



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 02:39 AM UTC

PDB ID : 4ZDI / pdb_00004zdi
Title : Crystal structure of the M. tuberculosis CTP synthase PyrG (apo form)
Authors : Bellinzoni, M.; Barilone, N.; Alzari, P.M.
Deposited on : 2015-04-17
Resolution : 3.52 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
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

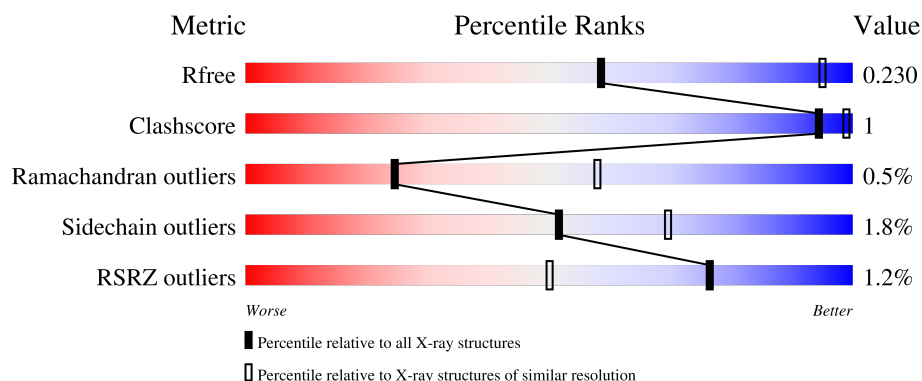
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.52 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	1025 (3.56-3.48)
Clashscore	190562	1079 (3.56-3.48)
Ramachandran outliers	187476	1052 (3.56-3.48)
Sidechain outliers	187428	1053 (3.56-3.48)
RSRZ outliers	180081	1024 (3.56-3.48)

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	587	86% 5% 10%
1	B	587	87% • 9%
1	C	587	85% 6% 9%
1	D	587	86% 5% 10%
1	E	587	2% 84% 6% 10%

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Mol	Chain	Length	Quality of chain
1	F	587	% 84% 6% 10%
1	G	587	% 85% 5% 10%
1	H	587	% 84% 5% 11%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 30937 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 CTP synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	531	Total	C	N	O	S	0	0	0
			3877	2451	676	739	11			
1	B	534	Total	C	N	O	S	0	0	0
			3888	2458	671	747	12			
1	C	533	Total	C	N	O	S	0	0	0
			3856	2442	662	740	12			
1	D	531	Total	C	N	O	S	0	0	0
			3932	2490	686	745	11			
1	E	530	Total	C	N	O	S	0	0	0
			3911	2479	684	738	10			
1	F	526	Total	C	N	O	S	0	0	0
			3862	2447	669	735	11			
1	G	527	Total	C	N	O	S	0	0	0
			3893	2466	678	738	11			
1	H	525	Total	C	N	O	S	0	0	0
			3710	2338	641	720	11			

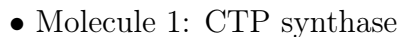
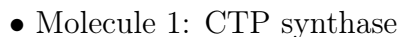
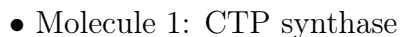
There are 8 discrepancies between the modelled and reference sequences:

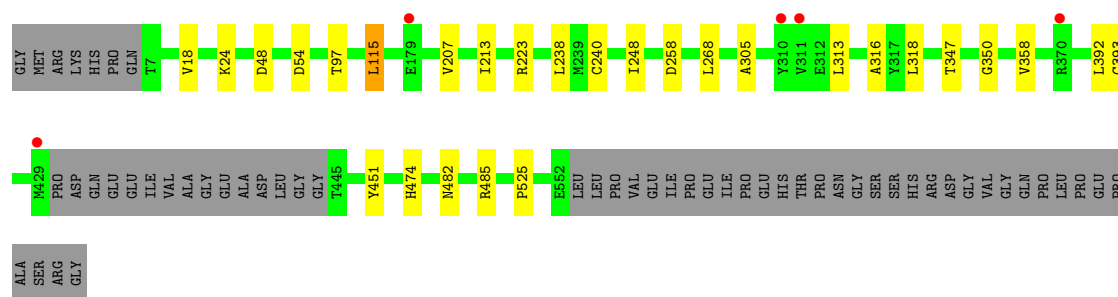
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP P9WHK7
B	0	GLY	-	expression tag	UNP P9WHK7
C	0	GLY	-	expression tag	UNP P9WHK7
D	0	GLY	-	expression tag	UNP P9WHK7
E	0	GLY	-	expression tag	UNP P9WHK7
F	0	GLY	-	expression tag	UNP P9WHK7
G	0	GLY	-	expression tag	UNP P9WHK7
H	0	GLY	-	expression tag	UNP P9WHK7

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

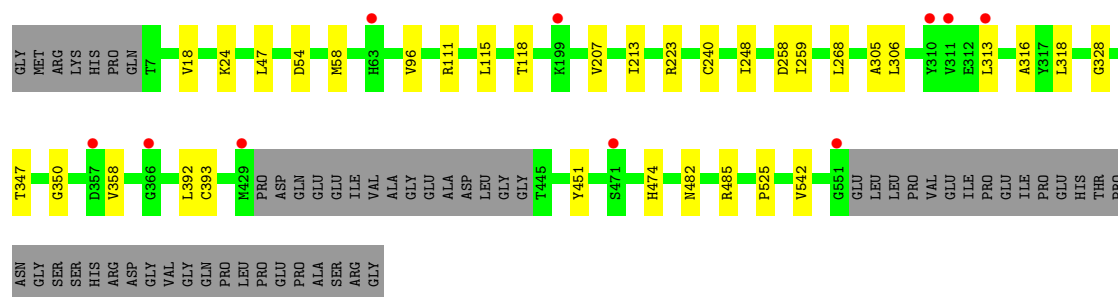
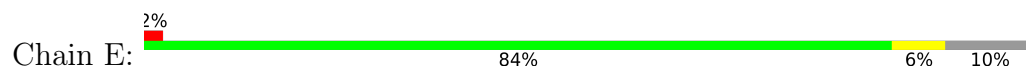
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 1	Ca 1	0	0
2	B	1	Total 1	Ca 1	0	0
2	C	1	Total 1	Ca 1	0	0
2	D	1	Total 1	Ca 1	0	0
2	E	1	Total 1	Ca 1	0	0
2	F	1	Total 1	Ca 1	0	0
2	G	1	Total 1	Ca 1	0	0
2	H	1	Total 1	Ca 1	0	0

- Molecule 1: CTP synthase

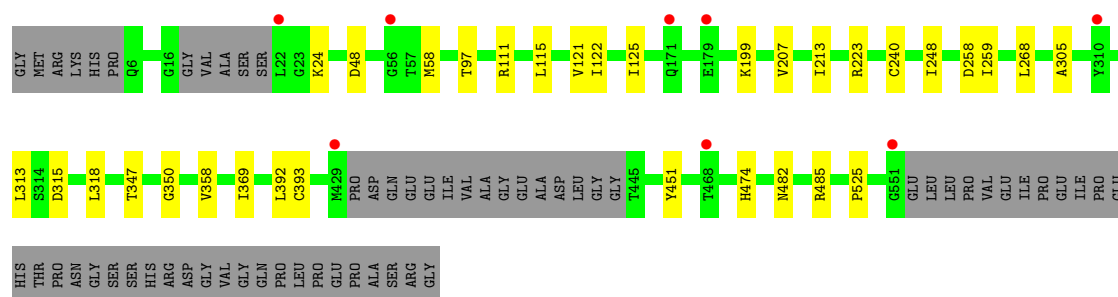
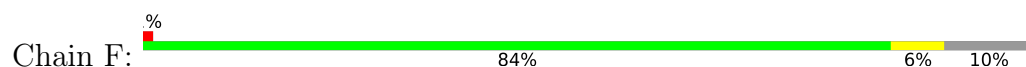




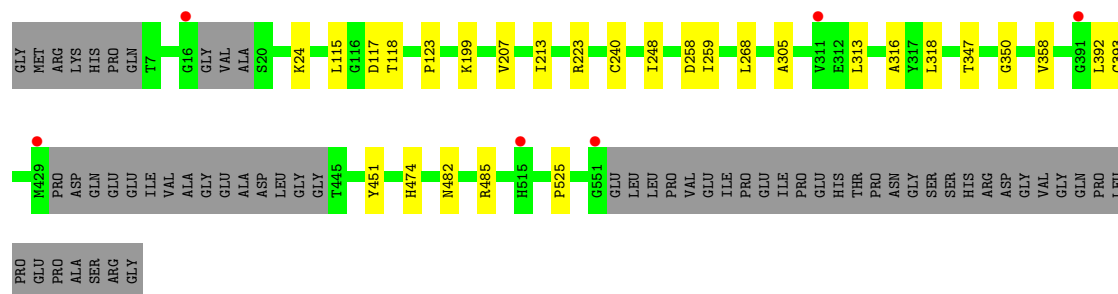
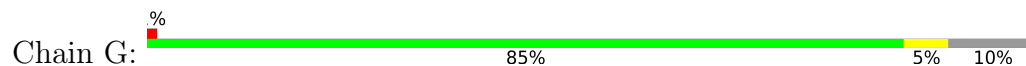
• Molecule 1: CTP synthase



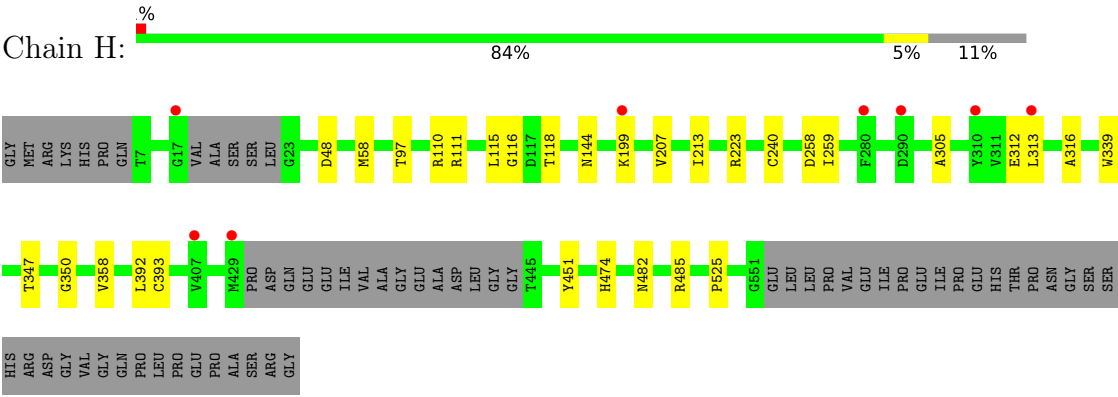
• Molecule 1: CTP synthase



• Molecule 1: CTP synthase



• Molecule 1: CTP synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 43	Depositor
Cell constants a, b, c, α , β , γ	196.83Å 196.83Å 184.05Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.21 – 3.52 49.21 – 3.52	Depositor EDS
% Data completeness (in resolution range)	98.6 (49.21-3.52) 98.6 (49.21-3.52)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.55 (at 3.48Å)	Xtriage
Refinement program	BUSTER 2.10.1	Depositor
R, R_{free}	0.213 , 0.221 0.220 , 0.230	Depositor DCC
R_{free} test set	4292 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	101.7	Xtriage
Anisotropy	0.721	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 81.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.089 for h,-k,-l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	30937	wwPDB-VP
Average B, all atoms (Å ²)	110.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.13% 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: CA

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	0.78	0/3965	1.27	2/5425 (0.0%)
1	B	0.78	1/3975 (0.0%)	1.27	4/5440 (0.1%)
1	C	0.78	1/3941 (0.0%)	1.27	2/5400 (0.0%)
1	D	0.78	0/4019	1.27	2/5494 (0.0%)
1	E	0.78	1/3999 (0.0%)	1.26	2/5470 (0.0%)
1	F	0.79	1/3948 (0.0%)	1.26	2/5401 (0.0%)
1	G	0.78	1/3977 (0.0%)	1.26	4/5433 (0.1%)
1	H	0.79	1/3791 (0.0%)	1.27	2/5204 (0.0%)
All	All	0.78	6/31615 (0.0%)	1.27	20/43267 (0.0%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	259	ILE	CA-C	5.20	1.56	1.52
1	C	259	ILE	CA-C	5.15	1.56	1.52
1	B	259	ILE	CA-C	5.14	1.56	1.52
1	F	259	ILE	CA-C	5.14	1.56	1.52
1	H	259	ILE	CA-C	5.06	1.56	1.52
1	G	259	ILE	CA-C	5.06	1.56	1.52

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	258	ASP	CA-C-N	9.07	125.95	120.24
1	E	258	ASP	C-N-CA	9.07	125.95	120.24
1	H	258	ASP	CA-C-N	9.05	125.94	120.24
1	H	258	ASP	C-N-CA	9.05	125.94	120.24
1	F	258	ASP	CA-C-N	8.98	125.90	120.24
1	F	258	ASP	C-N-CA	8.98	125.90	120.24
1	G	258	ASP	CA-C-N	8.91	125.85	120.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	258	ASP	C-N-CA	8.91	125.85	120.24
1	B	258	ASP	CA-C-N	8.87	125.83	120.24
1	B	258	ASP	C-N-CA	8.87	125.83	120.24
1	D	258	ASP	CA-C-N	8.83	125.80	120.24
1	D	258	ASP	C-N-CA	8.83	125.80	120.24
1	C	258	ASP	CA-C-N	8.81	125.79	120.24
1	C	258	ASP	C-N-CA	8.81	125.79	120.24
1	A	258	ASP	CA-C-N	8.60	125.66	120.24
1	A	258	ASP	C-N-CA	8.60	125.66	120.24
1	G	123	PRO	CA-C-N	5.03	127.27	120.38
1	G	123	PRO	C-N-CA	5.03	127.27	120.38
1	B	100	GLN	CA-C-N	5.01	126.87	120.56
1	B	100	GLN	C-N-CA	5.01	126.87	120.56

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	3877	0	3650	9	0
1	B	3888	0	3655	7	0
1	C	3856	0	3615	11	0
1	D	3932	0	3774	9	0
1	E	3911	0	3743	15	0
1	F	3862	0	3668	10	0
1	G	3893	0	3749	9	0
1	H	3710	0	3377	14	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	30937	0	29231	78	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 1.

All (78) 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:E:54:ASP:HB2	1:H:110:ARG:HH22	1.60	0.67
1:B:428:THR:HB	1:B:444:GLY:HA3	1.82	0.61
1:C:305:ALA:HB2	1:C:358:VAL:HG11	1.83	0.60
1:G:305:ALA:HB2	1:G:358:VAL:HG11	1.83	0.60
1:E:305:ALA:HB2	1:E:358:VAL:HG11	1.83	0.59
1:D:305:ALA:HB2	1:D:358:VAL:HG11	1.83	0.59
1:F:305:ALA:HB2	1:F:358:VAL:HG11	1.83	0.59
1:H:305:ALA:HB2	1:H:358:VAL:HG11	1.83	0.58
1:B:305:ALA:HB2	1:B:358:VAL:HG11	1.87	0.57
1:G:313:LEU:HD23	1:G:316:ALA:HB2	1.87	0.55
1:D:313:LEU:HD23	1:D:316:ALA:HB2	1.89	0.55
1:B:22:LEU:HD22	1:B:188:LEU:HD13	1.89	0.54
1:E:54:ASP:HB2	1:H:110:ARG:NH2	2.24	0.53
1:E:313:LEU:HD23	1:E:316:ALA:HB2	1.91	0.53
1:C:207:VAL:HG11	1:C:240:CYS:HB3	1.91	0.51
1:H:312:GLU:H	1:H:339:TRP:HB3	1.75	0.51
1:C:228:VAL:HG13	1:C:232:LEU:HD23	1.93	0.51
1:E:347:THR:HG23	1:E:350:GLY:H	1.77	0.49
1:G:347:THR:HG23	1:G:350:GLY:H	1.77	0.49
1:D:347:THR:HG23	1:D:350:GLY:H	1.78	0.49
1:A:428:THR:HB	1:A:444:GLY:HA3	1.95	0.49
1:C:347:THR:HG23	1:C:350:GLY:H	1.78	0.49
1:F:347:THR:HG23	1:F:350:GLY:H	1.77	0.49
1:B:347:THR:HG23	1:B:350:GLY:H	1.77	0.49
1:D:207:VAL:HG11	1:D:240:CYS:HB3	1.95	0.48
1:H:313:LEU:HD23	1:H:316:ALA:HB2	1.95	0.48
1:H:347:THR:HG23	1:H:350:GLY:H	1.77	0.48
1:A:347:THR:HG23	1:A:350:GLY:H	1.77	0.47
1:F:207:VAL:HG11	1:F:240:CYS:HB3	1.95	0.47
1:F:48:ASP:HB2	1:F:97:THR:HG22	1.97	0.47
1:A:121:VAL:HA	1:A:125:ILE:HB	1.96	0.47
1:G:207:VAL:HG11	1:G:240:CYS:HB3	1.95	0.47
1:H:207:VAL:HG11	1:H:240:CYS:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:48:ASP:HB2	1:D:97:THR:HG22	1.99	0.45
1:B:207:VAL:HG11	1:B:240:CYS:HB3	1.99	0.45
1:H:48:ASP:HB2	1:H:97:THR:HG22	1.99	0.45
1:C:497:GLY:HA3	1:C:507:PHE:HB2	1.99	0.45
1:C:389:VAL:HB	1:C:518:VAL:HG13	1.98	0.45
1:C:312:GLU:H	1:C:339:TRP:HB3	1.81	0.44
1:A:451:TYR:HB2	1:A:474:HIS:CD2	2.54	0.43
1:D:451:TYR:HB2	1:D:474:HIS:CD2	2.54	0.43
1:G:482:ASN:HA	1:G:485:ARG:HG3	2.01	0.43
1:A:482:ASN:HA	1:A:485:ARG:HG3	2.01	0.43
1:H:451:TYR:HB2	1:H:474:HIS:CD2	2.54	0.43
1:H:482:ASN:HA	1:H:485:ARG:HG3	2.01	0.43
1:G:392:LEU:HD22	1:G:525:PRO:HD2	2.01	0.42
1:D:392:LEU:HD22	1:D:525:PRO:HD2	2.01	0.42
1:E:451:TYR:HB2	1:E:474:HIS:CD2	2.53	0.42
1:F:482:ASN:HA	1:F:485:ARG:HG3	2.00	0.42
1:D:482:ASN:HA	1:D:485:ARG:HG3	2.01	0.42
1:E:392:LEU:HD22	1:E:525:PRO:HD2	2.01	0.42
1:G:451:TYR:HB2	1:G:474:HIS:CD2	2.53	0.42
1:A:207:VAL:HG11	1:A:240:CYS:HB3	2.01	0.42
1:E:482:ASN:HA	1:E:485:ARG:HG3	2.01	0.42
1:F:392:LEU:HD22	1:F:525:PRO:HD2	2.02	0.42
1:E:118:THR:HG22	1:H:58:MET:HE2	2.01	0.42
1:A:392:LEU:HD22	1:A:525:PRO:HD2	2.01	0.42
1:C:328:GLY:HA2	1:C:542:VAL:HG11	2.01	0.42
1:B:482:ASN:HA	1:B:485:ARG:HG3	2.01	0.42
1:F:451:TYR:HB2	1:F:474:HIS:CD2	2.54	0.42
1:E:248:ILE:HG13	1:E:268:LEU:HD13	2.02	0.41
1:F:58:MET:HE2	1:G:118:THR:HA	2.01	0.41
1:F:248:ILE:HG13	1:F:268:LEU:HD13	2.02	0.41
1:G:248:ILE:HG13	1:G:268:LEU:HD13	2.02	0.41
1:A:328:GLY:HA2	1:A:542:VAL:HG11	2.01	0.41
1:B:248:ILE:HG13	1:B:268:LEU:HD13	2.02	0.41
1:D:248:ILE:HG13	1:D:268:LEU:HD13	2.02	0.41
1:E:47:LEU:HD23	1:E:96:VAL:HB	2.01	0.41
1:C:248:ILE:HG13	1:C:268:LEU:HD13	2.03	0.41
1:C:392:LEU:HD22	1:C:525:PRO:HD2	2.02	0.41
1:E:58:MET:HE2	1:H:118:THR:HG22	2.02	0.41
1:A:248:ILE:HG13	1:A:268:LEU:HD13	2.03	0.41
1:F:121:VAL:O	1:F:125:ILE:HB	2.21	0.41
1:H:392:LEU:HD22	1:H:525:PRO:HD2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:207:VAL:HG11	1:E:240:CYS:HB3	2.02	0.41
1:E:58:MET:HA	1:H:116:GLY:HA2	2.02	0.40
1:E:328:GLY:HA2	1:E:542:VAL:HG11	2.04	0.40
1:C:482:ASN:HA	1:C:485:ARG:HG3	2.02	0.40

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	527/587 (90%)	510 (97%)	15 (3%)	2 (0%)	30	62
1	B	530/587 (90%)	511 (96%)	16 (3%)	3 (1%)	21	55
1	C	529/587 (90%)	507 (96%)	18 (3%)	4 (1%)	16	50
1	D	527/587 (90%)	511 (97%)	13 (2%)	3 (1%)	21	55
1	E	526/587 (90%)	508 (97%)	15 (3%)	3 (1%)	21	55
1	F	520/587 (89%)	504 (97%)	14 (3%)	2 (0%)	30	62
1	G	521/587 (89%)	507 (97%)	12 (2%)	2 (0%)	30	62
1	H	519/587 (88%)	504 (97%)	13 (2%)	2 (0%)	30	62
All	All	4199/4696 (89%)	4062 (97%)	116 (3%)	21 (0%)	24	58

All (21) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	393	CYS
1	B	18	VAL
1	B	393	CYS
1	C	18	VAL
1	C	393	CYS
1	D	393	CYS

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Mol	Chain	Res	Type
1	E	393	CYS
1	F	393	CYS
1	G	393	CYS
1	H	393	CYS
1	A	18	VAL
1	D	18	VAL
1	E	18	VAL
1	C	408	GLY
1	F	115	LEU
1	G	115	LEU
1	B	115	LEU
1	C	115	LEU
1	H	115	LEU
1	D	115	LEU
1	E	115	LEU

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	382/480 (80%)	376 (98%)	6 (2%)	55	70
1	B	384/480 (80%)	377 (98%)	7 (2%)	51	69
1	C	378/480 (79%)	370 (98%)	8 (2%)	47	66
1	D	397/480 (83%)	390 (98%)	7 (2%)	51	69
1	E	392/480 (82%)	386 (98%)	6 (2%)	57	71
1	F	386/480 (80%)	376 (97%)	10 (3%)	40	63
1	G	394/480 (82%)	388 (98%)	6 (2%)	57	71
1	H	350/480 (73%)	345 (99%)	5 (1%)	59	72
All	All	3063/3840 (80%)	3008 (98%)	55 (2%)	51	69

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	LYS
1	A	111	ARG
1	A	122	ILE
1	A	213	ILE
1	A	223	ARG
1	A	306	LEU
1	B	24	LYS
1	B	111	ARG
1	B	115	LEU
1	B	213	ILE
1	B	223	ARG
1	B	306	LEU
1	B	318	LEU
1	C	24	LYS
1	C	108	LYS
1	C	115	LEU
1	C	213	ILE
1	C	223	ARG
1	C	448	LEU
1	C	455	LEU
1	C	471	SER
1	D	24	LYS
1	D	54	ASP
1	D	115	LEU
1	D	213	ILE
1	D	223	ARG
1	D	238	LEU
1	D	318	LEU
1	E	24	LYS
1	E	111	ARG
1	E	213	ILE
1	E	223	ARG
1	E	306	LEU
1	E	318	LEU
1	F	24	LYS
1	F	111	ARG
1	F	122	ILE
1	F	199	LYS
1	F	213	ILE
1	F	223	ARG
1	F	313	LEU
1	F	315	ASP
1	F	318	LEU

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Mol	Chain	Res	Type
1	F	369	ILE
1	G	24	LYS
1	G	117	ASP
1	G	199	LYS
1	G	213	ILE
1	G	223	ARG
1	G	318	LEU
1	H	111	ARG
1	H	144	ASN
1	H	199	LYS
1	H	213	ILE
1	H	223	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	GLN
1	A	144	ASN
1	B	11	HIS
1	B	33	GLN
1	C	33	GLN
1	C	144	ASN
1	C	474	HIS
1	D	33	GLN
1	D	95	ASN
1	D	144	ASN
1	D	163	GLN
1	D	174	HIS
1	D	522	GLN
1	E	33	GLN
1	E	63	HIS
1	E	95	ASN
1	E	174	HIS
1	E	234	ASN
1	E	522	GLN
1	F	33	GLN
1	F	95	ASN
1	F	174	HIS
1	F	522	GLN
1	G	33	GLN
1	G	95	ASN
1	G	522	GLN

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Mol	Chain	Res	Type
1	H	33	GLN
1	H	59	ASN
1	H	95	ASN
1	H	522	GLN

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](#)

Of 8 ligands modelled in this entry, 8 are monoatomic - leaving 0 for Mogul analysis.

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 [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	531/587 (90%)	0.09	4 (0%)	82 58	68, 97, 122, 166	0
1	B	534/587 (90%)	0.04	5 (0%)	81 56	69, 97, 125, 159	0
1	C	533/587 (90%)	0.08	4 (0%)	82 58	68, 98, 133, 163	0
1	D	531/587 (90%)	0.10	5 (0%)	81 56	80, 107, 132, 174	0
1	E	530/587 (90%)	0.16	10 (1%)	66 39	87, 116, 139, 173	0
1	F	526/587 (89%)	0.18	8 (1%)	72 44	92, 118, 141, 168	0
1	G	527/587 (89%)	0.20	6 (1%)	78 52	96, 121, 142, 164	0
1	H	525/587 (89%)	0.17	8 (1%)	72 44	96, 120, 149, 188	0
All	All	4237/4696 (90%)	0.13	50 (1%)	76 50	68, 111, 140, 188	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	429	MET	4.0
1	A	429	MET	3.7
1	H	429	MET	3.5
1	D	370	ARG	3.4
1	D	310	TYR	3.3
1	F	310	TYR	3.1
1	A	551	GLY	3.1
1	E	429	MET	3.0
1	G	429	MET	3.0
1	H	313	LEU	2.9
1	C	313	LEU	2.8
1	H	280	PHE	2.8
1	B	310	TYR	2.7
1	E	366	GLY	2.7
1	E	199	LYS	2.7
1	E	310	TYR	2.6

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Mol	Chain	Res	Type	RSRZ
1	F	468	THR	2.6
1	D	311	VAL	2.6
1	G	551	GLY	2.6
1	B	313	LEU	2.5
1	B	410	THR	2.4
1	H	290	ASP	2.4
1	B	366	GLY	2.4
1	A	310	TYR	2.4
1	C	310	TYR	2.4
1	C	246	GLY	2.3
1	E	313	LEU	2.3
1	F	429	MET	2.3
1	C	368	GLY	2.3
1	E	311	VAL	2.3
1	E	551	GLY	2.2
1	F	551	GLY	2.2
1	E	357	ASP	2.2
1	F	22	LEU	2.2
1	B	311	VAL	2.2
1	H	17	GLY	2.2
1	G	515	HIS	2.2
1	G	16	GLY	2.2
1	E	63	HIS	2.1
1	A	411	ASN	2.1
1	F	171	GLN	2.1
1	H	407	VAL	2.1
1	F	56	GLY	2.1
1	F	179	GLU	2.1
1	H	310	TYR	2.1
1	E	471	SER	2.1
1	H	199	LYS	2.0
1	G	311	VAL	2.0
1	G	391	GLY	2.0
1	D	179	GLU	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 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
2	CA	D	601	1/1	0.77	0.11	119,119,119,119	0
2	CA	G	601	1/1	0.85	0.11	112,112,112,112	0
2	CA	E	601	1/1	0.91	0.17	114,114,114,114	0
2	CA	C	601	1/1	0.93	0.12	113,113,113,113	0
2	CA	F	601	1/1	0.94	0.08	124,124,124,124	0
2	CA	B	601	1/1	0.95	0.11	97,97,97,97	0
2	CA	A	601	1/1	0.95	0.13	94,94,94,94	0
2	CA	H	601	1/1	0.95	0.10	117,117,117,117	0

6.5 Other polymers [i](#)

There are no such residues in this entry.