



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 05:37 AM UTC

PDB ID : 5XP8 / pdb_00005xp8
Title : Crystal structure of T. thermophilus Argonaute protein complexed with a bulge 4A5 on the guide strand
Authors : Sheng, G.; Gogakos, T.; Wang, J.; Zhao, H.; Serganov, A.; Juranek, S.; Tuschl, T.; Patel, J.D.; Wang, Y.
Deposited on : 2017-06-01
Resolution : 3.10 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

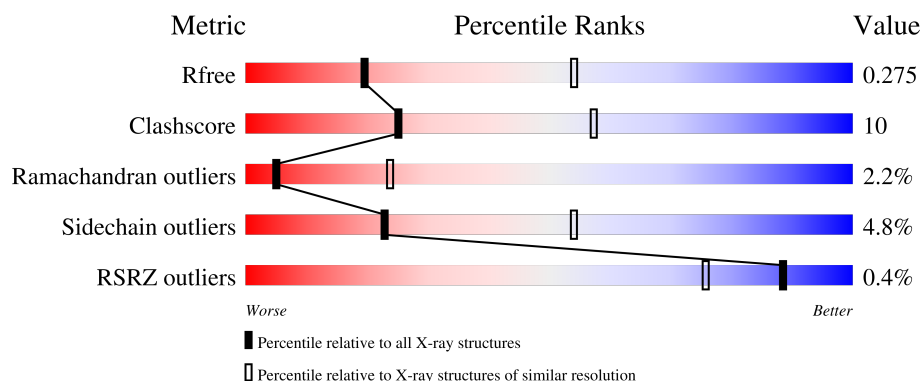
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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	685	71% 26% ..
2	E	22	36% 41% 23%
3	F	19	37% 37% 5% 21%
4	C	3	67% 33%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5808 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 TtAgo.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	678	Total	C	N	O	S	0	0	0
			5091	3266	938	881	6			

- Molecule 2 is a DNA chain called DNA (5'-D(P*TP*GP*AP*GP*AP*GP*TP*AP*GP*TP*AP*GP*GP*TP*TP*GP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	17	Total	C	N	O	P	0	0	0
			359	170	67	105	17			

- Molecule 3 is a DNA chain called DNA (5'-D(*CP*AP*AP*CP*C*AP*TP*AP*CP*TP*AP*CP*CP*TP*CP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	F	15	Total	C	N	O	P	0	0	0
			296	143	52	87	14			

- Molecule 4 is a DNA chain called DNA (5'-D(*AP*GP*T)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	C	3	Total	C	N	O	P	0	0	0
			59	30	12	15	2			

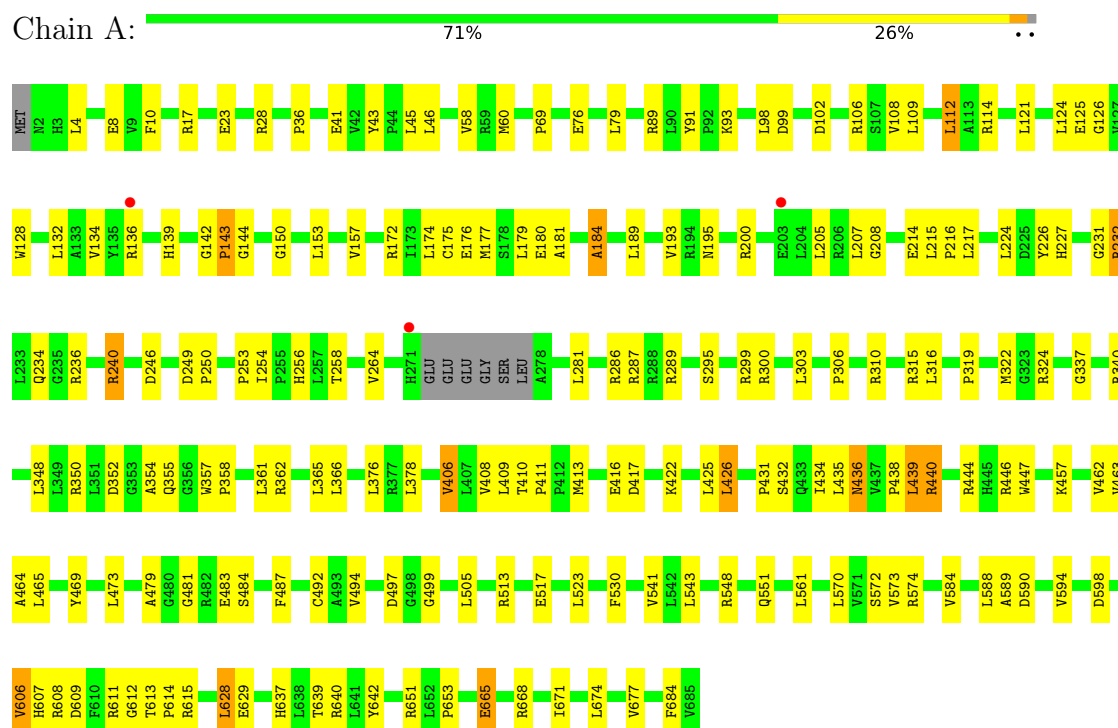
- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	3	Total	Mg	1	0
			3	3		

3 Residue-property plots

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: TtAgo





- Molecule 4: DNA (5'-D(*AP*GP*T)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 3 2	Depositor
Cell constants a, b, c, α , β , γ	202.14Å 202.14Å 202.14Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.20 – 3.10 45.20 – 3.10	Depositor EDS
% Data completeness (in resolution range)	98.9 (45.20-3.10) 98.8 (45.20-3.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.18 (at 3.12Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, R_{free}	0.214 , 0.276 0.218 , 0.275	Depositor DCC
R_{free} test set	1313 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	91.1	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 52.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5808	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.66% 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: MG

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	0.63	0/5213	1.18	38/7110 (0.5%)
2	E	0.38	0/403	1.01	0/621
3	F	0.75	2/330 (0.6%)	1.10	1/505 (0.2%)
4	C	0.28	0/66	0.88	0/101
All	All	0.62	2/6012 (0.0%)	1.16	39/8337 (0.5%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	9	DT	O3'-P	-8.32	1.48	1.61
3	F	7	DC	O3'-P	-7.38	1.50	1.61

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	99	ASP	CA-C-N	10.29	130.05	119.56
1	A	99	ASP	C-N-CA	10.29	130.05	119.56
1	A	139	HIS	N-CA-C	-9.54	101.77	113.41
1	A	358	PRO	N-CA-CB	8.60	110.96	103.31
1	A	642	TYR	CA-C-N	8.44	128.17	119.64
1	A	642	TYR	C-N-CA	8.44	128.17	119.64
1	A	469	TYR	CA-C-N	8.35	128.46	119.28
1	A	469	TYR	C-N-CA	8.35	128.46	119.28
1	A	598	ASP	N-CA-C	8.14	120.88	111.11
1	A	36	PRO	CA-C-N	6.90	127.07	120.31
1	A	36	PRO	C-N-CA	6.90	127.07	120.31
1	A	143	PRO	N-CA-CB	6.83	110.42	103.25
1	A	481	GLY	N-CA-C	-6.59	105.69	111.95
1	A	609	ASP	N-CA-C	6.21	118.85	111.71
1	A	136	ARG	N-CA-C	6.00	120.66	112.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	465	LEU	N-CA-C	5.79	118.99	110.59
1	A	406	VAL	N-CA-C	5.66	116.63	108.48
1	A	69	PRO	CA-C-N	5.62	126.00	119.47
1	A	69	PRO	C-N-CA	5.62	126.00	119.47
1	A	232	ARG	N-CA-C	-5.59	106.28	114.39
1	A	208	GLY	N-CA-C	5.59	120.49	111.38
1	A	463	VAL	N-CA-C	5.59	118.17	108.95
1	A	677	VAL	N-CA-C	5.53	116.06	107.99
1	A	175	CYS	N-CA-CB	-5.50	100.86	110.44
1	A	108	VAL	N-CA-C	5.43	116.20	110.72
1	A	492	CYS	N-CA-C	5.41	117.41	109.24
1	A	612	GLY	N-CA-C	-5.40	104.03	111.76
3	F	7	DC	C1'-O4'-C4'	-5.38	101.63	109.70
1	A	215	LEU	CA-C-N	-5.35	113.15	119.84
1	A	215	LEU	C-N-CA	-5.35	113.15	119.84
1	A	69	PRO	O-C-N	5.26	123.62	121.15
1	A	483	GLU	N-CA-C	5.25	117.98	110.68
1	A	322	MET	N-CA-C	5.18	117.34	108.90
1	A	594	VAL	N-CA-C	5.13	113.23	108.15
1	A	102	ASP	CA-C-N	5.13	124.92	119.28
1	A	102	ASP	C-N-CA	5.13	124.92	119.28
1	A	207	LEU	N-CA-C	-5.06	103.36	110.50
1	A	254	ILE	CA-C-N	-5.00	115.62	120.98
1	A	254	ILE	C-N-CA	-5.00	115.62	120.98

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	5091	0	4990	97	0
2	E	359	0	194	12	0
3	F	296	0	170	9	0
4	C	59	0	33	1	0
5	A	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5808	0	5387	107	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 10.

All (107) 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)
2:E:12:DG:H1	3:F:8:DC:H42	1.14	0.87
2:E:12:DG:H1	3:F:8:DC:N4	1.78	0.81
2:E:16:DG:H1	3:F:4:DC:H42	1.33	0.74
1:A:315:ARG:HH11	1:A:589:ALA:HB3	1.53	0.73
1:A:410:THR:O	1:A:436:ASN:HA	1.91	0.70
1:A:295:SER:O	1:A:299:ARG:HG3	1.94	0.67
1:A:365:LEU:HD13	1:A:376:LEU:HD21	1.79	0.65
1:A:410:THR:HG21	1:A:413:MET:HE2	1.77	0.65
1:A:513:ARG:NH2	1:A:551:GLN:O	2.32	0.63
2:E:12:DG:N2	3:F:8:DC:N3	2.44	0.62
1:A:350:ARG:NH2	1:A:354:ALA:HB3	2.16	0.61
1:A:28:ARG:HB3	1:A:93:LYS:HE3	1.81	0.60
1:A:365:LEU:HD11	1:A:378:LEU:HD11	1.83	0.60
3:F:8:DC:H2''	3:F:9:DT:H5'	1.84	0.60
1:A:295:SER:HA	1:A:306:PRO:HG3	1.83	0.59
1:A:340:ARG:NH1	1:A:499:GLY:O	2.34	0.59
1:A:473:LEU:HB3	1:A:541:VAL:HG12	1.85	0.59
1:A:350:ARG:NH2	1:A:354:ALA:CB	2.66	0.58
1:A:17:ARG:HG3	1:A:303:LEU:O	2.03	0.57
1:A:439:LEU:HD11	1:A:447:TRP:HB3	1.85	0.57
1:A:315:ARG:NH1	1:A:589:ALA:HB3	2.20	0.56
1:A:319:PRO:HB3	1:A:637:HIS:CG	2.40	0.56
1:A:109:LEU:HB2	1:A:157:VAL:HG21	1.87	0.56
1:A:128:TRP:CZ3	1:A:172:ARG:HG2	2.41	0.55
2:E:15:DT:H3	3:F:5:DA:H61	1.54	0.55
1:A:350:ARG:HG3	1:A:355:GLN:O	2.07	0.55
1:A:494:VAL:HG13	1:A:530:PHE:HD1	1.71	0.55
1:A:615:ARG:O	1:A:651:ARG:NH1	2.39	0.54
2:E:11:DA:H2''	2:E:12:DG:H5''	1.90	0.54
1:A:590:ASP:OD2	3:F:18:DG:N1	2.41	0.54
1:A:17:ARG:HD3	1:A:303:LEU:HA	1.90	0.53
1:A:114:ARG:HD3	1:A:132:LEU:HD11	1.92	0.52
1:A:416:GLU:HG2	1:A:417:ASP:N	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:350:ARG:CZ	1:A:354:ALA:HB3	2.40	0.51
1:A:172:ARG:NH1	2:E:9:DG:OP1	2.39	0.51
1:A:352:ASP:HB3	1:A:411:PRO:HD3	1.91	0.51
1:A:43:TYR:CZ	2:E:17:DT:H2''	2.46	0.51
1:A:606:VAL:HG13	1:A:611:ARG:HH12	1.75	0.51
1:A:408:VAL:HG13	1:A:434:ILE:HA	1.93	0.49
3:F:13:DA:H2'	3:F:14:DC:O4'	2.12	0.49
1:A:195:ASN:ND2	1:A:200:ARG:HB2	2.28	0.49
1:A:439:LEU:HA	1:A:446:ARG:NH2	2.27	0.49
1:A:439:LEU:O	1:A:440:ARG:HG2	2.13	0.49
1:A:76:GLU:HG2	1:A:89:ARG:NE	2.28	0.48
1:A:227:HIS:HD1	1:A:232:ARG:HH11	1.62	0.48
1:A:639:THR:HA	1:A:653:PRO:HA	1.94	0.48
1:A:174:LEU:HD12	1:A:174:LEU:C	2.38	0.48
1:A:431:PRO:HB2	1:A:457:LYS:HB3	1.96	0.47
1:A:444:ARG:HA	1:A:447:TRP:NE1	2.28	0.47
1:A:10:PHE:CE2	1:A:584:VAL:HG12	2.50	0.47
1:A:79:LEU:HD12	1:A:79:LEU:O	2.16	0.46
1:A:128:TRP:HZ3	1:A:172:ARG:HG2	1.81	0.46
1:A:142:GLY:O	1:A:144:GLY:N	2.49	0.46
1:A:409:LEU:HD21	1:A:435:LEU:HD23	1.98	0.46
1:A:8:GLU:OE1	1:A:310:ARG:NH1	2.49	0.46
1:A:464:ALA:HB1	1:A:497:ASP:O	2.16	0.46
1:A:300:ARG:HD3	1:A:300:ARG:HA	1.76	0.45
1:A:446:ARG:HG3	2:E:2:DG:C8	2.51	0.45
1:A:286:ARG:HD2	1:A:613:THR:HG21	1.99	0.45
1:A:124:LEU:HD23	1:A:124:LEU:HA	1.81	0.45
1:A:422:LYS:NZ	1:A:432:SER:O	2.50	0.45
1:A:181:ALA:HA	1:A:184:ALA:HB3	1.98	0.44
1:A:523:LEU:HD21	1:A:561:LEU:HD11	1.99	0.44
1:A:246:ASP:HB3	1:A:249:ASP:CB	2.48	0.44
1:A:479:ALA:HA	1:A:487:PHE:O	2.18	0.44
1:A:543:LEU:HB3	1:A:570:LEU:HD12	1.99	0.44
1:A:189:LEU:H	1:A:189:LEU:HD12	1.83	0.44
1:A:425:LEU:HD12	1:A:432:SER:HB3	2.00	0.44
1:A:607:HIS:O	1:A:608:ARG:HG2	2.18	0.43
2:E:13:DG:H2'	2:E:14:DT:H6	1.83	0.43
1:A:179:LEU:HD23	1:A:258:THR:HG23	2.00	0.43
1:A:439:LEU:HA	1:A:446:ARG:HH21	1.82	0.43
1:A:671:ILE:HA	1:A:674:LEU:HD12	2.00	0.43
1:A:548:ARG:HA	1:A:572:SER:OG	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:43:TYR:CE1	2:E:17:DT:H2''	2.54	0.43
1:A:98:LEU:HD23	1:A:98:LEU:HA	1.86	0.43
1:A:41:GLU:O	1:A:45:LEU:HB2	2.19	0.42
1:A:246:ASP:HB3	1:A:249:ASP:HB3	2.01	0.42
1:A:58:VAL:HG22	1:A:112:LEU:HD13	2.00	0.42
1:A:324:ARG:N	1:A:337:GLY:O	2.41	0.42
1:A:361:LEU:O	1:A:365:LEU:HG	2.20	0.42
2:E:15:DT:H3	3:F:5:DA:N6	2.18	0.42
1:A:180:GLU:OE2	1:A:240:ARG:HD2	2.19	0.42
1:A:226:TYR:OH	4:C:21:DT:OP2	2.34	0.42
1:A:350:ARG:HD2	1:A:409:LEU:HB2	2.02	0.42
1:A:17:ARG:HH22	1:A:23:GLU:CD	2.28	0.41
1:A:348:LEU:HD21	1:A:350:ARG:HD3	2.01	0.41
1:A:4:LEU:HD13	1:A:316:LEU:HD23	2.01	0.41
1:A:426:LEU:HA	1:A:426:LEU:HD12	1.71	0.41
1:A:121:LEU:HD11	1:A:153:LEU:HD12	2.02	0.41
1:A:224:LEU:HD12	1:A:224:LEU:HA	1.77	0.41
1:A:362:ARG:HG2	1:A:366:LEU:HD12	2.03	0.41
1:A:134:VAL:O	1:A:150:GLY:HA3	2.21	0.41
1:A:348:LEU:HD22	1:A:357:TRP:HA	2.03	0.41
1:A:45:LEU:HA	1:A:45:LEU:HD12	1.75	0.41
1:A:106:ARG:HG3	1:A:157:VAL:HG23	2.03	0.41
1:A:217:LEU:HD23	1:A:217:LEU:HA	1.93	0.41
1:A:665:GLU:HG3	1:A:684:PHE:HA	2.02	0.41
1:A:125:GLU:HA	1:A:126:GLY:HA2	1.68	0.41
1:A:548:ARG:HG2	1:A:574:ARG:NE	2.36	0.41
1:A:89:ARG:HG2	1:A:91:TYR:CZ	2.56	0.40
1:A:303:LEU:HA	1:A:303:LEU:HD23	1.88	0.40
1:A:588:LEU:HD21	1:A:614:PRO:HG3	2.03	0.40
1:A:174:LEU:HD13	1:A:176:GLU:OE1	2.22	0.40
1:A:17:ARG:NH2	1:A:23:GLU:OE1	2.54	0.40
1:A:628:LEU:HD12	1:A:628:LEU:HA	1.71	0.40
1:A:76:GLU:HG2	1:A:89:ARG:CD	2.52	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	674/685 (98%)	634 (94%)	25 (4%)	15 (2%)	5	24

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	436	ASN
1	A	439	LEU
1	A	214	GLU
1	A	216	PRO
1	A	250	PRO
1	A	440	ARG
1	A	143	PRO
1	A	184	ALA
1	A	438	PRO
1	A	205	LEU
1	A	253	PRO
1	A	256	HIS
1	A	281	LEU
1	A	484	SER
1	A	231	GLY

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	475/549 (86%)	452 (95%)	23 (5%)	23	54

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

Mol	Chain	Res	Type
1	A	46	LEU
1	A	60	MET
1	A	112	LEU
1	A	177	MET
1	A	193	VAL
1	A	234	GLN
1	A	236	ARG
1	A	240	ARG
1	A	264	VAL
1	A	287	ARG
1	A	289	ARG
1	A	406	VAL
1	A	426	LEU
1	A	462	VAL
1	A	505	LEU
1	A	517	GLU
1	A	573	VAL
1	A	606	VAL
1	A	628	LEU
1	A	629	GLU
1	A	640	ARG
1	A	665	GLU
1	A	668	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	433	GLN
1	A	509	GLN
1	A	633	HIS
1	A	657	HIS

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 3 ligands modelled in this entry, 3 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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	678/685 (98%)	-0.66	3 (0%) 88 76	14, 55, 97, 134	0
2	E	17/22 (77%)	-0.94	0 100 100	30, 44, 91, 113	0
3	F	15/19 (78%)	-0.33	0 100 100	42, 62, 137, 142	0
4	C	3/3 (100%)	-0.01	0 100 100	76, 76, 98, 122	0
All	All	713/729 (97%)	-0.66	3 (0%) 88 76	14, 56, 98, 142	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	136	ARG	3.4
1	A	271	HIS	3.1
1	A	203	GLU	2.9

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
5	MG	A	701	1/1	0.80	0.11	12,12,12,12	0
5	MG	A	702	1/1	-	-	29,29,29,29	1
5	MG	A	703	1/1	0.95	0.05	28,28,28,28	0

6.5 Other polymers [i](#)

There are no such residues in this entry.