



wwPDB X-ray Structure Validation Summary Report

Nov 20, 2014 – 10:48 PM EST

PDB ID : 4KPE
Title : Novel fluoroquinolones in complex with topoisomerase IV from *S. pneumoniae* and E-site G-gate
Authors : Laponogov, I.; Pan, X.-S.; Vesekov, D.A.; Cirz, R.T.; Wagman, A.S.; Moser, H.E.; Fisher, L.M.; Sanderson, M.R.
Deposited on : 2013-05-13
Resolution : 3.43 Å(reported)

This is a wwPDB validation summary 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/ValidationPDFNotes.html>

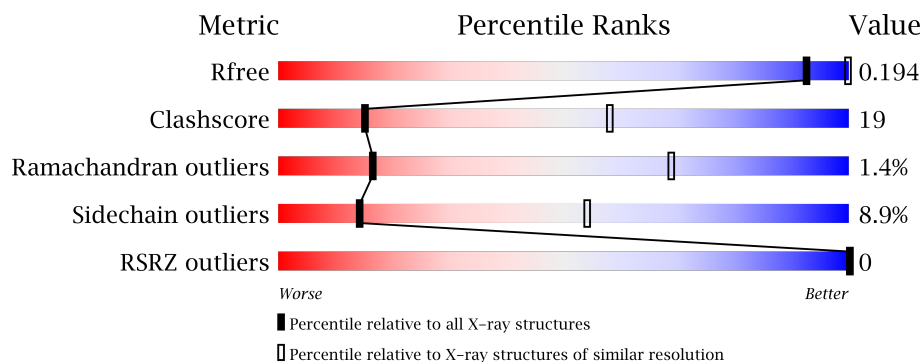
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.16 November 2013
Xtriage (Phenix) : dev-1439
EDS : stable24195
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.1.3
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable24195

1 Overall quality at a glance

The reported resolution of this entry is 3.43 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}	66092	1032 (3.58-3.30)
Clashscore	79885	1296 (3.58-3.30)
Ramachandran outliers	78287	1256 (3.58-3.30)
Sidechain outliers	78261	1256 (3.58-3.30)
RSRZ outliers	66119	1032 (3.58-3.30)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	496	
1	B	496	
2	C	268	
2	D	268	
3	E	7	
4	F	11	
5	G	7	
6	H	11	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
7	MG	A	502	-	X
7	MG	B	502	-	X
7	MG	C	701	-	X
7	MG	D	701	-	X

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 11256 atoms, of which 38 are hydrogens and 0 are deuterium.

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 DNA topoisomerase 4 subunit A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	482	Total	C	N	O	S	0	1	0
			3738	2371	645	709	13			
1	B	482	Total	C	N	O	S	0	1	0
			3713	2358	638	704	13			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	257	THR	ILE	ENGINEERED MUTATION	UNP P72525
A	489	LEU	-	EXPRESSION TAG	UNP P72525
A	490	GLU	-	EXPRESSION TAG	UNP P72525
A	491	HIS	-	EXPRESSION TAG	UNP P72525
A	492	HIS	-	EXPRESSION TAG	UNP P72525
A	493	HIS	-	EXPRESSION TAG	UNP P72525
A	494	HIS	-	EXPRESSION TAG	UNP P72525
A	495	HIS	-	EXPRESSION TAG	UNP P72525
A	496	HIS	-	EXPRESSION TAG	UNP P72525
B	257	THR	ILE	ENGINEERED MUTATION	UNP P72525
B	489	LEU	-	EXPRESSION TAG	UNP P72525
B	490	GLU	-	EXPRESSION TAG	UNP P72525
B	491	HIS	-	EXPRESSION TAG	UNP P72525
B	492	HIS	-	EXPRESSION TAG	UNP P72525
B	493	HIS	-	EXPRESSION TAG	UNP P72525
B	494	HIS	-	EXPRESSION TAG	UNP P72525
B	495	HIS	-	EXPRESSION TAG	UNP P72525
B	496	HIS	-	EXPRESSION TAG	UNP P72525

- Molecule 2 is a protein called DNA topoisomerase 4 subunit B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	208	Total	C	N	O	S	0	0	0
			1479	940	259	274	6			

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	210	Total	C	N	O	S	0	0	0
			1474	939	256	274	5			

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	380	MET	-	EXPRESSION TAG	UNP Q59961
C	381	GLY	-	EXPRESSION TAG	UNP Q59961
C	382	HIS	-	EXPRESSION TAG	UNP Q59961
C	383	HIS	-	EXPRESSION TAG	UNP Q59961
C	384	HIS	-	EXPRESSION TAG	UNP Q59961
C	385	HIS	-	EXPRESSION TAG	UNP Q59961
C	386	HIS	-	EXPRESSION TAG	UNP Q59961
C	387	HIS	-	EXPRESSION TAG	UNP Q59961
C	388	HIS	-	EXPRESSION TAG	UNP Q59961
C	389	HIS	-	EXPRESSION TAG	UNP Q59961
C	390	HIS	-	EXPRESSION TAG	UNP Q59961
C	391	HIS	-	EXPRESSION TAG	UNP Q59961
C	392	SER	-	EXPRESSION TAG	UNP Q59961
C	393	SER	-	EXPRESSION TAG	UNP Q59961
C	394	GLY	-	EXPRESSION TAG	UNP Q59961
C	395	HIS	-	EXPRESSION TAG	UNP Q59961
C	396	ILE	-	EXPRESSION TAG	UNP Q59961
C	397	ASP	-	EXPRESSION TAG	UNP Q59961
C	398	ASP	-	EXPRESSION TAG	UNP Q59961
C	399	ASP	-	EXPRESSION TAG	UNP Q59961
C	400	ASP	-	EXPRESSION TAG	UNP Q59961
C	401	LYS	-	EXPRESSION TAG	UNP Q59961
C	402	HIS	-	EXPRESSION TAG	UNP Q59961
C	403	MET	-	EXPRESSION TAG	UNP Q59961
C	460	ILE	VAL	ENGINEERED MUTATION	UNP Q59961
C	644	ALA	THR	ENGINEERED MUTATION	UNP Q59961
D	380	MET	-	EXPRESSION TAG	UNP Q59961
D	381	GLY	-	EXPRESSION TAG	UNP Q59961
D	382	HIS	-	EXPRESSION TAG	UNP Q59961
D	383	HIS	-	EXPRESSION TAG	UNP Q59961
D	384	HIS	-	EXPRESSION TAG	UNP Q59961
D	385	HIS	-	EXPRESSION TAG	UNP Q59961
D	386	HIS	-	EXPRESSION TAG	UNP Q59961
D	387	HIS	-	EXPRESSION TAG	UNP Q59961
D	388	HIS	-	EXPRESSION TAG	UNP Q59961
D	389	HIS	-	EXPRESSION TAG	UNP Q59961

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	390	HIS	-	EXPRESSION TAG	UNP Q59961
D	391	HIS	-	EXPRESSION TAG	UNP Q59961
D	392	SER	-	EXPRESSION TAG	UNP Q59961
D	393	SER	-	EXPRESSION TAG	UNP Q59961
D	394	GLY	-	EXPRESSION TAG	UNP Q59961
D	395	HIS	-	EXPRESSION TAG	UNP Q59961
D	396	ILE	-	EXPRESSION TAG	UNP Q59961
D	397	ASP	-	EXPRESSION TAG	UNP Q59961
D	398	ASP	-	EXPRESSION TAG	UNP Q59961
D	399	ASP	-	EXPRESSION TAG	UNP Q59961
D	400	ASP	-	EXPRESSION TAG	UNP Q59961
D	401	LYS	-	EXPRESSION TAG	UNP Q59961
D	402	HIS	-	EXPRESSION TAG	UNP Q59961
D	403	MET	-	EXPRESSION TAG	UNP Q59961
D	460	ILE	VAL	ENGINEERED MUTATION	UNP Q59961
D	644	ALA	THR	ENGINEERED MUTATION	UNP Q59961

- Molecule 3 is a DNA chain called E-site DNA1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	7	Total	C	N	O	P	0	0	0
			140	69	27	38	6			

- Molecule 4 is a DNA chain called E-site DNA2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	11	Total	C	N	O	P	0	0	0
			225	108	39	67	11			

- Molecule 5 is a DNA chain called E-site DNA3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	G	7	Total	C	N	O	P	0	0	0
			139	68	25	40	6			

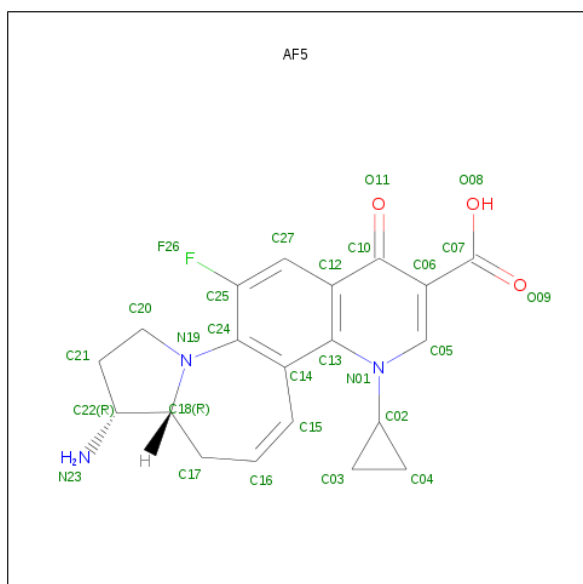
- Molecule 6 is a DNA chain called E-site DNA4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	H	11	Total	C	N	O	P	0	0	0
			226	107	43	65	11			

- Molecule 7 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	B	2	Total Mg 2 2	0	0
7	A	2	Total Mg 2 2	0	0
7	D	1	Total Mg 1 1	0	0
7	C	1	Total Mg 1 1	0	0

- Molecule 8 is (7AR,8R)-8-AMINO-4-CYCLOPROPYL-12-FLUORO-1-OXO-4,7,7A,8,9,10-HEXAHYDRO-1H-PYRROLO[1',2':1,7]AZEPINO[2,3-H]QUINOLINE-2-CARBOXYLIC ACID (three-letter code: AF5) (formula: C₂₀H₂₀FN₃O₃).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
8	F	1	Total	C	F	H	N	O	0	0
			46	20	1	19	3	3		
8	H	1	Total	C	F	H	N	O	0	0
			46	20	1	19	3	3		

- Molecule 9 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	13	Total O 13 13	0	0
9	B	9	Total O 9 9	0	0
9	C	1	Total O 1 1	0	0

Continued on next page...

Continued from previous page...

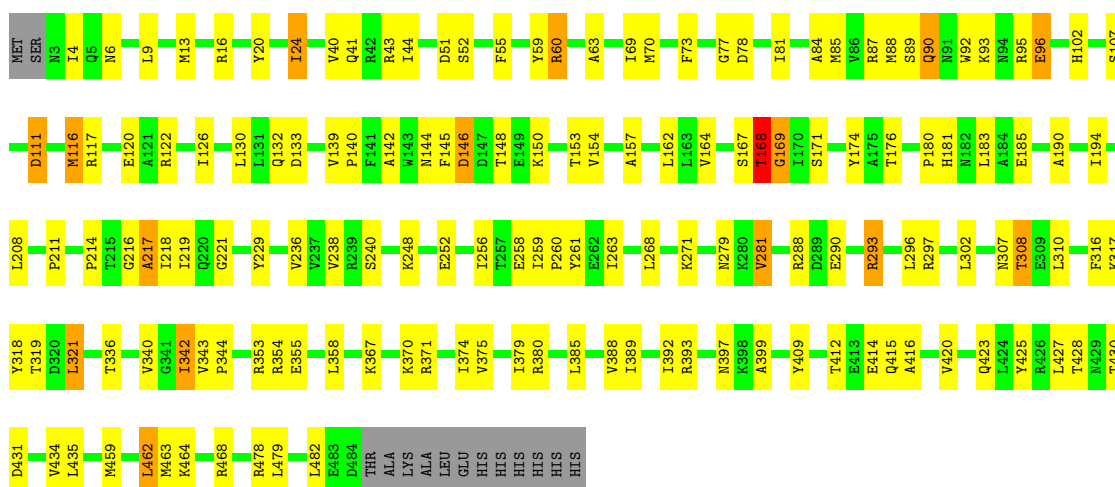
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	D	1	Total	O	0	0
			1	1		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

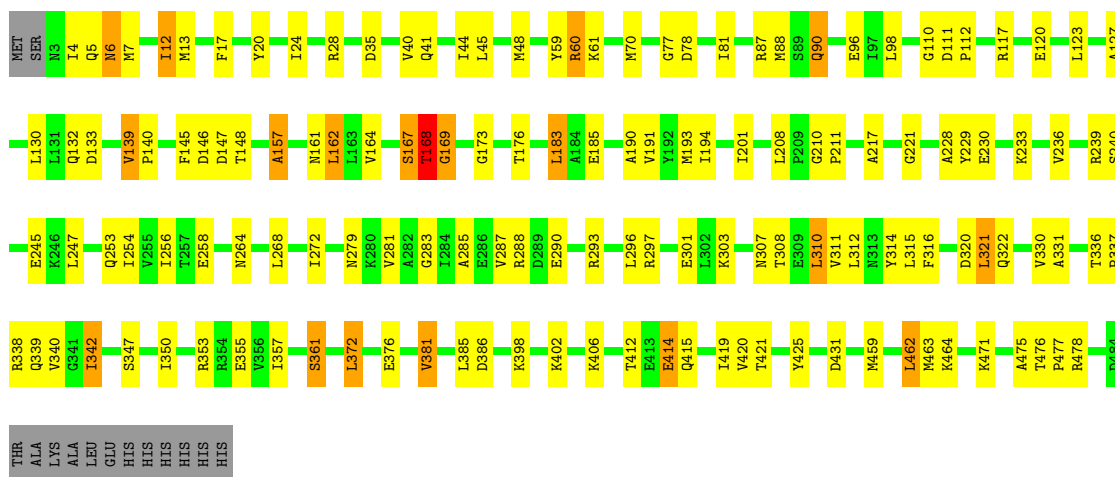
• Molecule 1: DNA topoisomerase 4 subunit A

Chain A:



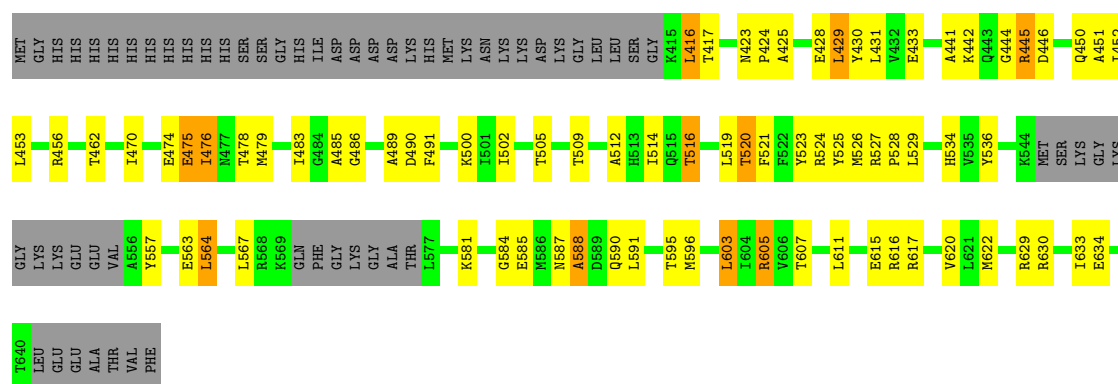
• Molecule 1: DNA topoisomerase 4 subunit A

Chain B:



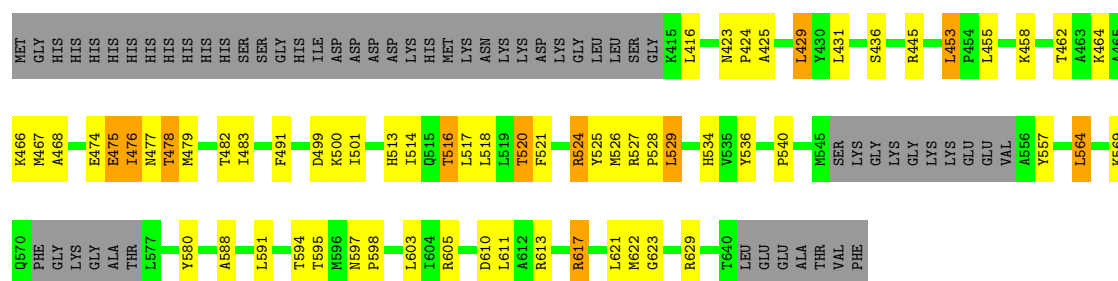
• Molecule 2: DNA topoisomerase 4 subunit B

Chain C:



- Molecule 2: DNA topoisomerase 4 subunit B

Chain D:



- Molecule 3: E-site DNA1

Chain E: 



- Molecule 4: E-site DNA2

Chain F:



- Molecule 5: E-site DNA3

Chain G:



- Molecule 6: E-site DNA4

Chain H: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	157.83Å 157.83Å 210.71Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	41.82 – 3.43 43.81 – 3.43	Depositor EDS
% Data completeness (in resolution range)	97.1 (41.82-3.43) 97.2 (43.81-3.43)	Depositor EDS
R_{merge}	12.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.13 (at 3.40Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1069)	Depositor
R, R_{free}	0.154 , 0.195 0.152 , 0.194	Depositor DCC
R_{free} test set	2000 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	54.2	Xtriage
Anisotropy	0.621	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 20.8	EDS
Estimated twinning fraction	0.024 for -h,-k,l	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 40036 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11256	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.99% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: AF5, 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	0.43	0/3802	0.62	0/5150
1	B	0.45	0/3777	0.62	0/5122
2	C	0.35	0/1505	0.56	0/2053
2	D	0.35	0/1500	0.55	0/2049
3	E	0.87	0/157	1.54	2/241 (0.8%)
4	F	0.86	0/251	1.80	10/385 (2.6%)
5	G	0.78	0/155	1.56	3/238 (1.3%)
6	H	0.79	0/253	1.69	7/388 (1.8%)
All	All	0.46	0/11400	0.75	22/15626 (0.1%)

There are no bond length outliers.

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	H	1	DG	O4'-C1'-N9	8.93	114.25	108.00
6	H	10	DC	O4'-C4'-C3'	-7.95	101.23	106.00
4	F	3	DT	O4'-C4'-C3'	-7.53	101.48	106.00
4	F	10	DT	O4'-C4'-C3'	-7.50	101.50	106.00
6	H	1	DG	C4'-C3'-C2'	-7.35	96.48	103.10

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the

chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3738	0	3664	138	1
1	B	3713	0	3628	131	1
2	C	1479	0	1308	70	0
2	D	1474	0	1287	57	0
3	E	140	0	78	1	0
4	F	225	0	126	5	0
5	G	139	0	78	5	0
6	H	226	0	124	13	0
7	A	2	0	0	0	0
7	B	2	0	0	0	0
7	C	1	0	0	0	0
7	D	1	0	0	0	0
8	F	27	19	0	3	0
8	H	27	19	0	2	0
9	A	13	0	0	3	0
9	B	9	0	0	0	0
9	C	1	0	0	0	0
9	D	1	0	0	0	0
All	All	11218	38	10293	403	1

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 19.

The worst 5 of 403 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:70:MET:HE1	1:A:78:ASP:CB	1.75	1.16
2:C:526:MET:CE	2:C:529:LEU:HD12	1.80	1.11
1:A:146:ASP:HB3	1:A:148:THR:HG23	1.33	1.10
1:B:146:ASP:HB3	1:B:148:THR:HG23	1.14	1.08
1:A:60:ARG:HH11	1:A:60:ARG:HG3	1.16	1.06

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:393:ARG:NH2	1:B:279:ASN:O[4_545]	2.10	0.10

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	481/496 (97%)	451 (94%)	23 (5%)	7 (2%)	15	68
1	B	481/496 (97%)	448 (93%)	29 (6%)	4 (1%)	27	81
2	C	202/268 (75%)	179 (89%)	19 (9%)	4 (2%)	11	62
2	D	204/268 (76%)	186 (91%)	14 (7%)	4 (2%)	11	62
All	All	1368/1528 (90%)	1264 (92%)	85 (6%)	19 (1%)	16	69

5 of 19 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	168	THR
2	D	569	LYS
1	A	168	THR
2	C	424	PRO
2	D	588	ALA

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	380/431 (88%)	355 (93%)	25 (7%)	24	70
1	B	376/431 (87%)	351 (93%)	25 (7%)	24	70
2	C	120/224 (54%)	101 (84%)	19 (16%)	4	22
2	D	116/224 (52%)	97 (84%)	19 (16%)	3	20
All	All	992/1310 (76%)	904 (91%)	88 (9%)	14	54

5 of 88 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	308	THR
1	B	462	LEU
2	D	524	ARG
1	B	310	LEU
1	B	372	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	B	53	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

Of 8 ligands modelled in this entry, 6 are monoatomic - leaving 2 for Mogul analysis.

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$
8	AF5	F	101	7	31,31,31	1.94	7 (22%)	45,48,48	3.41	21 (46%)
8	AF5	H	101	7	31,31,31	1.92	6 (19%)	45,48,48	3.69	22 (48%)

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
8	AF5	F	101	7	-	0/8/33/33	0/4/5/5
8	AF5	H	101	7	-	0/8/33/33	0/4/5/5

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	H	101	AF5	C15-C16	7.20	1.48	1.33
8	F	101	AF5	C15-C16	6.92	1.47	1.33
8	H	101	AF5	C02-N01	-3.71	1.43	1.49
8	F	101	AF5	C14-C15	3.42	1.49	1.46
8	F	101	AF5	C02-N01	-3.38	1.44	1.49

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	H	101	AF5	C04-C02-N01	15.70	140.98	118.92
8	F	101	AF5	C04-C02-N01	15.44	140.62	118.92
8	H	101	AF5	C24-C14-C15	-10.71	114.03	122.94
8	F	101	AF5	C24-C14-C15	-7.97	116.30	122.94
8	H	101	AF5	C03-C02-N01	-6.57	109.68	118.92

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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	482/496 (97%)	-0.44	0 100 100	28, 45, 78, 109	0
1	B	482/496 (97%)	-0.45	0 100 100	26, 44, 73, 100	0
2	C	208/268 (77%)	-0.24	0 100 100	49, 78, 113, 150	0
2	D	210/268 (78%)	-0.18	0 100 100	49, 81, 118, 153	0
3	E	7/7 (100%)	-0.63	0 100 100	48, 53, 80, 110	0
4	F	11/11 (100%)	-0.54	0 100 100	54, 64, 80, 97	0
5	G	7/7 (100%)	-0.42	0 100 100	45, 51, 82, 100	0
6	H	11/11 (100%)	-0.31	0 100 100	55, 64, 73, 94	0
All	All	1418/1564 (90%)	-0.37	0 100 100	26, 52, 101, 153	0

There are no RSRZ outliers to report.

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 carbohydrates in this entry.

6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
7	MG	B	502	1/1	0.33	11.92	64,64,64,64	0
7	MG	D	701	1/1	0.63	9.28	52,52,52,52	0
7	MG	A	502	1/1	0.24	7.83	53,53,53,53	0
7	MG	C	701	1/1	0.37	6.13	59,59,59,59	0
8	AF5	H	101	27/27	0.26	1.00	66,92,133,155	0
8	AF5	F	101	27/27	0.23	0.86	51,71,87,90	0
7	MG	B	501	1/1	0.14	-0.66	54,54,54,54	0
7	MG	A	501	1/1	0.11	-1.69	43,43,43,43	0

6.5 Other polymers ⓘ

There are no such residues in this entry.