



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 08:21 AM UTC

PDB ID : 3SAM / pdb_00003sam
Title : Structure of D13, the scaffolding protein of vaccinia virus (mutant D513G)
Authors : Coulibaly, F.
Deposited on : 2011-06-03
Resolution : 2.55 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

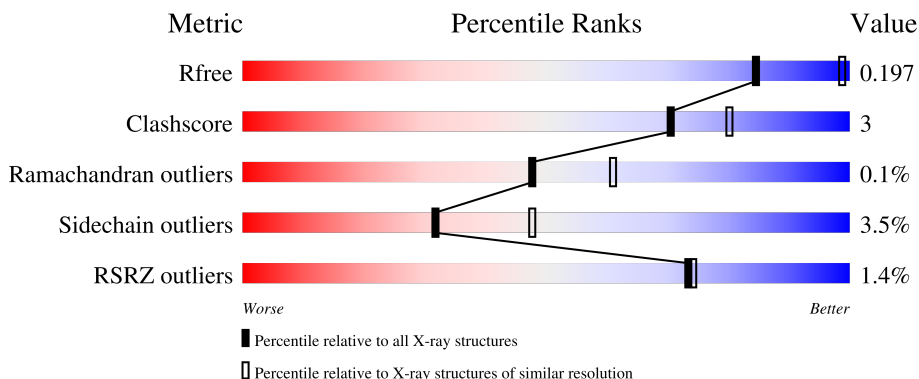
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 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	1091 (2.54-2.54)
Clashscore	190562	1120 (2.54-2.54)
Ramachandran outliers	187476	1106 (2.54-2.54)
Sidechain outliers	187428	1106 (2.54-2.54)
RSRZ outliers	180081	1091 (2.54-2.54)

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	576	 82% 10% • 6%
1	B	576	 83% 11% • 6%
1	C	576	 81% 12% • 6%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 13528 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 Rifampicin resistance protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	541	Total 4296	C 2744	N 704	O 834	S 14	0	3	0
1	B	544	Total 4288	C 2739	N 695	O 841	S 13	0	0	0
1	C	542	Total 4298	C 2752	N 700	O 832	S 14	0	2	0

There are 78 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-24	MET	-	expression tag	UNP P68440
A	-23	SER	-	expression tag	UNP P68440
A	-22	TYR	-	expression tag	UNP P68440
A	-21	TYR	-	expression tag	UNP P68440
A	-20	HIS	-	expression tag	UNP P68440
A	-19	HIS	-	expression tag	UNP P68440
A	-18	HIS	-	expression tag	UNP P68440
A	-17	HIS	-	expression tag	UNP P68440
A	-16	HIS	-	expression tag	UNP P68440
A	-15	HIS	-	expression tag	UNP P68440
A	-14	ASP	-	expression tag	UNP P68440
A	-13	TYR	-	expression tag	UNP P68440
A	-12	ASP	-	expression tag	UNP P68440
A	-11	ILE	-	expression tag	UNP P68440
A	-10	PRO	-	expression tag	UNP P68440
A	-9	THR	-	expression tag	UNP P68440
A	-8	THR	-	expression tag	UNP P68440
A	-7	GLU	-	expression tag	UNP P68440
A	-6	ASN	-	expression tag	UNP P68440
A	-5	LEU	-	expression tag	UNP P68440
A	-4	TYR	-	expression tag	UNP P68440
A	-3	PHE	-	expression tag	UNP P68440
A	-2	GLN	-	expression tag	UNP P68440

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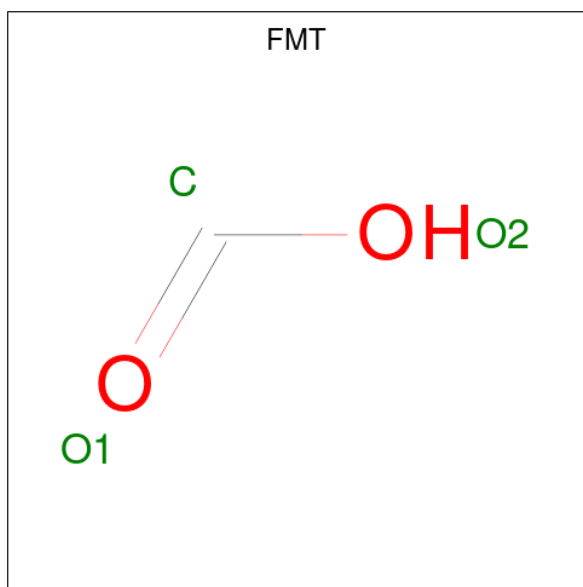
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P68440
A	0	ALA	-	expression tag	UNP P68440
A	513	GLY	ASP	engineered mutation	UNP P68440
B	-24	MET	-	expression tag	UNP P68440
B	-23	SER	-	expression tag	UNP P68440
B	-22	TYR	-	expression tag	UNP P68440
B	-21	TYR	-	expression tag	UNP P68440
B	-20	HIS	-	expression tag	UNP P68440
B	-19	HIS	-	expression tag	UNP P68440
B	-18	HIS	-	expression tag	UNP P68440
B	-17	HIS	-	expression tag	UNP P68440
B	-16	HIS	-	expression tag	UNP P68440
B	-15	HIS	-	expression tag	UNP P68440
B	-14	ASP	-	expression tag	UNP P68440
B	-13	TYR	-	expression tag	UNP P68440
B	-12	ASP	-	expression tag	UNP P68440
B	-11	ILE	-	expression tag	UNP P68440
B	-10	PRO	-	expression tag	UNP P68440
B	-9	THR	-	expression tag	UNP P68440
B	-8	THR	-	expression tag	UNP P68440
B	-7	GLU	-	expression tag	UNP P68440
B	-6	ASN	-	expression tag	UNP P68440
B	-5	LEU	-	expression tag	UNP P68440
B	-4	TYR	-	expression tag	UNP P68440
B	-3	PHE	-	expression tag	UNP P68440
B	-2	GLN	-	expression tag	UNP P68440
B	-1	GLY	-	expression tag	UNP P68440
B	0	ALA	-	expression tag	UNP P68440
B	513	GLY	ASP	engineered mutation	UNP P68440
C	-24	MET	-	expression tag	UNP P68440
C	-23	SER	-	expression tag	UNP P68440
C	-22	TYR	-	expression tag	UNP P68440
C	-21	TYR	-	expression tag	UNP P68440
C	-20	HIS	-	expression tag	UNP P68440
C	-19	HIS	-	expression tag	UNP P68440
C	-18	HIS	-	expression tag	UNP P68440
C	-17	HIS	-	expression tag	UNP P68440
C	-16	HIS	-	expression tag	UNP P68440
C	-15	HIS	-	expression tag	UNP P68440
C	-14	ASP	-	expression tag	UNP P68440
C	-13	TYR	-	expression tag	UNP P68440
C	-12	ASP	-	expression tag	UNP P68440

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-11	ILE	-	expression tag	UNP P68440
C	-10	PRO	-	expression tag	UNP P68440
C	-9	THR	-	expression tag	UNP P68440
C	-8	THR	-	expression tag	UNP P68440
C	-7	GLU	-	expression tag	UNP P68440
C	-6	ASN	-	expression tag	UNP P68440
C	-5	LEU	-	expression tag	UNP P68440
C	-4	TYR	-	expression tag	UNP P68440
C	-3	PHE	-	expression tag	UNP P68440
C	-2	GLN	-	expression tag	UNP P68440
C	-1	GLY	-	expression tag	UNP P68440
C	0	ALA	-	expression tag	UNP P68440
C	513	GLY	ASP	engineered mutation	UNP P68440

- Molecule 2 is FORMIC ACID (CCD ID: FMT) (formula: CH₂O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	3	1	2	0	0
2	A	1	3	1	2	0	0
2	A	1	3	1	2	0	0
2	A	1	3	1	2	0	0
2	C	1	3	1	2	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	C	O	0	0
			3	1	2		
2	C	1	Total	C	O	0	0
			3	1	2		

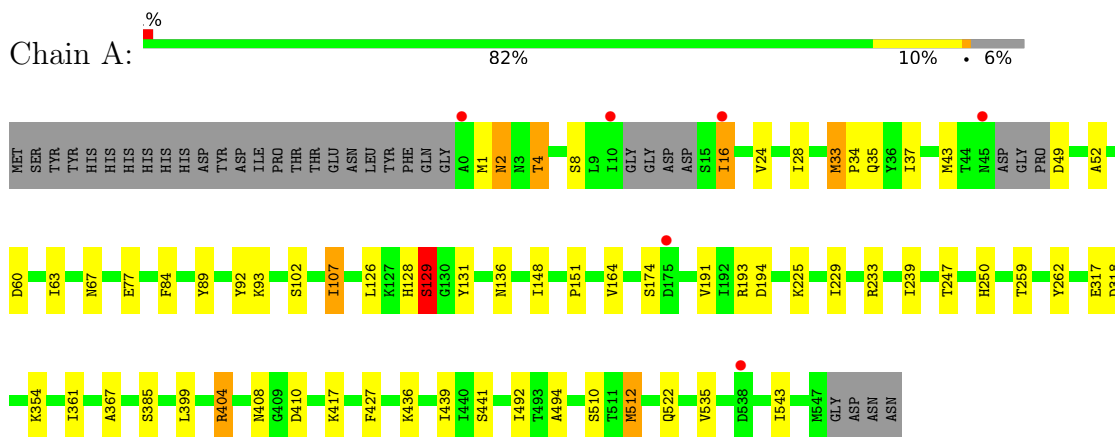
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	248	Total	O	0	0
			248	248		
3	B	175	Total	O	0	0
			175	175		
3	C	202	Total	O	0	0
			202	202		

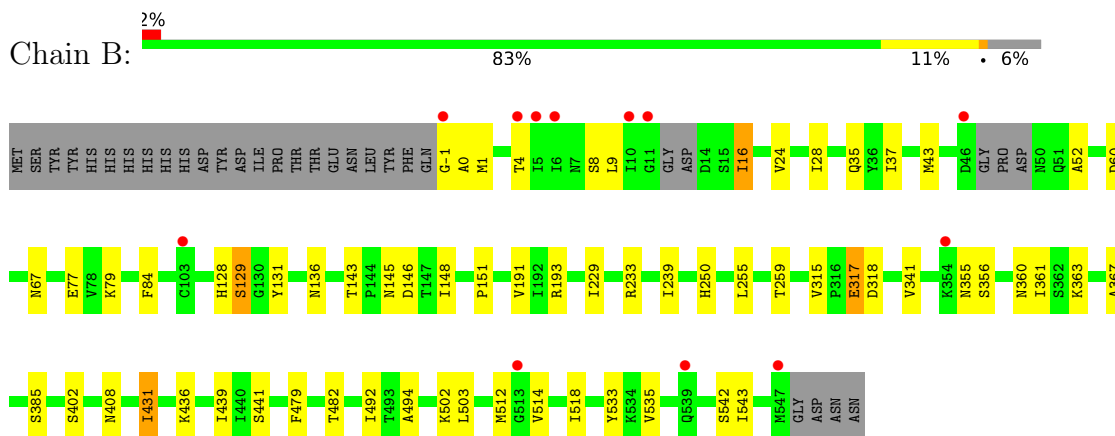
3 Residue-property plots [i](#)

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.

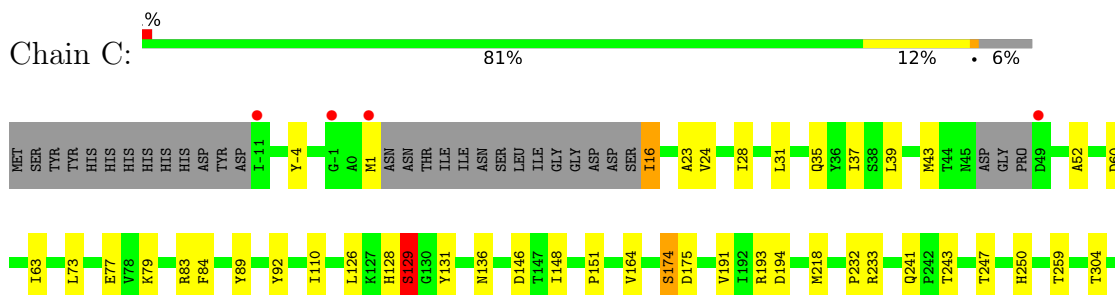
- Molecule 1: Rifampicin resistance protein



- Molecule 1: Rifampicin resistance protein



- Molecule 1: Rifampicin resistance protein





4 Data and refinement statistics

Property	Value	Source
Space group	P 61 2 2	Depositor
Cell constants a, b, c, α , β , γ	189.63Å 189.63Å 255.13Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	17.99 – 2.55 17.99 – 2.55	Depositor EDS
% Data completeness (in resolution range)	99.6 (17.99-2.55) 99.6 (17.99-2.55)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.44 (at 2.56Å)	Xtrriage
Refinement program	BUSTER 2.8.0	Depositor
R, R_{free}	0.175 , 0.201 0.173 , 0.197	Depositor DCC
R_{free} test set	4413 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	52.0	Xtrriage
Anisotropy	0.135	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 51.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	13528	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.68% 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 i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: FMT

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	0.85	1/4387 (0.0%)	1.19	20/5968 (0.3%)
1	B	0.83	1/4379 (0.0%)	1.19	17/5960 (0.3%)
1	C	0.84	0/4395	1.18	17/5979 (0.3%)
All	All	0.84	2/13161 (0.0%)	1.19	54/17907 (0.3%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	33	MET	SD-CE	-6.91	1.62	1.79
1	B	129	SER	CA-C	5.33	1.59	1.52

All (54) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	128	HIS	CA-C-N	10.75	134.69	120.28
1	B	128	HIS	C-N-CA	10.75	134.69	120.28
1	A	129	SER	N-CA-C	9.65	121.80	111.28
1	B	129	SER	N-CA-C	9.54	121.68	111.28
1	A	128	HIS	CA-C-N	9.36	132.82	120.28
1	A	128	HIS	C-N-CA	9.36	132.82	120.28
1	C	128	HIS	CA-C-N	9.08	132.79	120.54
1	C	128	HIS	C-N-CA	9.08	132.79	120.54
1	C	129	SER	N-CA-C	7.98	120.68	111.11
1	A	510	SER	CA-C-N	-7.80	111.23	122.94
1	A	510	SER	C-N-CA	-7.80	111.23	122.94
1	A	2	ASN	CA-CB-CG	7.56	120.16	112.60
1	A	408	ASN	CA-C-N	7.43	135.08	121.70
1	A	408	ASN	C-N-CA	7.43	135.08	121.70
1	C	408	ASN	CA-C-N	7.43	135.07	121.70
1	C	408	ASN	C-N-CA	7.43	135.07	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	317	GLU	CA-C-N	7.23	129.97	120.28
1	B	317	GLU	C-N-CA	7.23	129.97	120.28
1	A	354	LYS	CA-C-N	-7.16	111.15	123.25
1	A	354	LYS	C-N-CA	-7.16	111.15	123.25
1	A	317	GLU	CA-C-N	6.77	130.03	120.28
1	A	317	GLU	C-N-CA	6.77	130.03	120.28
1	C	174	SER	CA-C-N	6.63	131.81	122.46
1	C	174	SER	C-N-CA	6.63	131.81	122.46
1	B	492	ILE	N-CA-CB	6.63	117.75	110.53
1	A	512	MET	N-CA-C	-6.50	99.98	110.32
1	C	129	SER	CA-C-N	6.46	133.32	121.70
1	C	129	SER	C-N-CA	6.46	133.32	121.70
1	C	317	GLU	CA-C-N	6.33	129.40	120.28
1	C	317	GLU	C-N-CA	6.33	129.40	120.28
1	C	-4	TYR	CA-C-N	6.04	130.70	122.07
1	C	-4	TYR	C-N-CA	6.04	130.70	122.07
1	B	129	SER	CA-C-N	5.91	132.34	121.70
1	B	129	SER	C-N-CA	5.91	132.34	121.70
1	B	60	ASP	CA-CB-CG	5.73	118.33	112.60
1	C	194	ASP	CA-CB-CG	5.65	118.25	112.60
1	A	194	ASP	CA-CB-CG	5.64	118.25	112.60
1	A	129	SER	CA-C-N	5.56	131.72	121.70
1	A	129	SER	C-N-CA	5.56	131.72	121.70
1	B	514	VAL	CA-C-N	5.48	129.96	122.34
1	B	514	VAL	C-N-CA	5.48	129.96	122.34
1	B	129	SER	O-C-N	-5.44	116.35	122.12
1	A	67	ASN	CA-CB-CG	5.34	117.94	112.60
1	C	146	ASP	CA-CB-CG	5.25	117.85	112.60
1	A	107	ILE	N-CA-C	-5.24	107.31	111.81
1	B	408	ASN	CA-C-N	5.18	131.03	121.70
1	B	408	ASN	C-N-CA	5.18	131.03	121.70
1	B	318	ASP	CA-CB-CG	5.12	117.72	112.60
1	A	318	ASP	CA-CB-CG	5.11	117.71	112.60
1	C	129	SER	CA-C-O	-5.08	115.46	120.90
1	A	492	ILE	N-CA-C	-5.07	102.20	108.89
1	B	146	ASP	CA-CB-CG	5.06	117.66	112.60
1	B	67	ASN	CA-CB-CG	5.03	117.63	112.60
1	C	318	ASP	CA-CB-CG	5.00	117.61	112.60

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	4296	0	4240	31	0
1	B	4288	0	4221	31	0
1	C	4298	0	4243	37	0
2	A	12	0	4	0	0
2	C	9	0	3	0	0
3	A	248	0	0	0	0
3	B	175	0	0	2	0
3	C	202	0	0	1	0
All	All	13528	0	12711	86	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 (86) 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:33:MET:HE3	1:A:34:PRO:HD2	1.37	1.02
1:B:1:MET:HE2	1:C:63:ILE:HD13	1.58	0.83
1:A:259:THR:HG21	1:A:439:ILE:HD11	1.64	0.78
1:B:259:THR:HG21	1:B:439:ILE:HD11	1.66	0.78
1:B:360:ASN:O	1:B:363:LYS:HG2	1.85	0.77
1:C:259:THR:HG21	1:C:439:ILE:HD11	1.66	0.77
1:A:126:LEU:O	1:A:129:SER:HB2	1.88	0.74
1:B:16:ILE:HD11	1:C:28:ILE:HG21	1.70	0.73
1:A:33:MET:HE3	1:A:34:PRO:CD	2.21	0.67
1:B:1:MET:HE3	1:C:218:MET:HB2	1.75	0.67
1:A:89:TYR:HA	1:A:129:SER:HB3	1.79	0.65
1:A:233:ARG:NH2	1:A:247:THR:O	2.23	0.62
1:A:16:ILE:HD11	1:B:28:ILE:HG21	1.81	0.61
1:C:369:THR:HG22	1:C:382:ALA:HB3	1.82	0.61
1:C:367:ALA:HB3	1:C:385:SER:HB2	1.82	0.61
1:A:191:VAL:HG12	1:A:193[A]:ARG:HD2	1.83	0.59
1:A:33:MET:CE	1:A:34:PRO:HD2	2.23	0.59
1:B:143:THR:HG22	1:B:145:ASN:H	1.66	0.59
1:B:360:ASN:H	1:B:363:LYS:HE3	1.66	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:233:ARG:NH2	1:C:247:THR:O	2.23	0.57
1:C:126:LEU:O	1:C:129:SER:HB2	2.03	0.57
1:C:89:TYR:HA	1:C:129:SER:HB3	1.88	0.55
1:A:399:LEU:HD22	1:A:404:ARG:HH12	1.72	0.55
1:A:33:MET:HE1	1:B:479:PHE:CD1	2.44	0.53
1:A:4:THR:HG21	1:C:451:VAL:O	2.09	0.53
1:A:92:TYR:CD2	1:A:129:SER:OG	2.62	0.53
1:C:60:ASP:HB3	1:C:63:ILE:HG12	1.90	0.53
1:C:43:MET:HE1	1:C:52:ALA:HB1	1.91	0.53
1:B:255:LEU:HD13	1:B:503:LEU:HD13	1.91	0.52
1:C:191:VAL:HG12	1:C:193:ARG:HD2	1.92	0.52
1:B:84:PHE:HB3	1:B:148:ILE:HG21	1.92	0.51
1:B:533:TYR:CD1	1:B:543:ILE:HD12	2.45	0.51
1:B:43:MET:HE1	1:B:52:ALA:HB1	1.93	0.51
1:B:1:MET:HE2	1:C:63:ILE:CD1	2.38	0.51
1:C:174:SER:HB3	1:C:540:GLY:HA2	1.93	0.50
1:B:35:GLN:HG2	1:B:37:ILE:HG13	1.92	0.50
1:C:92:TYR:CD1	1:C:129:SER:OG	2.64	0.50
1:A:84:PHE:HB3	1:A:148:ILE:HG21	1.94	0.50
1:B:367:ALA:HB3	1:B:385:SER:HB2	1.94	0.50
1:C:535:VAL:HG22	1:C:543:ILE:HG22	1.94	0.50
1:C:84:PHE:HB3	1:C:148:ILE:HG21	1.93	0.49
1:C:241:GLN:HG2	1:C:243:THR:HG22	1.94	0.49
1:B:191:VAL:HG12	1:B:193:ARG:HD2	1.94	0.49
1:C:35:GLN:HG2	1:C:37:ILE:HG13	1.93	0.49
1:A:28:ILE:HG21	1:C:16:ILE:HD11	1.93	0.49
1:B:-1:GLY:HA2	1:C:39:LEU:HD23	1.93	0.49
1:A:367:ALA:HB3	1:A:385:SER:HB2	1.94	0.48
1:B:431:ILE:HG12	1:B:439:ILE:HG21	1.95	0.48
1:C:250:HIS:HA	1:C:494:ALA:HB2	1.95	0.48
1:B:250:HIS:HA	1:B:494:ALA:HB2	1.96	0.48
1:A:43:MET:HE1	1:A:52:ALA:HB1	1.96	0.48
1:B:535:VAL:HG22	1:B:543:ILE:HG22	1.96	0.47
1:A:93:LYS:HD3	1:A:427:PHE:CD2	2.50	0.47
1:C:353:ARG:HB2	1:C:356:SER:HB3	1.95	0.47
1:C:453:TYR:CD2	1:C:477:LEU:HD21	2.50	0.47
1:C:534:LYS:HB2	1:C:546:ILE:HD11	1.98	0.46
1:A:535:VAL:HG22	1:A:543:ILE:HG22	1.98	0.45
1:A:77:GLU:HB2	1:A:151:PRO:HD3	1.96	0.45
1:C:110:ILE:HG13	1:C:232:PRO:HG2	1.99	0.45
1:A:35:GLN:HG2	1:A:37:ILE:HG13	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:92:TYR:HD1	1:C:129:SER:OG	1.97	0.45
1:A:262:TYR:HB3	1:A:522:GLN:HB2	1.99	0.45
1:A:250:HIS:HA	1:A:494:ALA:HB2	1.98	0.44
1:B:239:ILE:HG12	3:B:813:HOH:O	2.17	0.44
1:C:77:GLU:HB2	1:C:151:PRO:HD3	2.00	0.43
1:C:233:ARG:HD3	1:C:531:ASP:OD2	2.18	0.43
1:B:0:ALA:HB1	1:C:60:ASP:OD2	2.18	0.43
1:B:77:GLU:HB2	1:B:151:PRO:HD3	1.99	0.43
1:A:60:ASP:HB3	1:A:63:ILE:HG13	1.99	0.43
1:A:92:TYR:HD2	1:A:129:SER:HG	1.65	0.43
1:C:512:MET:HE3	1:C:512:MET:HB2	1.81	0.43
1:B:512:MET:HG2	1:B:518:ILE:HG23	2.01	0.43
1:A:92:TYR:HD2	1:A:129:SER:OG	2.02	0.43
1:A:225:LYS:HB2	1:C:23:ALA:HB1	2.00	0.43
1:A:131:TYR:HA	1:A:136:ASN:OD1	2.19	0.42
1:B:131:TYR:HA	1:B:136:ASN:OD1	2.20	0.42
1:A:410:ASP:CG	1:A:417:LYS:HE2	2.45	0.41
1:B:229:ILE:HD13	1:B:229:ILE:HG21	1.87	0.41
1:C:92:TYR:HD1	1:C:129:SER:HG	1.58	0.41
1:B:233:ARG:NH1	3:B:1175:HOH:O	2.51	0.41
1:A:102:SER:HB3	1:A:107:ILE:HD11	2.02	0.41
1:C:131:TYR:HA	1:C:136:ASN:OD1	2.21	0.41
1:C:83[B]:ARG:NH2	3:C:1116:HOH:O	2.54	0.41
1:B:315:VAL:HG22	1:B:341:VAL:HB	2.03	0.40
1:A:34:PRO:HG2	1:B:479:PHE:HA	2.04	0.40
1:B:9:LEU:HD22	1:C:31:LEU:HG	2.02	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	538/576 (93%)	520 (97%)	17 (3%)	1 (0%)	43	56
1	B	538/576 (93%)	517 (96%)	21 (4%)	0	100	100
1	C	538/576 (93%)	516 (96%)	22 (4%)	0	100	100
All	All	1614/1728 (93%)	1553 (96%)	60 (4%)	1 (0%)	48	61

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	174	SER

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	493/527 (94%)	477 (97%)	16 (3%)	34	51
1	B	493/527 (94%)	476 (97%)	17 (3%)	32	48
1	C	492/527 (93%)	473 (96%)	19 (4%)	28	43
All	All	1478/1581 (94%)	1426 (96%)	52 (4%)	32	48

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	2	ASN
1	A	4	THR
1	A	8	SER
1	A	16	ILE
1	A	24	VAL
1	A	49	ASP
1	A	129	SER
1	A	164	VAL
1	A	229	ILE
1	A	239	ILE
1	A	361	ILE

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Mol	Chain	Res	Type
1	A	404	ARG
1	A	436	LYS
1	A	441	SER
1	A	512	MET
1	B	4	THR
1	B	8	SER
1	B	16	ILE
1	B	24	VAL
1	B	79	LYS
1	B	129	SER
1	B	317	GLU
1	B	355	ASN
1	B	356	SER
1	B	361	ILE
1	B	402	SER
1	B	431	ILE
1	B	436	LYS
1	B	441	SER
1	B	482	THR
1	B	502	LYS
1	B	542	SER
1	C	1	MET
1	C	16	ILE
1	C	24	VAL
1	C	73	LEU
1	C	79	LYS
1	C	129	SER
1	C	164	VAL
1	C	175	ASP
1	C	304	THR
1	C	353	ARG
1	C	369	THR
1	C	385	SER
1	C	402	SER
1	C	436	LYS
1	C	441	SER
1	C	518	ILE
1	C	536	SER
1	C	541	VAL
1	C	542	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	7	ASN
1	A	96	ASN
1	B	7	ASN
1	B	61	GLN
1	B	221	ASN
1	B	268	ASN
1	B	324	GLN
1	C	45	ASN
1	C	96	ASN
1	C	203	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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](#)

7 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	FMT	C	552	-	2,2,2	0.79	0	1,1,1	0.71	0
2	FMT	C	554	-	2,2,2	0.69	0	1,1,1	0.35	0
2	FMT	A	552	-	2,2,2	0.56	0	1,1,1	0.05	0
2	FMT	A	553	-	2,2,2	0.57	0	1,1,1	0.07	0
2	FMT	C	553	-	2,2,2	0.77	0	1,1,1	0.31	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	FMT	A	555	-	2,2,2	0.71	0	1,1,1	0.57	0
2	FMT	A	554	-	2,2,2	0.61	0	1,1,1	0.63	0

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.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	541/576 (93%)	-0.43	6 (1%) 78 79	19, 47, 73, 109	3 (0%)
1	B	544/576 (94%)	-0.17	12 (2%) 62 63	38, 55, 87, 124	0
1	C	542/576 (94%)	-0.41	4 (0%) 84 86	26, 49, 74, 103	2 (0%)
All	All	1627/1728 (94%)	-0.34	22 (1%) 73 74	19, 50, 80, 124	5 (0%)

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	10	ILE	6.1
1	B	46	ASP	4.4
1	B	10	ILE	3.9
1	B	-1	GLY	3.7
1	A	538	ASP	3.2
1	B	11	GLY	3.0
1	B	539	GLN	2.9
1	C	-11	ILE	2.8
1	C	-1	GLY	2.6
1	B	6	ILE	2.6
1	B	103	CYS	2.4
1	B	513	GLY	2.4
1	A	175	ASP	2.4
1	B	5	ILE	2.4
1	B	547	MET	2.4
1	A	16	ILE	2.4
1	C	1	MET	2.3
1	A	0	ALA	2.3
1	B	4	THR	2.1
1	B	354	LYS	2.1
1	A	45	ASN	2.1
1	C	49	ASP	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(Å ²)	Q<0.9
2	FMT	C	552	3/3	0.77	0.16	61,61,64,65	0
2	FMT	A	552	3/3	0.82	0.15	71,71,74,75	0
2	FMT	A	554	3/3	0.84	0.14	61,61,61,63	0
2	FMT	A	553	3/3	0.86	0.18	75,75,76,77	0
2	FMT	C	554	3/3	0.86	0.15	60,60,64,64	0
2	FMT	C	553	3/3	0.92	0.09	62,62,64,65	0
2	FMT	A	555	3/3	0.93	0.08	70,70,74,74	0

6.5 Other polymers [i](#)

There are no such residues in this entry.