



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 16, 2023 – 09:26 PM EDT

PDB ID : 4TMA
Title : Crystal structure of gyrase bound to its inhibitor YacG
Authors : Vos, S.M.; Lyubimov, A.Y.; Hershey, D.M.; Schoeffler, A.J.; Berger, J.M.
Deposited on : 2014-05-31
Resolution : 3.30 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.35.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

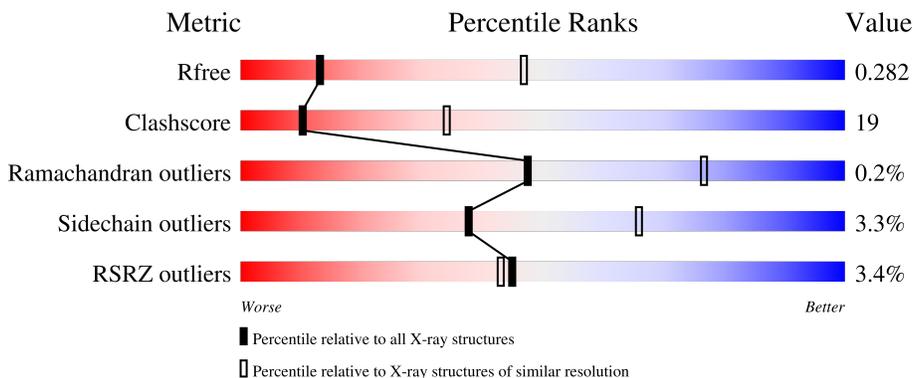
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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}	130704	1149 (3.34-3.26)
Clashscore	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)
RSRZ outliers	127900	1115 (3.34-3.26)

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	525	
1	C	525	
1	E	525	
1	G	525	
2	B	417	

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Mol	Chain	Length	Quality of chain
2	D	417	
2	F	417	
2	H	417	
3	I	65	
3	J	65	
3	K	65	
3	L	65	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 26792 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 DNA gyrase subunit A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	505	Total 3983	C 2510	N 711	O 747	S 15	0	0	0
1	C	475	Total 3733	C 2345	N 672	O 701	S 15	0	0	0
1	E	486	Total 3841	C 2413	N 698	O 715	S 15	0	1	0
1	G	483	Total 3800	C 2391	N 682	O 713	S 14	0	0	0

- Molecule 2 is a protein called DNA gyrase subunit B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	374	Total 2995	C 1875	N 527	O 579	S 14	0	0	0
2	D	251	Total 1990	C 1252	N 347	O 379	S 12	0	0	0
2	F	371	Total 2971	C 1863	N 523	O 571	S 14	0	0	0
2	H	233	Total 1863	C 1170	N 326	O 356	S 11	0	1	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	385	SER	-	expression tag	UNP U6NGU8
B	386	ASN	-	expression tag	UNP U6NGU8
B	387	ALA	-	expression tag	UNP U6NGU8
B	458	TYR	PHE	engineered mutation	UNP U6NGU8
D	385	SER	-	expression tag	UNP U6NGU8
D	386	ASN	-	expression tag	UNP U6NGU8
D	387	ALA	-	expression tag	UNP U6NGU8
D	458	TYR	PHE	engineered mutation	UNP U6NGU8

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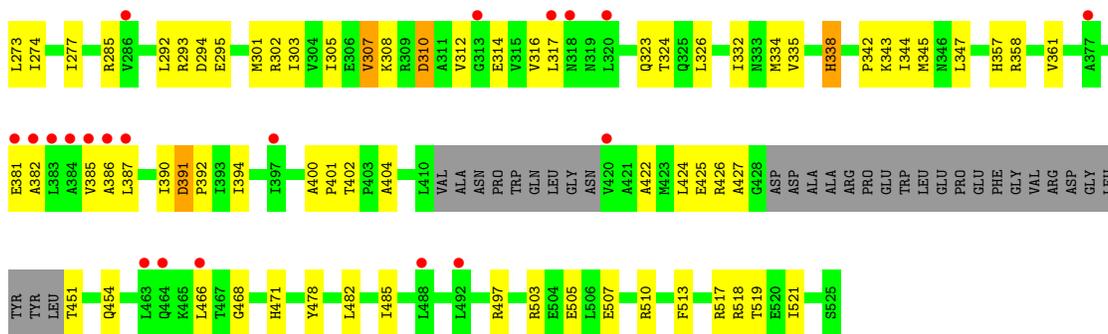
Chain	Residue	Modelled	Actual	Comment	Reference
F	385	SER	-	expression tag	UNP U6NGU8
F	386	ASN	-	expression tag	UNP U6NGU8
F	387	ALA	-	expression tag	UNP U6NGU8
F	458	TYR	PHE	engineered mutation	UNP U6NGU8
H	385	SER	-	expression tag	UNP U6NGU8
H	386	ASN	-	expression tag	UNP U6NGU8
H	387	ALA	-	expression tag	UNP U6NGU8
H	458	TYR	PHE	engineered mutation	UNP U6NGU8

- Molecule 3 is a protein called DNA gyrase inhibitor YacG.

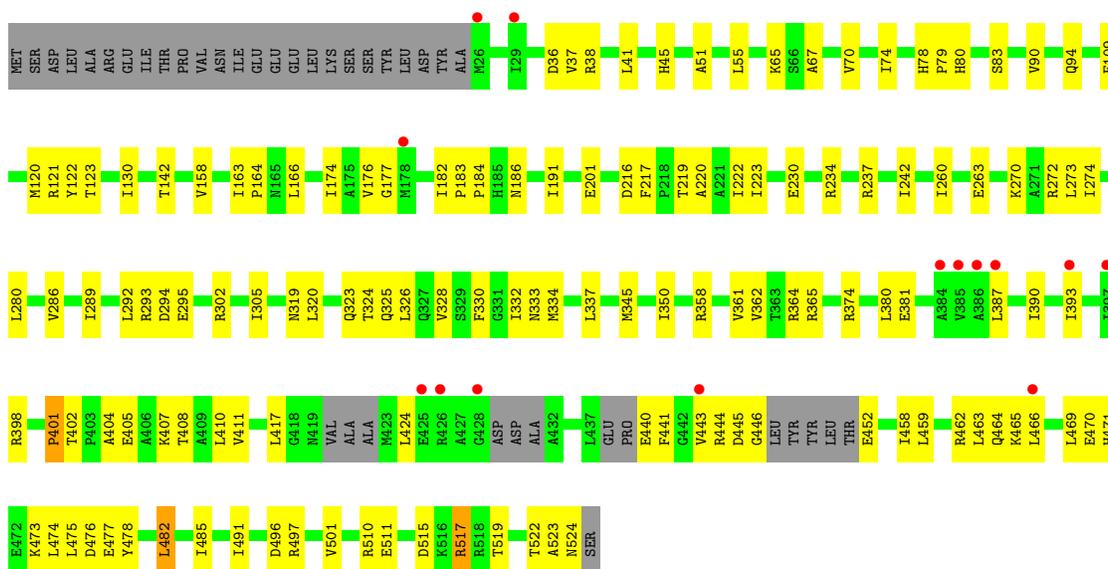
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	I	47	Total	C	N	O	S	0	0	0
			363	230	63	66	4			
3	J	57	Total	C	N	O	S	0	0	0
			446	279	74	89	4			
3	K	55	Total	C	N	O	S	0	0	0
			430	270	72	84	4			
3	L	48	Total	C	N	O	S	0	0	0
			371	234	64	69	4			

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

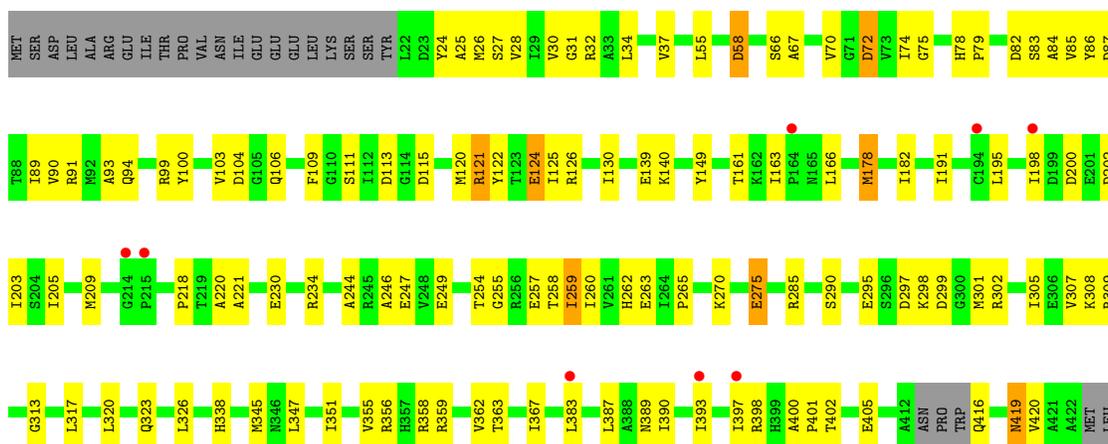
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Zn	0	0
			1	1		
4	E	1	Total	Zn	0	0
			1	1		
4	I	1	Total	Zn	0	0
			1	1		
4	J	1	Total	Zn	0	0
			1	1		
4	K	1	Total	Zn	0	0
			1	1		
4	L	1	Total	Zn	0	0
			1	1		



• Molecule 1: DNA gyrase subunit A

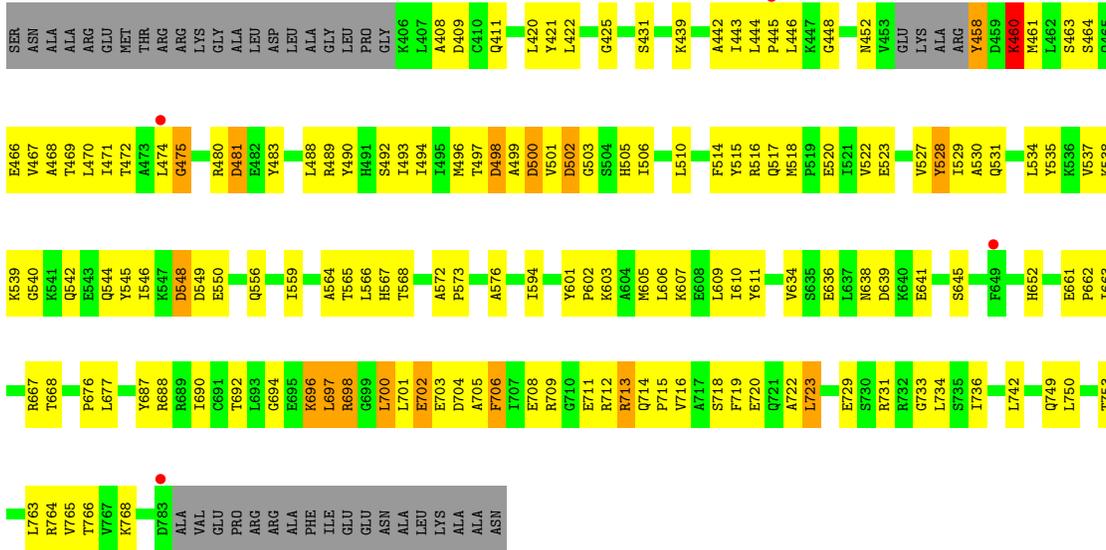


• Molecule 1: DNA gyrase subunit A

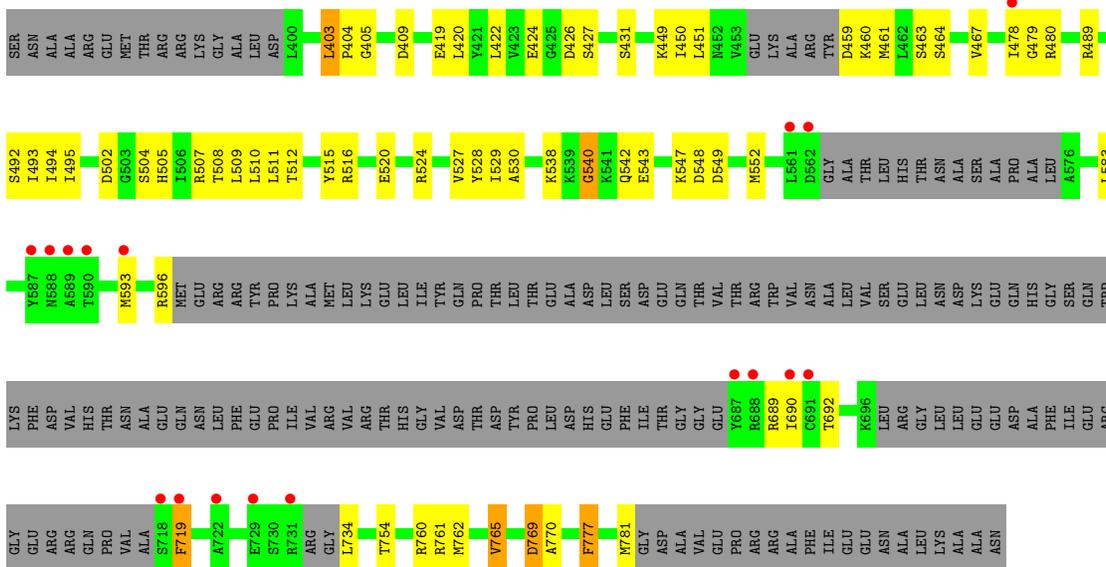




- Molecule 2: DNA gyrase subunit B



- Molecule 2: DNA gyrase subunit B

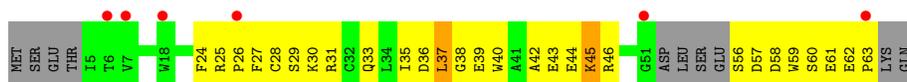


- Molecule 2: DNA gyrase subunit B





- Molecule 3: DNA gyrase inhibitor YacG



- Molecule 3: DNA gyrase inhibitor YacG



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	107.21Å 114.46Å 462.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.32 – 3.30 49.32 – 3.30	Depositor EDS
% Data completeness (in resolution range)	77.7 (49.32-3.30) 77.7 (49.32-3.30)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.10 (at 3.33Å)	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.243 , 0.283 0.244 , 0.282	Depositor DCC
R_{free} test set	3399 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	109.9	Xtrriage
Anisotropy	0.025	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 61.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	26792	wwPDB-VP
Average B, all atoms (Å ²)	140.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.20% 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:
ZN

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	0.60	2/4044 (0.0%)	0.71	12/5466 (0.2%)
1	C	0.44	0/3785	0.61	4/5111 (0.1%)
1	E	0.47	0/3896	0.57	2/5258 (0.0%)
1	G	0.40	0/3855	0.51	1/5209 (0.0%)
2	B	0.47	1/3046 (0.0%)	0.73	8/4111 (0.2%)
2	D	0.37	0/2015	0.57	0/2705
2	F	0.40	0/3021	0.66	7/4074 (0.2%)
2	H	0.43	0/1887	0.66	4/2534 (0.2%)
3	I	0.65	0/372	0.92	4/504 (0.8%)
3	J	0.35	0/457	0.67	2/620 (0.3%)
3	K	0.81	1/441 (0.2%)	0.63	1/598 (0.2%)
3	L	0.73	2/380 (0.5%)	0.73	1/515 (0.2%)
All	All	0.47	6/27199 (0.0%)	0.64	46/36705 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1
2	D	0	1
2	H	0	1
All	All	0	3

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	K	63	PRO	N-CD	-15.54	1.26	1.47
3	L	26	PRO	N-CD	9.27	1.60	1.47
3	L	48	PRO	N-CD	5.42	1.55	1.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	502	ASP	CA-C	5.37	1.67	1.52
1	A	218	PRO	N-CD	5.17	1.55	1.47

The worst 5 of 46 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	28	CYS	O-C-N	-9.19	107.99	122.70
2	B	475	GLY	N-CA-C	8.69	134.84	113.10
1	A	419	ASN	N-CA-C	8.50	133.96	111.00
2	F	603	LYS	N-CA-C	8.06	132.76	111.00
3	I	47	ILE	CB-CA-C	-7.48	96.64	111.60

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	251	ASP	Peptide
2	D	540	GLY	Peptide
2	H	449	LYS	Peptide

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	3983	0	4040	184	1
1	C	3733	0	3810	152	1
1	E	3841	0	3910	120	14
1	G	3800	0	3867	106	0
2	B	2995	0	2972	159	1
2	D	1990	0	2013	83	0
2	F	2971	0	2959	128	14
2	H	1863	0	1887	69	1
3	I	363	0	357	17	0
3	J	446	0	416	11	0
3	K	430	0	404	38	0
3	L	371	0	362	18	0
4	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	E	1	0	0	0	0
4	I	1	0	0	0	0
4	J	1	0	0	0	0
4	K	1	0	0	0	0
4	L	1	0	0	0	0
All	All	26792	0	26997	1011	16

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 19.

The worst 5 of 1011 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:D:760:ARG:HD3	2:D:762:MET:CE	1.40	1.52
1:G:257:GLU:OE2	1:G:313:GLY:N	1.61	1.31
2:D:760:ARG:CD	2:D:762:MET:CE	2.09	1.30
2:D:760:ARG:CD	2:D:762:MET:HE2	1.63	1.28
1:G:255:GLY:O	1:G:309:ARG:HD3	1.17	1.27

The worst 5 of 16 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	Interatomic distance (Å)	Clash overlap (Å)
1:E:476:ASP:OD2	2:F:596:ARG:CZ[3_757]	1.27	0.93
1:E:476:ASP:OD2	2:F:596:ARG:NE[3_757]	1.27	0.93
1:E:476:ASP:CG	2:F:596:ARG:NE[3_757]	1.32	0.88
1:E:476:ASP:CG	2:F:596:ARG:CZ[3_757]	1.33	0.87
1:E:476:ASP:CG	2:F:596:ARG:NH2[3_757]	1.39	0.81

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	497/525 (95%)	473 (95%)	22 (4%)	2 (0%)	34	66
1	C	469/525 (89%)	438 (93%)	30 (6%)	1 (0%)	47	77
1	E	477/525 (91%)	454 (95%)	22 (5%)	1 (0%)	47	77
1	G	475/525 (90%)	443 (93%)	31 (6%)	1 (0%)	47	77
2	B	370/417 (89%)	341 (92%)	28 (8%)	1 (0%)	41	71
2	D	239/417 (57%)	225 (94%)	13 (5%)	1 (0%)	34	66
2	F	365/417 (88%)	347 (95%)	18 (5%)	0	100	100
2	H	224/417 (54%)	206 (92%)	17 (8%)	1 (0%)	34	66
3	I	45/65 (69%)	42 (93%)	3 (7%)	0	100	100
3	J	53/65 (82%)	50 (94%)	3 (6%)	0	100	100
3	K	51/65 (78%)	47 (92%)	4 (8%)	0	100	100
3	L	46/65 (71%)	46 (100%)	0	0	100	100
All	All	3311/4028 (82%)	3112 (94%)	191 (6%)	8 (0%)	47	77

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	220	ALA
1	E	401	PRO
2	B	696	LYS
1	A	136	ALA
1	G	439	PRO

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	422/440 (96%)	406 (96%)	16 (4%)	33	62
1	C	397/440 (90%)	387 (98%)	10 (2%)	47	72
1	E	407/440 (92%)	397 (98%)	10 (2%)	47	72
1	G	403/440 (92%)	387 (96%)	16 (4%)	31	61

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	322/352 (92%)	306 (95%)	16 (5%)	24	55
2	D	214/352 (61%)	207 (97%)	7 (3%)	38	66
2	F	319/352 (91%)	311 (98%)	8 (2%)	47	72
2	H	202/352 (57%)	196 (97%)	6 (3%)	41	68
3	I	41/59 (70%)	40 (98%)	1 (2%)	49	73
3	J	51/59 (86%)	48 (94%)	3 (6%)	19	49
3	K	49/59 (83%)	47 (96%)	2 (4%)	30	61
3	L	42/59 (71%)	41 (98%)	1 (2%)	49	73
All	All	2869/3404 (84%)	2773 (97%)	96 (3%)	38	66

5 of 96 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	496	ASP
1	G	72	ASP
2	F	409	ASP
2	F	683	THR
1	G	202	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	57	ASN
2	H	544	GLN
1	G	106	GLN
1	G	338	HIS
2	H	746	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 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	505/525 (96%)	-0.03	14 (2%) 53 51	67, 110, 249, 473	0
1	C	475/525 (90%)	0.11	23 (4%) 30 28	75, 145, 252, 431	0
1	E	486/525 (92%)	-0.01	14 (2%) 51 50	65, 104, 254, 314	0
1	G	483/525 (92%)	0.01	13 (2%) 54 52	59, 139, 235, 370	0
2	B	374/417 (89%)	-0.11	4 (1%) 80 81	69, 132, 176, 208	0
2	D	251/417 (60%)	0.26	17 (6%) 17 17	86, 145, 270, 299	0
2	F	371/417 (88%)	-0.02	4 (1%) 80 81	59, 121, 200, 247	0
2	H	233/417 (55%)	0.20	16 (6%) 16 16	79, 132, 263, 362	0
3	I	47/65 (72%)	-0.35	0 100 100	65, 106, 140, 149	0
3	J	57/65 (87%)	-0.09	2 (3%) 44 42	66, 108, 144, 153	0
3	K	55/65 (84%)	0.47	6 (10%) 5 5	136, 176, 205, 211	0
3	L	48/65 (73%)	0.11	2 (4%) 36 34	166, 194, 227, 283	0
All	All	3385/4028 (84%)	0.03	115 (3%) 45 43	59, 130, 246, 473	0

The worst 5 of 115 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	386	ALA	8.2
2	D	719	PHE	7.9
1	A	385	VAL	7.4
1	A	17	LEU	6.1
3	K	51	GLY	5.7

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 monosaccharides 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(\AA^2)	Q<0.9
4	ZN	K	101	1/1	0.71	0.12	202,202,202,202	0
4	ZN	E	601	1/1	0.76	0.27	346,346,346,346	0
4	ZN	L	101	1/1	0.80	0.14	225,225,225,225	0
4	ZN	B	1001	1/1	0.84	0.54	346,346,346,346	0
4	ZN	I	101	1/1	0.97	0.16	95,95,95,95	0
4	ZN	J	101	1/1	0.99	0.10	137,137,137,137	0

6.5 Other polymers [i](#)

There are no such residues in this entry.