRESSION TAG	UNP Q5YXQ1
C	-21	MET	-	EXPRESSION TAG	UNP Q5YXQ1
C	-20	GLY	-	EXPRESSION TAG	UNP Q5YXQ1
C	-19	SER	-	EXPRESSION TAG	UNP Q5YXQ1
C	-18	SER	-	EXPRESSION TAG	UNP Q5YXQ1
C	-17	HIS	-	EXPRESSION TAG	UNP Q5YXQ1
C	-16	HIS	-	EXPRESSION TAG	UNP Q5YXQ1
C	-15	HIS	-	EXPRESSION TAG	UNP Q5YXQ1
C	-14	HIS	-	EXPRESSION TAG	UNP Q5YXQ1
C	-13	HIS	-	EXPRESSION TAG	UNP Q5YXQ1
C	-12	HIS	-	EXPRESSION TAG	UNP Q5YXQ1
C	-11	SER	-	EXPRESSION TAG	UNP Q5YXQ1
C	-10	SER	-	EXPRESSION TAG	UNP Q5YXQ1
C	-9	GLY	-	EXPRESSION TAG	UNP Q5YXQ1
C	-8	LEU	-	EXPRESSION TAG	UNP Q5YXQ1
C	-7	GLU	-	EXPRESSION TAG	UNP Q5YXQ1
C	-6	VAL	-	EXPRESSION TAG	UNP Q5YXQ1
C	-5	LEU	-	EXPRESSION TAG	UNP Q5YXQ1
C	-4	PHE	-	EXPRESSION TAG	UNP Q5YXQ1
C	-3	GLN	-	EXPRESSION TAG	UNP Q5YXQ1

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	GLY	-	EXPRESSION TAG	UNP Q5YXQ1
C	-1	PRO	-	EXPRESSION TAG	UNP Q5YXQ1
C	0	ALA	-	EXPRESSION TAG	UNP Q5YXQ1
D	-21	MET	-	EXPRESSION TAG	UNP Q5YXQ1
D	-20	GLY	-	EXPRESSION TAG	UNP Q5YXQ1
D	-19	SER	-	EXPRESSION TAG	UNP Q5YXQ1
D	-18	SER	-	EXPRESSION TAG	UNP Q5YXQ1
D	-17	HIS	-	EXPRESSION TAG	UNP Q5YXQ1
D	-16	HIS	-	EXPRESSION TAG	UNP Q5YXQ1
D	-15	HIS	-	EXPRESSION TAG	UNP Q5YXQ1
D	-14	HIS	-	EXPRESSION TAG	UNP Q5YXQ1
D	-13	HIS	-	EXPRESSION TAG	UNP Q5YXQ1
D	-12	HIS	-	EXPRESSION TAG	UNP Q5YXQ1
D	-11	SER	-	EXPRESSION TAG	UNP Q5YXQ1
D	-10	SER	-	EXPRESSION TAG	UNP Q5YXQ1
D	-9	GLY	-	EXPRESSION TAG	UNP Q5YXQ1
D	-8	LEU	-	EXPRESSION TAG	UNP Q5YXQ1
D	-7	GLU	-	EXPRESSION TAG	UNP Q5YXQ1
D	-6	VAL	-	EXPRESSION TAG	UNP Q5YXQ1
D	-5	LEU	-	EXPRESSION TAG	UNP Q5YXQ1
D	-4	PHE	-	EXPRESSION TAG	UNP Q5YXQ1
D	-3	GLN	-	EXPRESSION TAG	UNP Q5YXQ1
D	-2	GLY	-	EXPRESSION TAG	UNP Q5YXQ1
D	-1	PRO	-	EXPRESSION TAG	UNP Q5YXQ1
D	0	ALA	-	EXPRESSION TAG	UNP Q5YXQ1
A	194	ALA	CYS	ENGINEERED MUTATION	UNP Q5YXQ1
B	194	ALA	CYS	ENGINEERED MUTATION	UNP Q5YXQ1
C	194	ALA	CYS	ENGINEERED MUTATION	UNP Q5YXQ1
D	194	ALA	CYS	ENGINEERED MUTATION	UNP Q5YXQ1

- Molecule 2 is SUCCINIC ACID (three-letter code: SIN) (formula: C₄H₆O₄).



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

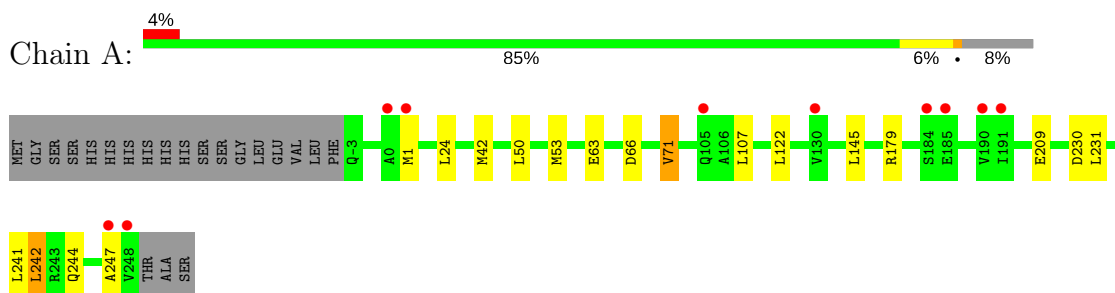
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	216	Total	O	0	0
			216	216		
3	B	151	Total	O	0	0
			151	151		
3	C	141	Total	O	0	0
			141	141		
3	D	127	Total	O	0	0
			127	127		

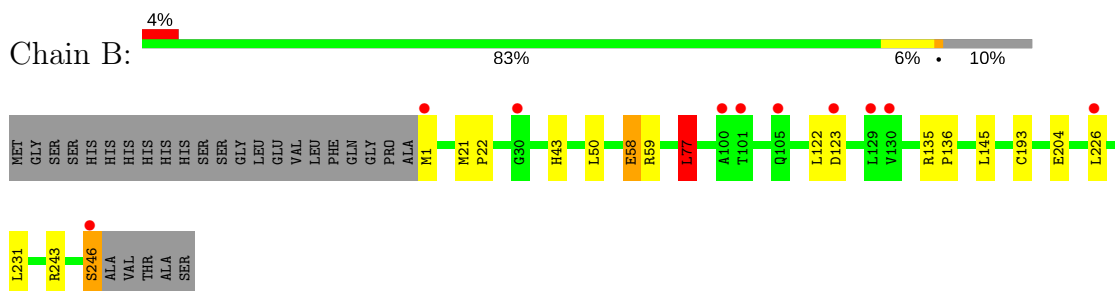
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

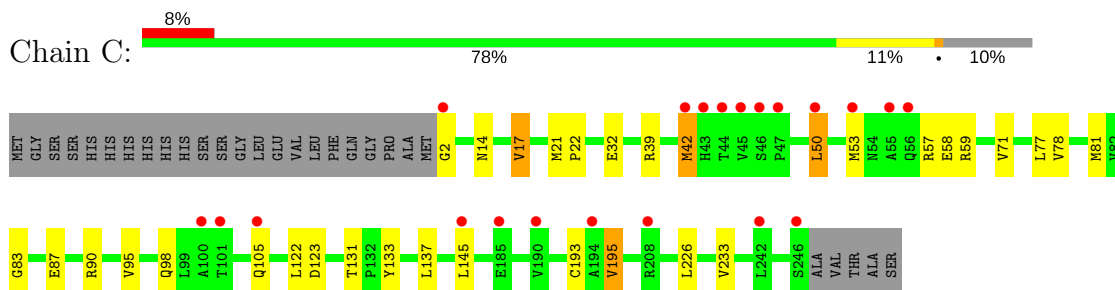
• Molecule 1: PUTATIVE MALEATE ISOMERASE



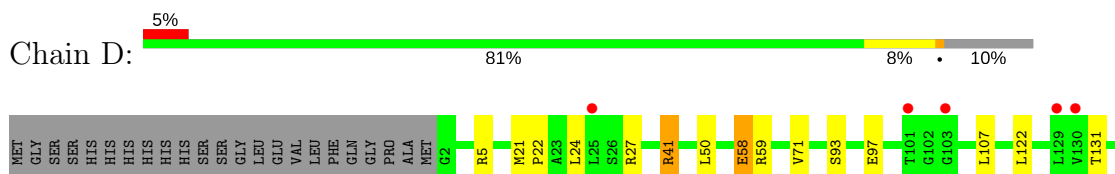
• Molecule 1: PUTATIVE MALEATE ISOMERASE

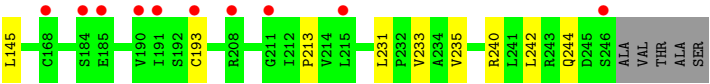


• Molecule 1: PUTATIVE MALEATE ISOMERASE



• Molecule 1: PUTATIVE MALEATE ISOMERASE





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	52.98Å 85.67Å 239.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.95 20.00 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.2 (20.00-1.95) 99.2 (20.00-1.95)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.86 (at 1.94Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.222 , 0.260 0.242 , 0.273	Depositor DCC
R_{free} test set	3994 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	26.7	Xtriage
Anisotropy	0.149	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 31.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	7976	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.14% 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: SIN

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	0.59	0/1883	0.71	2/2564 (0.1%)
1	B	0.47	0/1863	0.63	1/2535 (0.0%)
1	C	0.49	0/1848	0.64	0/2515
1	D	0.47	0/1837	0.68	4/2501 (0.2%)
All	All	0.51	0/7431	0.67	7/10115 (0.1%)

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	59	ARG	NE-CZ-NH2	-9.68	115.46	120.30
1	A	242	LEU	CA-CB-CG	-8.01	96.88	115.30
1	B	77	LEU	CA-CB-CG	7.07	131.55	115.30
1	A	71	VAL	CB-CA-C	-6.59	98.87	111.40
1	D	59	ARG	NE-CZ-NH1	6.00	123.30	120.30
1	D	41	ARG	NE-CZ-NH2	-5.84	117.38	120.30
1	D	41	ARG	NE-CZ-NH1	5.61	123.11	120.30

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	1854	0	1880	7	0
1	B	1829	0	1857	6	0
1	C	1817	0	1844	16	0
1	D	1809	0	1831	16	0
2	A	8	0	3	0	0
2	B	8	0	3	0	0
2	C	8	0	2	1	0
2	D	8	0	3	0	0
3	A	216	0	0	0	0
3	B	151	0	0	0	0
3	C	141	0	0	2	0
3	D	127	0	0	2	0
All	All	7976	0	7423	42	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 (42) 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:58[A]:GLU:OE1	1:B:59:ARG:N	2.15	0.76
1:B:243:ARG:HB2	1:B:246:SER:OG	1.87	0.74
1:A:66:ASP:OD2	1:D:41:ARG:HD2	1.92	0.69
1:C:195:VAL:HG22	2:C:300:SIN:O2	1.95	0.66
1:C:87:GLU:OE1	1:C:90:ARG:NH2	2.32	0.63
1:B:77:LEU:HG	1:B:193:CYS:O	1.99	0.62
1:C:77:LEU:HG	1:C:193:CYS:O	2.01	0.61
1:D:58:GLU:CD	1:D:58:GLU:H	2.04	0.61
1:C:131:THR:HG22	1:C:193:CYS:HB2	1.82	0.60
1:D:24:LEU:HD23	1:D:235:VAL:HG11	1.82	0.60
1:C:77:LEU:HD13	1:C:81:MET:HG3	1.84	0.58
1:D:5:ARG:NH1	3:D:2005:HOH:O	2.39	0.56
1:C:50:LEU:HD21	1:C:78:VAL:HG13	1.88	0.56
1:B:21:MET:HB3	1:B:22:PRO:HD3	1.89	0.54
1:D:131:THR:HG22	1:D:193:CYS:HB2	1.91	0.52
1:A:241:LEU:O	1:A:244:GLN:HG2	2.11	0.51
1:C:21:MET:HB2	1:C:22:PRO:HD3	1.93	0.51
1:C:57:ARG:HD3	1:C:95:VAL:HG22	1.94	0.50
1:D:233:VAL:CG2	1:D:244:GLN:HB2	2.42	0.50
1:C:39:ARG:O	1:C:59:ARG:NH2	2.40	0.50
1:A:179:ARG:HD3	1:A:209:GLU:OE2	2.12	0.49
1:D:21:MET:HB3	1:D:22:PRO:HD3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:5:ARG:NH2	3:D:2006:HOH:O	2.44	0.48
1:C:58:GLU:HA	1:C:98:GLN:HE22	1.78	0.48
1:C:83:GLY:O	3:C:2056:HOH:O	2.20	0.48
1:A:63:GLU:HA	1:D:41:ARG:HD3	1.94	0.47
1:C:42:MET:HG2	1:C:53:MET:SD	2.55	0.47
1:D:58:GLU:CD	1:D:58:GLU:N	2.67	0.47
1:D:24:LEU:HD21	1:D:242:LEU:HD13	1.98	0.45
1:A:247:ALA:HA	1:B:243:ARG:NH2	2.31	0.45
1:D:93:SER:O	1:D:97:GLU:HG3	2.16	0.45
1:C:14:ASN:OD1	1:C:17:VAL:HG13	2.16	0.45
1:D:27:ARG:HB2	1:D:235:VAL:HG13	1.98	0.45
1:D:213:PRO:HG3	1:D:240:ARG:HH11	1.81	0.44
1:D:233:VAL:HG23	1:D:233:VAL:O	2.17	0.44
1:C:2:GLY:N	3:C:2001:HOH:O	2.52	0.43
1:A:24:LEU:HD23	1:A:24:LEU:C	2.39	0.43
1:C:131:THR:HB	1:C:133:TYR:CD2	2.54	0.42
1:C:137:LEU:HD23	1:C:137:LEU:HA	1.91	0.42
1:D:233:VAL:HG21	1:D:244:GLN:HB2	2.00	0.42
1:B:135:ARG:HB2	1:B:136:PRO:HD3	2.01	0.42
1:A:42:MET:HB2	1:A:53:MET:HB2	2.02	0.41

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	250/273 (92%)	245 (98%)	5 (2%)	0	100	100
1	B	246/273 (90%)	241 (98%)	5 (2%)	0	100	100
1	C	244/273 (89%)	236 (97%)	8 (3%)	0	100	100
1	D	243/273 (89%)	239 (98%)	4 (2%)	0	100	100
All	All	983/1092 (90%)	961 (98%)	22 (2%)	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	195/213 (92%)	186 (95%)	9 (5%)	31	16
1	B	194/213 (91%)	181 (93%)	13 (7%)	19	7
1	C	192/213 (90%)	180 (94%)	12 (6%)	21	8
1	D	191/213 (90%)	184 (96%)	7 (4%)	39	25
All	All	772/852 (91%)	731 (95%)	41 (5%)	27	12

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	50	LEU
1	A	71	VAL
1	A	107	LEU
1	A	122	LEU
1	A	145	LEU
1	A	230	ASP
1	A	231	LEU
1	A	242	LEU
1	B	1	MET
1	B	43	HIS
1	B	50	LEU
1	B	58[A]	GLU
1	B	58[B]	GLU
1	B	77	LEU
1	B	122	LEU
1	B	123	ASP
1	B	145	LEU
1	B	204	GLU
1	B	226	LEU
1	B	231	LEU
1	B	246	SER

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Mol	Chain	Res	Type
1	C	17	VAL
1	C	32	GLU
1	C	42	MET
1	C	50	LEU
1	C	71	VAL
1	C	105	GLN
1	C	122	LEU
1	C	123	ASP
1	C	145	LEU
1	C	195	VAL
1	C	226	LEU
1	C	233	VAL
1	D	50	LEU
1	D	58	GLU
1	D	71	VAL
1	D	107	LEU
1	D	122	LEU
1	D	145	LEU
1	D	231	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	98	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

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
2	SIN	A	300	1	1,7,7	0.02	0	2,8,8	1.98	1 (50%)
2	SIN	B	300	1	1,7,7	0.07	0	2,8,8	2.01	1 (50%)
2	SIN	C	300	1	1,7,7	0.01	0	2,8,8	0.42	0
2	SIN	D	300	1	1,7,7	0.05	0	2,8,8	1.09	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
2	SIN	A	300	1	-	0/1/5/5	0/0/0/0
2	SIN	B	300	1	-	0/1/5/5	0/0/0/0
2	SIN	C	300	1	-	0/1/5/5	0/0/0/0
2	SIN	D	300	1	-	0/1/5/5	0/0/0/0

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	300	SIN	C2-C3-C4	2.79	117.43	112.66
2	B	300	SIN	C2-C3-C4	2.84	117.51	112.66

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	300	SIN	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	252/273 (92%)	0.20	10 (3%) 39 49	16, 24, 40, 55	0
1	B	246/273 (90%)	0.38	10 (4%) 38 48	22, 32, 47, 63	0
1	C	245/273 (89%)	0.52	21 (8%) 11 17	24, 35, 53, 61	0
1	D	245/273 (89%)	0.51	15 (6%) 22 31	17, 37, 61, 75	0
All	All	988/1092 (90%)	0.40	56 (5%) 24 34	16, 32, 54, 75	0

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1	MET	4.9
1	C	55	ALA	4.0
1	C	208	ARG	3.8
1	D	246	SER	3.8
1	C	42	MET	3.7
1	A	247	ALA	3.6
1	D	185	GLU	3.6
1	D	190	VAL	3.5
1	B	130	VAL	3.4
1	C	185	GLU	3.2
1	D	191	ILE	3.2
1	C	43	HIS	3.2
1	D	208	ARG	3.2
1	D	168	CYS	3.1
1	B	30	GLY	3.1
1	B	101	THR	3.1
1	B	129	LEU	3.1
1	C	105	GLN	3.1
1	A	248	VAL	3.0
1	D	129	LEU	2.9
1	D	130	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
1	C	246	SER	2.9
1	A	185	GLU	2.8
1	B	100	ALA	2.8
1	B	226	LEU	2.8
1	A	184	SER	2.8
1	C	45	VAL	2.8
1	A	0	ALA	2.7
1	A	1	MET	2.7
1	D	211	GLY	2.6
1	D	25	LEU	2.6
1	C	190	VAL	2.6
1	D	184	SER	2.5
1	D	103	GLY	2.5
1	C	100	ALA	2.5
1	C	101	THR	2.5
1	C	56	GLN	2.4
1	B	105	GLN	2.4
1	B	246	SER	2.4
1	B	123	ASP	2.3
1	D	101	THR	2.3
1	C	46	SER	2.3
1	C	2	GLY	2.2
1	D	215	LEU	2.2
1	C	50	LEU	2.2
1	A	130	VAL	2.2
1	C	44	THR	2.1
1	A	105	GLN	2.1
1	C	47	PRO	2.1
1	D	193	CYS	2.1
1	C	145	LEU	2.1
1	A	190	VAL	2.1
1	C	194	ALA	2.0
1	A	191	ILE	2.0
1	C	242	LEU	2.0
1	C	53	MET	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
2	SIN	C	300	8/8	0.83	0.17	0.23	40,42,45,46	0
2	SIN	D	300	8/8	0.91	0.14	0.21	29,32,34,34	0
2	SIN	B	300	8/8	0.95	0.12	-0.13	25,26,27,28	0
2	SIN	A	300	8/8	0.95	0.10	-0.59	18,22,23,23	0

6.5 Other polymers [i](#)

There are no such residues in this entry.