



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 02:11 PM UTC

PDB ID : 2FGT / pdb_00002fgt
Title : Crystal Structure of YycH from Bacillus subtilis
Authors : Szurmant, H.; Zhao, H.; Mohan, M.A.; James, H.A.; Varughese, K.I.
Deposited on : 2005-12-22
Resolution : 2.30 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

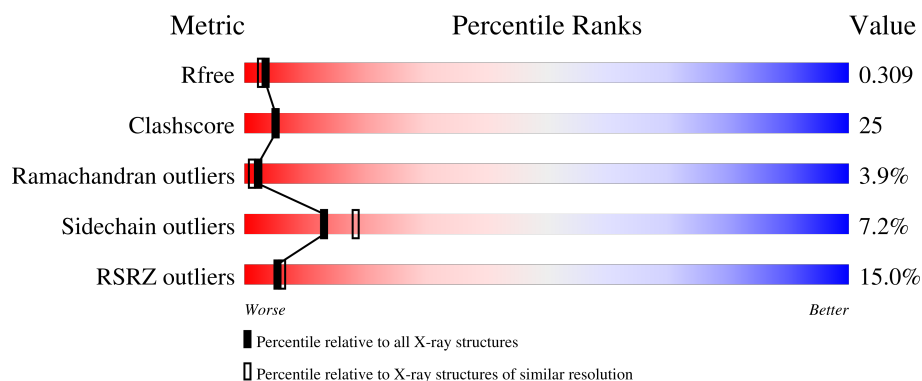
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	417	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3058 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 Two-component system yycF/yycG regulatory protein yycH.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	373	Total	C	N	O	S	0	0	0
			2964	1904	478	574	8			

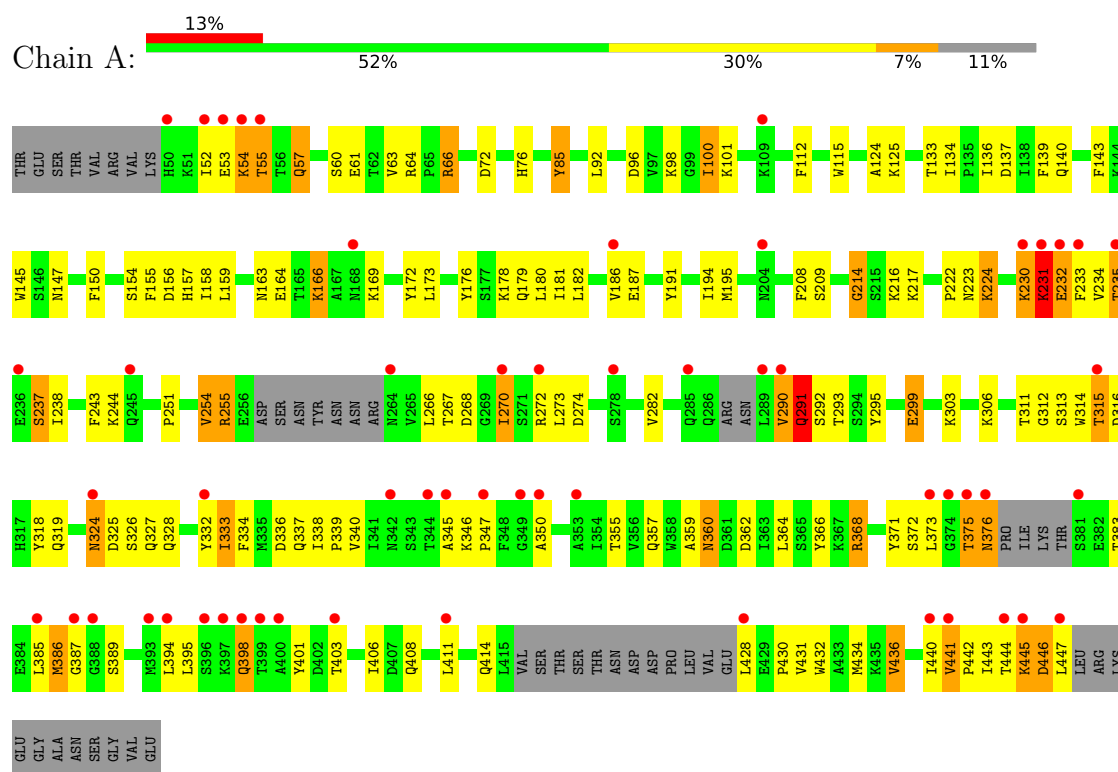
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	94	Total	O	0	0
			94	94		

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: Two-component system yycF/yyeG regulatory protein yycH



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	63.58Å 63.58Å 192.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.35 – 2.30 38.35 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.2 (38.35-2.30) 99.3 (38.35-2.30)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.92 (at 2.29Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.251 , 0.304 0.257 , 0.309	Depositor DCC
R_{free} test set	1800 reflections (9.86%)	wwPDB-VP
Wilson B-factor (Å ²)	37.7	Xtriage
Anisotropy	0.094	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 46.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	3058	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.71% 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](#)

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	0.44	0/3029	1.01	17/4105 (0.4%)

There are no bond length outliers.

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	389	SER	N-CA-C	-9.40	100.38	112.23
1	A	441	VAL	N-CA-C	7.62	116.20	107.89
1	A	325	ASP	N-CA-C	-7.62	102.98	111.82
1	A	176	TYR	N-CA-C	7.57	120.25	111.02
1	A	368	ARG	N-CA-C	7.56	114.80	108.07
1	A	214	GLY	N-CA-C	-6.72	100.71	112.53
1	A	232	GLU	N-CA-C	-6.67	96.59	110.80
1	A	345	ALA	N-CA-C	-6.01	101.87	110.59
1	A	231	LYS	N-CA-C	5.83	123.23	110.80
1	A	327	GLN	N-CA-C	5.64	119.18	111.39
1	A	230	LYS	N-CA-C	5.54	117.88	109.63
1	A	446	ASP	N-CA-C	-5.43	106.69	113.15
1	A	359	ALA	N-CA-C	-5.43	102.13	109.95
1	A	158	ILE	N-CA-C	-5.42	99.84	107.75
1	A	181	ILE	N-CA-C	5.31	115.63	107.77
1	A	173	LEU	N-CA-C	-5.23	100.20	108.73
1	A	55	THR	N-CA-C	5.20	118.03	110.17

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	2964	0	2820	143	0
2	A	94	0	0	5	0
All	All	3058	0	2820	143	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 25.

All (143) 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:315:THR:HG21	1:A:368:ARG:HH22	1.24	0.99
1:A:54:LYS:HG2	1:A:55:THR:HG23	1.48	0.91
1:A:53:GLU:HB2	1:A:312:GLY:O	1.73	0.89
1:A:316:ASP:HB3	1:A:333:ILE:HD13	1.58	0.85
1:A:100:ILE:HD13	1:A:101:LYS:N	1.93	0.84
1:A:315:THR:HG21	1:A:368:ARG:NH2	1.94	0.82
1:A:209:SER:HB3	1:A:223:ASN:HD21	1.44	0.82
1:A:315:THR:CG2	1:A:368:ARG:HH22	1.93	0.82
1:A:333:ILE:HG23	1:A:340:VAL:HB	1.61	0.81
1:A:434:MET:HB3	1:A:443:ILE:HD11	1.65	0.76
1:A:267:THR:CG2	1:A:272:ARG:HG2	2.15	0.76
1:A:290:VAL:O	1:A:291:GLN:HB2	1.85	0.76
1:A:100:ILE:HD12	1:A:150:PHE:CE1	2.21	0.75
1:A:324:ASN:CB	1:A:328:GLN:H	2.02	0.72
1:A:159:LEU:HD12	1:A:172:TYR:HB2	1.71	0.72
1:A:376:ASN:OD1	1:A:376:ASN:C	2.33	0.71
1:A:316:ASP:CB	1:A:333:ILE:HD13	2.21	0.71
1:A:324:ASN:HD22	1:A:326:SER:H	1.38	0.71
1:A:100:ILE:HD11	1:A:182:LEU:HG	1.71	0.71
1:A:140:GLN:HE21	1:A:147:ASN:HD22	1.36	0.71
1:A:194:ILE:HG22	1:A:195:MET:HE2	1.72	0.69
1:A:179:GLN:HG2	2:A:496:HOH:O	1.93	0.68
1:A:267:THR:HG22	1:A:272:ARG:HG2	1.74	0.68
1:A:398:GLN:HE22	1:A:401:TYR:H	1.42	0.67
1:A:230:LYS:HD2	1:A:383:THR:HG23	1.76	0.66
1:A:115:TRP:CH2	1:A:159:LEU:HD11	2.31	0.66
1:A:372:SER:O	1:A:373:LEU:HD23	1.96	0.65
1:A:328:GLN:OE1	1:A:355:THR:HG21	1.98	0.64
1:A:267:THR:HG22	1:A:272:ARG:HA	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:334:PHE:CZ	1:A:339:PRO:HG3	2.32	0.64
1:A:136:ILE:O	1:A:140:GLN:HG3	1.99	0.63
1:A:235:THR:HA	1:A:373:LEU:CD2	2.29	0.62
1:A:255:ARG:HG2	1:A:255:ARG:HH11	1.65	0.62
1:A:140:GLN:NE2	1:A:147:ASN:HD22	1.98	0.62
1:A:324:ASN:HB2	1:A:328:GLN:H	1.64	0.62
1:A:100:ILE:HD13	1:A:100:ILE:C	2.25	0.61
1:A:159:LEU:CD1	1:A:172:TYR:HB2	2.31	0.61
1:A:324:ASN:HB3	1:A:328:GLN:H	1.65	0.61
1:A:57:GLN:HE22	1:A:318:TYR:H	1.49	0.60
1:A:52:ILE:HG12	1:A:312:GLY:HA3	1.84	0.59
1:A:336:ASP:O	1:A:338:ILE:HG12	2.02	0.59
1:A:230:LYS:HD2	1:A:383:THR:CG2	2.33	0.58
1:A:52:ILE:HG23	1:A:53:GLU:N	2.18	0.58
1:A:222:PRO:O	1:A:387:GLY:O	2.22	0.58
1:A:155:PHE:CZ	1:A:182:LEU:HD22	2.37	0.58
1:A:76:HIS:HB2	1:A:208:PHE:O	2.05	0.57
1:A:61:GLU:O	1:A:64:ARG:HD3	2.04	0.57
1:A:346:LYS:N	1:A:347:PRO:CD	2.68	0.56
1:A:346:LYS:N	1:A:347:PRO:HD3	2.20	0.56
1:A:267:THR:HG21	1:A:272:ARG:HG2	1.86	0.55
1:A:163:ASN:HA	2:A:542:HOH:O	2.06	0.55
1:A:315:THR:HG23	1:A:318:TYR:HE1	1.70	0.54
1:A:66:ARG:HG2	1:A:66:ARG:HH11	1.71	0.54
1:A:244:LYS:HD3	1:A:266:LEU:HD13	1.89	0.54
1:A:166:LYS:N	1:A:166:LYS:HD3	2.23	0.54
1:A:328:GLN:HG2	1:A:355:THR:HG23	1.88	0.54
1:A:85:TYR:CD2	1:A:85:TYR:C	2.86	0.54
1:A:414:GLN:NE2	2:A:551:HOH:O	2.41	0.54
1:A:235:THR:HA	1:A:373:LEU:HD23	1.90	0.54
1:A:209:SER:HB3	1:A:223:ASN:ND2	2.18	0.53
1:A:216:LYS:C	1:A:217:LYS:HG2	2.34	0.53
1:A:237:SER:HA	1:A:371:TYR:HA	1.89	0.53
1:A:357:GLN:HG2	1:A:364:LEU:HD22	1.91	0.53
1:A:164:GLU:HB2	1:A:191:TYR:CZ	2.44	0.53
1:A:375:THR:HG22	1:A:376:ASN:N	2.24	0.53
1:A:268:ASP:OD1	1:A:270:ILE:HD13	2.09	0.52
1:A:169:LYS:HE2	2:A:484:HOH:O	2.09	0.52
1:A:316:ASP:HB3	1:A:333:ILE:CD1	2.35	0.52
1:A:445:LYS:C	1:A:447:LEU:H	2.16	0.52
1:A:98:LYS:HZ1	1:A:187:GLU:CD	2.18	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:431:VAL:HG12	1:A:432:TRP:N	2.25	0.52
1:A:403:THR:HA	1:A:406:ILE:HG12	1.91	0.51
1:A:143:PHE:HB2	1:A:145:TRP:CD1	2.45	0.51
1:A:251:PRO:O	1:A:254:VAL:HG12	2.11	0.51
1:A:191:TYR:CZ	1:A:195:MET:HG3	2.45	0.51
1:A:96:ASP:C	1:A:186:VAL:HG23	2.35	0.50
1:A:319:GLN:HE22	1:A:337:GLN:NE2	2.10	0.50
1:A:72:ASP:CG	1:A:124:ALA:HB2	2.36	0.49
1:A:270:ILE:HD13	1:A:270:ILE:H	1.77	0.49
1:A:315:THR:HG22	1:A:368:ARG:HH12	1.78	0.49
1:A:366:TYR:OH	1:A:368:ARG:HD2	2.11	0.49
1:A:406:ILE:HD13	1:A:436:VAL:HG22	1.94	0.49
1:A:125:LYS:HG2	1:A:159:LEU:HD22	1.93	0.48
1:A:293:THR:HG22	1:A:360:ASN:OD1	2.12	0.48
1:A:53:GLU:H	1:A:312:GLY:HA3	1.77	0.48
1:A:315:THR:HG23	1:A:318:TYR:CE1	2.49	0.48
1:A:155:PHE:HZ	1:A:182:LEU:HD22	1.79	0.48
1:A:243:PHE:CE2	1:A:282:VAL:HG21	2.48	0.47
1:A:398:GLN:HE22	1:A:401:TYR:N	2.09	0.47
1:A:313:SER:O	1:A:315:THR:HG22	2.13	0.47
1:A:444:THR:C	1:A:446:ASP:H	2.22	0.47
1:A:53:GLU:HG3	1:A:311:THR:O	2.15	0.47
1:A:238:ILE:HB	1:A:243:PHE:CE2	2.50	0.47
1:A:295:TYR:CE1	1:A:303:LYS:HE2	2.50	0.47
1:A:444:THR:HG22	1:A:445:LYS:N	2.29	0.47
1:A:134:ILE:HB	1:A:139:PHE:CZ	2.50	0.47
1:A:445:LYS:O	1:A:447:LEU:HD22	2.14	0.46
1:A:398:GLN:NE2	1:A:401:TYR:H	2.09	0.46
1:A:444:THR:CG2	1:A:445:LYS:N	2.77	0.46
1:A:143:PHE:HB2	1:A:145:TRP:NE1	2.30	0.46
1:A:394:LEU:C	1:A:394:LEU:HD23	2.40	0.46
1:A:230:LYS:HB3	1:A:231:LYS:H	1.59	0.46
1:A:395:LEU:HA	1:A:398:GLN:HG2	1.97	0.46
1:A:332:TYR:OH	1:A:440:ILE:HD12	2.15	0.46
1:A:112:PHE:CG	1:A:179:GLN:HG3	2.51	0.45
1:A:295:TYR:CD2	1:A:299:GLU:HG2	2.51	0.45
1:A:57:GLN:HB2	1:A:314:TRP:CD1	2.51	0.45
1:A:270:ILE:HD13	1:A:270:ILE:N	2.32	0.45
1:A:319:GLN:HE22	1:A:337:GLN:HE22	1.62	0.45
1:A:100:ILE:HD11	1:A:182:LEU:CG	2.43	0.45
1:A:244:LYS:HD3	1:A:266:LEU:CD1	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:156:ASP:OD1	1:A:157:HIS:HD2	2.00	0.45
1:A:208:PHE:CZ	1:A:222:PRO:HG3	2.53	0.44
1:A:274:ASP:OD1	1:A:274:ASP:C	2.61	0.44
1:A:214:GLY:HA2	1:A:403:THR:OG1	2.19	0.43
1:A:143:PHE:HD2	1:A:145:TRP:CZ2	2.37	0.43
1:A:319:GLN:NE2	1:A:337:GLN:HE22	2.17	0.43
1:A:231:LYS:N	1:A:428:LEU:O	2.52	0.43
1:A:115:TRP:HH2	1:A:159:LEU:HD11	1.80	0.43
1:A:60:SER:O	1:A:64:ARG:HD2	2.19	0.43
1:A:255:ARG:HG2	1:A:255:ARG:NH1	2.30	0.43
1:A:166:LYS:HD3	1:A:166:LYS:H	1.83	0.42
1:A:191:TYR:CE2	1:A:195:MET:HG3	2.55	0.42
1:A:431:VAL:CG1	1:A:432:TRP:N	2.82	0.42
1:A:66:ARG:HG2	1:A:66:ARG:NH1	2.33	0.42
1:A:411:LEU:HG	1:A:432:TRP:CZ3	2.55	0.42
1:A:66:ARG:NH2	1:A:408:GLN:NE2	2.68	0.42
1:A:96:ASP:O	1:A:186:VAL:HG23	2.20	0.42
1:A:223:ASN:C	1:A:224:LYS:HD3	2.43	0.42
1:A:328:GLN:HG2	1:A:355:THR:CG2	2.50	0.42
1:A:137:ASP:HB2	2:A:537:HOH:O	2.19	0.41
1:A:66:ARG:HH22	1:A:408:GLN:NE2	2.18	0.41
1:A:98:LYS:NZ	1:A:187:GLU:CD	2.78	0.41
1:A:441:VAL:HA	1:A:442:PRO:HD3	1.91	0.41
1:A:434:MET:HE3	1:A:436:VAL:HG21	2.01	0.41
1:A:251:PRO:O	1:A:254:VAL:CG1	2.69	0.41
1:A:133:THR:HB	1:A:154:SER:OG	2.21	0.41
1:A:178:LYS:HB3	1:A:180:LEU:HG	2.02	0.41
1:A:430:PRO:C	1:A:431:VAL:HG23	2.46	0.41
1:A:324:ASN:HB2	1:A:328:GLN:O	2.22	0.40
1:A:100:ILE:C	1:A:100:ILE:CD1	2.92	0.40
1:A:179:GLN:HG2	1:A:179:GLN:O	2.21	0.40
1:A:385:LEU:O	1:A:386:MET:C	2.64	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	363/417 (87%)	325 (90%)	24 (7%)	14 (4%)	2 1

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	231	LYS
1	A	235	THR
1	A	290	VAL
1	A	291	GLN
1	A	54	LYS
1	A	232	GLU
1	A	350	ALA
1	A	386	MET
1	A	445	LYS
1	A	234	VAL
1	A	292	SER
1	A	375	THR
1	A	233	PHE
1	A	237	SER

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	319/384 (83%)	296 (93%)	23 (7%)	13 18

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	GLN
1	A	63	VAL
1	A	66	ARG

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Mol	Chain	Res	Type
1	A	85	TYR
1	A	92	LEU
1	A	100	ILE
1	A	166	LYS
1	A	224	LYS
1	A	254	VAL
1	A	255	ARG
1	A	270	ILE
1	A	273	LEU
1	A	291	GLN
1	A	299	GLU
1	A	306	LYS
1	A	315	THR
1	A	324	ASN
1	A	333	ILE
1	A	360	ASN
1	A	362	ASP
1	A	376	ASN
1	A	398	GLN
1	A	436	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	GLN
1	A	82	ASN
1	A	129	GLN
1	A	140	GLN
1	A	200	ASN
1	A	204	ASN
1	A	223	ASN
1	A	305	GLN
1	A	322	ASN
1	A	324	ASN
1	A	327	GLN
1	A	337	GLN
1	A	398	GLN
1	A	408	GLN
1	A	414	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](#)

There are no ligands in this entry.

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	373/417 (89%)	0.83	56 (15%) 5 6	18, 38, 63, 83	0

All (56) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	373	LEU	6.0
1	A	376	ASN	5.2
1	A	233	PHE	5.0
1	A	374	GLY	4.5
1	A	393	MET	4.4
1	A	447	LEU	3.8
1	A	381	SER	3.7
1	A	289	LEU	3.7
1	A	236	GLU	3.2
1	A	400	ALA	3.2
1	A	387	GLY	3.2
1	A	50	HIS	3.2
1	A	444	THR	3.1
1	A	385	LEU	3.1
1	A	231	LYS	3.0
1	A	264	ASN	3.0
1	A	232	GLU	3.0
1	A	54	LYS	2.9
1	A	290	VAL	2.9
1	A	285	GLN	2.8
1	A	342	ASN	2.7
1	A	398	GLN	2.7
1	A	349	GLY	2.6
1	A	278	SER	2.6
1	A	53	GLU	2.6
1	A	396	SER	2.6
1	A	347	PRO	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	235	THR	2.6
1	A	350	ALA	2.5
1	A	441	VAL	2.5
1	A	52	ILE	2.5
1	A	445	LYS	2.5
1	A	55	THR	2.5
1	A	344	THR	2.5
1	A	270	ILE	2.5
1	A	428	LEU	2.5
1	A	345	ALA	2.5
1	A	375	THR	2.4
1	A	353	ALA	2.4
1	A	403	THR	2.4
1	A	186	VAL	2.3
1	A	394	LEU	2.3
1	A	315	THR	2.3
1	A	397	LYS	2.3
1	A	440	ILE	2.3
1	A	324	ASN	2.2
1	A	168	ASN	2.2
1	A	332	TYR	2.1
1	A	230	LYS	2.1
1	A	272	ARG	2.1
1	A	109	LYS	2.1
1	A	245	GLN	2.0
1	A	204	ASN	2.0
1	A	411	LEU	2.0
1	A	388	GLY	2.0
1	A	399	THR	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 ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.