Full wwPDB X-ray Structure Validation Report (i)

May 15, 2019 – 10:51 AM EDT

PDB ID	:	5ZXH
Title	:	The structure of MT189-tubulin complex
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Deposited on	:	2018-05-21
Resolution	:	2.80 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

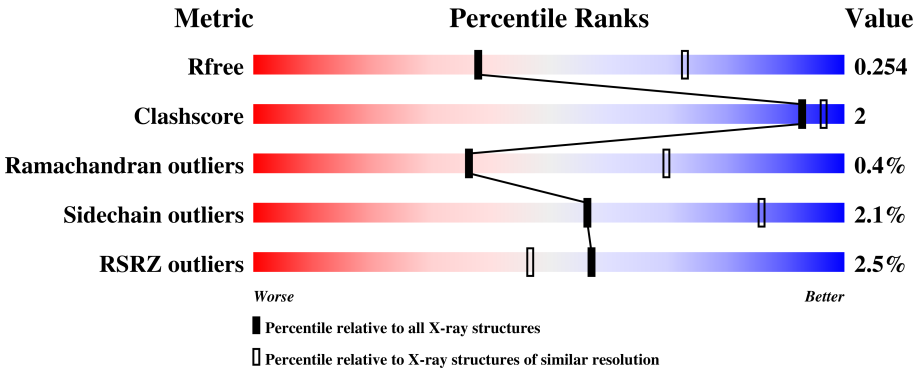
MolProbity	:	4.02b-467
Mogul	:	1.8.0 (224370), CSD as540be (2019)
Xtriage (Phenix)	:	1.13
EDS	:	rb-20031633
Percentile statistics	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac	:	5.8.0158
CCP4	:	7.0 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20031633

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 2.80 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}	111664	2792 (2.80-2.80)
Clashscore	122126	3209 (2.80-2.80)
Ramachandran outliers	120053	3158 (2.80-2.80)
Sidechain outliers	120020	3160 (2.80-2.80)
RSRZ outliers	108989	2726 (2.80-2.80)

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. 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 <=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	450	93%
1	C	450	91% 7%
2	B	445	% 87% 7% 5%
2	D	445	5% 89% 6% 5%
3	E	143	% 83% 16%

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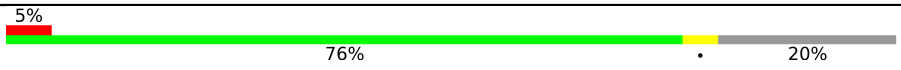
Mol	Chain	Length	Quality of chain
4	F	384	

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 17367 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 Tubulin alpha-1B chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	437	Total	C	N	O	S	0	4	0
			3441	2179	586	652	24			
1	C	440	Total	C	N	O	S	0	7	0
			3469	2193	588	663	25			

- Molecule 2 is a protein called Tubulin beta-2B chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	424	Total	C	N	O	S	0	2	0
			3351	2106	574	645	26			
2	D	421	Total	C	N	O	S	0	1	0
			3304	2078	562	638	26			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	170	VAL	MET	engineered mutation	UNP Q6B856
B	316	VAL	ILE	engineered mutation	UNP Q6B856
D	170	VAL	MET	engineered mutation	UNP Q6B856
D	316	VAL	ILE	engineered mutation	UNP Q6B856

- Molecule 3 is a protein called Stathmin-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	120	Total	C	N	O	S	0	0	0
			994	614	180	195	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	3	MET	-	expression tag	UNP P63043
E	4	ALA	-	expression tag	UNP P63043

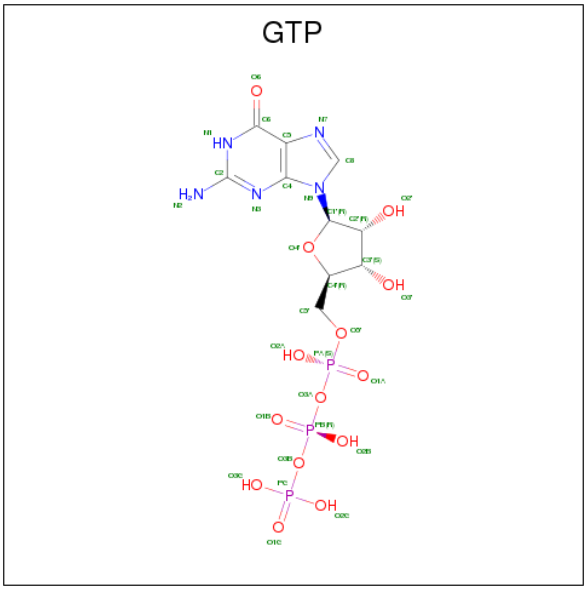
- Molecule 4 is a protein called Tubulin tyrosine ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	309	Total	C	N	O	S	0	3	0
			2553	1645	438	455	15			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	379	HIS	-	expression tag	UNP E1BQ43
F	380	HIS	-	expression tag	UNP E1BQ43
F	381	HIS	-	expression tag	UNP E1BQ43
F	382	HIS	-	expression tag	UNP E1BQ43
F	383	HIS	-	expression tag	UNP E1BQ43
F	384	HIS	-	expression tag	UNP E1BQ43

- Molecule 5 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			32	10	5	14	3		
5	C	1	Total	C	N	O	P	0	0
			32	10	5	14	3		
5	D	1	Total	C	N	O	P	0	0
			32	10	5	14	3		

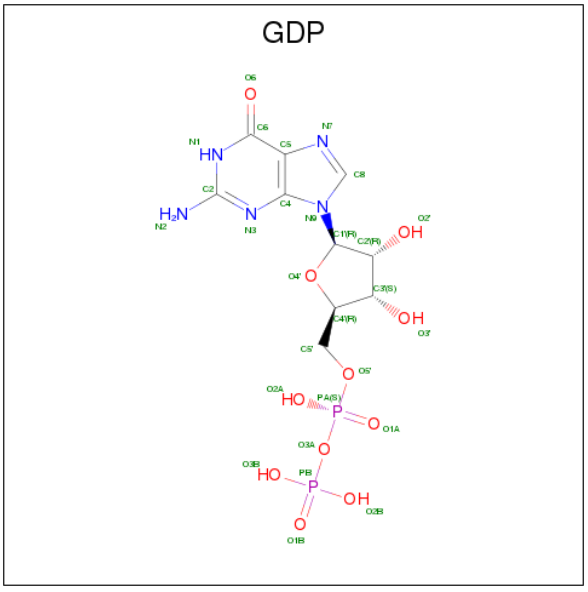
- Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 7 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	B	1	Total Ca 1 1	0	0
7	A	1	Total Ca 1 1	0	0
7	C	1	Total Ca 1 1	0	0

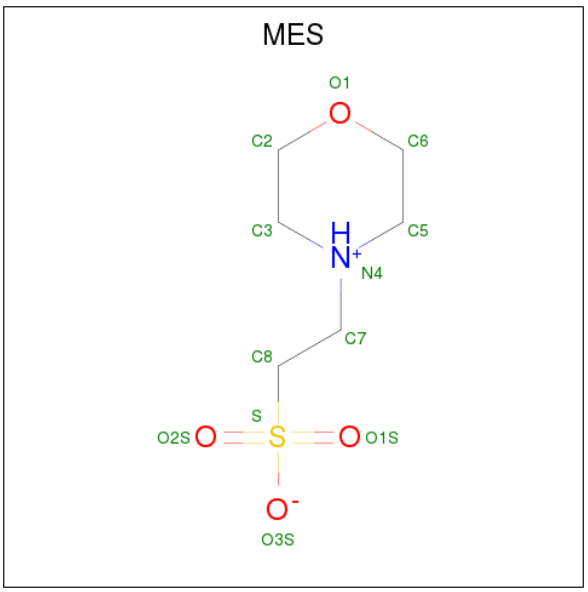
- Molecule 8 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	B	1	Total C N O P 28 10 5 11 2	0	0

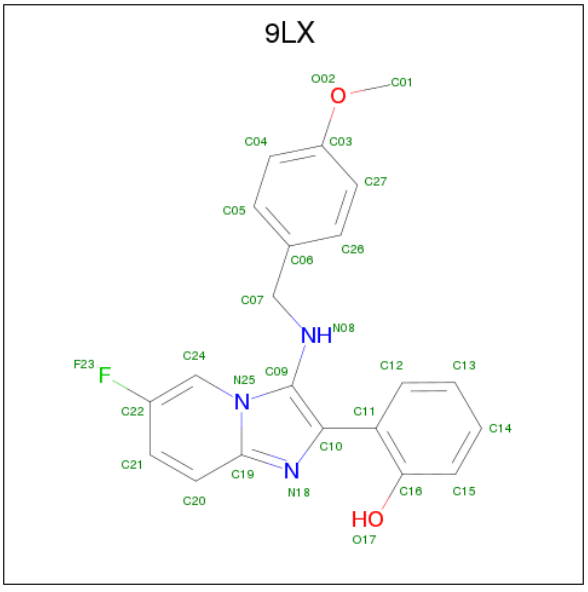
- Molecule 9 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES)

(formula: $C_6H_{13}NO_4S$).



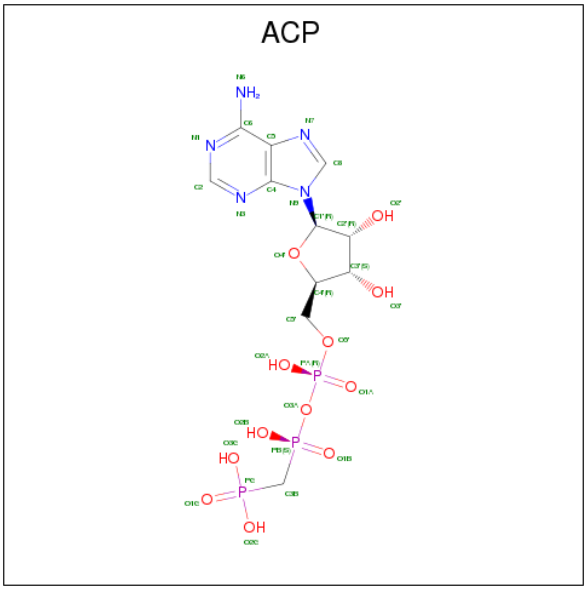
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
9	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 10 is 2-(6-fluoro-3-{[(4-methoxyphenyl)methyl]amino}imidazo[1,2-a]pyridin-2-yl)phenol (three-letter code: 9LX) (formula: $C_{21}H_{18}FN_3O_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
10	B	1	Total	C	F	N	O	0	0
			27	21	1	3	2		
10	D	1	Total	C	F	N	O	0	0
			27	21	1	3	2		

- Molecule 11 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (three-letter code: ACP) (formula: $C_{11}H_{18}N_5O_{12}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
11	F	1	Total	C	N	O	P	0	0
			31	11	5	12	3		

- Molecule 12 is water.

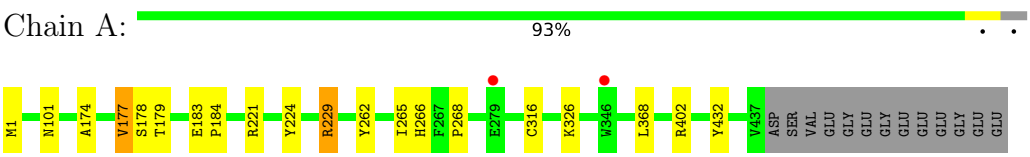
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	7	Total	O	0	0
			7	7		
12	B	4	Total	O	0	0
			4	4		
12	C	4	Total	O	0	0
			4	4		

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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 geometryand 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.

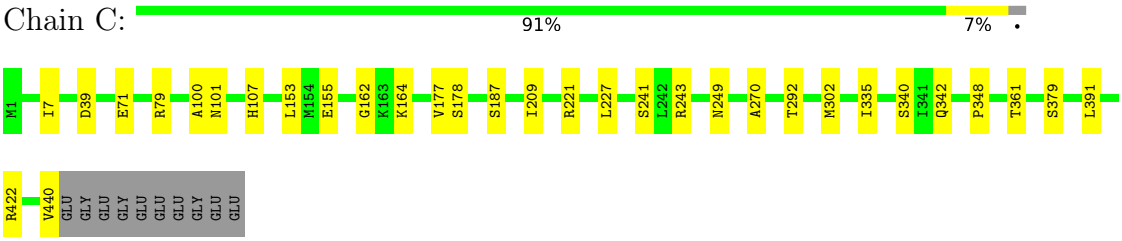
• Molecule 1: Tubulin alpha-1B chain

Chain A:



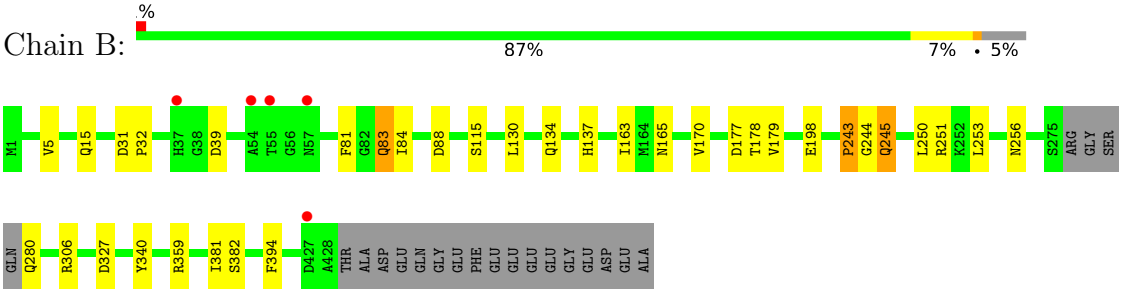
• Molecule 1: Tubulin alpha-1B chain

Chain C:



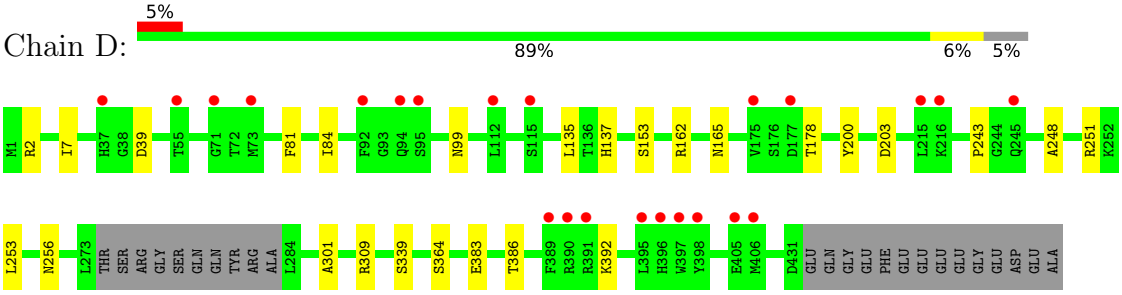
• Molecule 2: Tubulin beta-2B chain

Chain B:



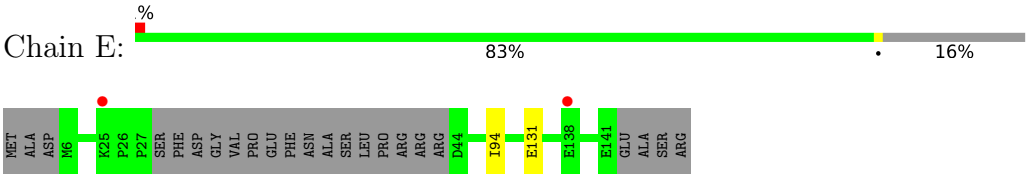
• Molecule 2: Tubulin beta-2B chain

Chain D:



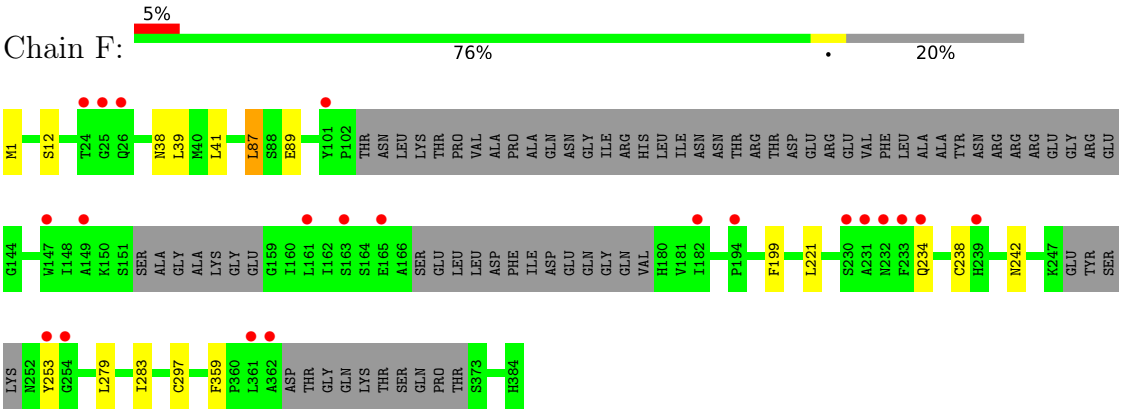
• Molecule 3: Stathmin-4

Chain E:



• Molecule 4: Tubulin tyrosine ligase

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	104.91Å 157.06Å 182.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.80 46.84 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.4 (50.00-2.80) 99.5 (46.84-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.40 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.208 , 0.259 0.210 , 0.254	Depositor DCC
R_{free} test set	3753 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å^2)	42.8	Xtriage
Anisotropy	0.062	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 29.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	17367	wwPDB-VP
Average B, all atoms (Å^2)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.76% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: GDP, MG, CA, 9LX, GTP, ACP, MES

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	0.52	0/3525	0.73	0/4784
1	C	0.55	0/3556	0.74	4/4828 (0.1%)
2	B	0.53	0/3425	0.72	0/4639
2	D	0.49	0/3377	0.68	0/4576
3	E	0.52	0/1002	0.68	0/1329
4	F	0.49	0/2618	0.65	0/3537
All	All	0.52	0/17503	0.71	4/23693 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	39	ASP	CB-CG-OD1	5.69	123.42	118.30
1	C	243	ARG	NE-CZ-NH1	5.33	122.96	120.30
1	C	79	ARG	NE-CZ-NH1	5.24	122.92	120.30
1	C	422	ARG	NE-CZ-NH2	-5.01	117.80	120.30

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	3441	0	3362	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	3469	0	3377	13	0
2	B	3351	0	3226	17	0
2	D	3304	0	3179	10	0
3	E	994	0	1013	1	0
4	F	2553	0	2519	6	0
5	A	32	0	12	0	0
5	C	32	0	12	0	0
5	D	32	0	12	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
7	A	1	0	0	0	0
7	B	1	0	0	0	0
7	C	1	0	0	0	0
8	B	28	0	12	0	0
9	B	24	0	26	1	0
10	B	27	0	0	0	0
10	D	27	0	0	0	0
11	F	31	0	14	1	0
12	A	7	0	0	0	0
12	B	4	0	0	0	0
12	C	4	0	0	0	0
All	All	17367	0	16764	56	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 2.

All (56) 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:229[A]:ARG:CG	1:A:229[A]:ARG:HH11	1.83	0.90
1:A:229[A]:ARG:HG2	1:A:229[A]:ARG:HH11	1.52	0.74
1:A:174:ALA:O	1:A:178:SER:HB2	1.96	0.66
1:A:229[A]:ARG:HH11	1:A:229[A]:ARG:HG3	1.60	0.66
2:B:251:ARG:NH1	9:B:503:MES:O2S	2.27	0.65
1:A:229[A]:ARG:NH1	1:A:229[A]:ARG:HG2	2.10	0.62
1:A:368[B]:LEU:H	1:A:368[B]:LEU:HD12	1.64	0.62
1:A:101:ASN:HD22	2:B:256:ASN:HD21	1.50	0.60
4:F:87:LEU:HD21	4:F:297:CYS:HB2	1.87	0.56
1:A:229[A]:ARG:NH1	1:A:229[A]:ARG:CG	2.53	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:368[B]:LEU:N	1:A:368[B]:LEU:HD12	2.21	0.55
2:B:163:ILE:HG21	2:B:250:LEU:HB3	1.90	0.53
1:C:209:ILE:HG22	1:C:227:LEU:HD22	1.90	0.52
1:A:265:ILE:HG23	1:A:432:TYR:CE2	2.45	0.52
2:D:99:ASN:HD22	2:D:178:THR:HG21	1.73	0.52
1:A:177:VAL:HG22	1:A:177:VAL:O	2.10	0.51
2:D:7:ILE:O	2:D:135:LEU:HD12	2.10	0.51
1:C:101:ASN:HD22	2:D:256:ASN:HD21	1.57	0.51
2:D:81:PHE:O	2:D:84:ILE:HG22	2.11	0.50
2:D:203:ASP:HB3	2:D:301:ALA:HA	1.93	0.50
2:B:306:ARG:NH1	2:B:340:TYR:OH	2.45	0.50
1:C:270:ALA:HB3	1:C:302:MET:CE	2.43	0.49
2:B:179:VAL:HG12	1:C:348:PRO:HG2	1.96	0.48
2:B:177:ASP:O	2:B:178:THR:HG23	2.13	0.48
2:B:198:GLU:OE2	2:B:253:LEU:HD23	2.14	0.47
1:A:177:VAL:HG21	1:A:224:TYR:CE1	2.50	0.47
1:C:162:GLY:HA2	3:E:94:ILE:HD11	1.97	0.47
1:C:100:ALA:CB	2:D:251:ARG:HG2	2.45	0.46
2:B:170:VAL:HG13	2:B:381:ILE:HD11	1.97	0.46
1:A:221:ARG:NE	2:B:327:ASP:OD2	2.49	0.46
2:B:83:GLN:HA	2:B:83:GLN:HE21	1.80	0.46
2:B:5:VAL:HG23	2:B:130:LEU:CD1	2.45	0.46
4:F:279:LEU:HD12	4:F:283:ILE:HB	1.97	0.46
1:C:292:THR:HG22	1:C:335:ILE:CD1	2.46	0.45
2:B:243:PRO:CB	2:B:244:GLY:CA	2.94	0.45
1:C:209:ILE:HG22	1:C:227:LEU:CD2	2.47	0.45
2:B:5:VAL:HG23	2:B:130:LEU:HD11	1.99	0.45
2:D:309:ARG:NH1	2:D:339:SER:O	2.46	0.45
2:D:165:ASN:HD21	2:D:200:TYR:HE2	1.63	0.45
2:B:81:PHE:O	2:B:84:ILE:HG22	2.17	0.44
2:D:383:GLU:HA	2:D:386:THR:HG22	1.99	0.44
4:F:39:LEU:HD21	4:F:41:LEU:HD21	1.99	0.44
1:C:107:HIS:HE1	1:C:155:GLU:OE1	2.01	0.44
1:A:266:HIS:O	1:A:268:PRO:HD3	2.17	0.43
4:F:242:ASN:HD21	11:F:401:ACP:H5'2	1.83	0.43
2:B:179:VAL:HG21	2:B:394:PHE:CZ	2.54	0.43
1:C:270:ALA:HB3	1:C:302:MET:HE3	2.01	0.42
1:A:183:GLU:N	1:A:184:PRO:CD	2.82	0.42
1:C:187:SER:HB3	1:C:391:LEU:HD21	2.01	0.42
2:B:31:ASP:HB2	2:B:32:PRO:CD	2.50	0.41
1:C:7:ILE:HG21	1:C:153:LEU:HD21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:199:PHE:CD2	4:F:221:LEU:HD23	2.55	0.41
1:C:241:SER:HA	1:C:249:ASN:HD21	1.85	0.41
2:D:203:ASP:C	2:D:203:ASP:OD1	2.58	0.41
2:B:134:GLN:HA	2:B:165:ASN:O	2.22	0.40
4:F:38:ASN:HB3	4:F:359:PHE:CZ	2.56	0.40

There are no symmetry-related clashes.

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	439/450 (98%)	429 (98%)	10 (2%)	0	100	100
1	C	444/450 (99%)	434 (98%)	9 (2%)	1 (0%)	49	81
2	B	422/445 (95%)	404 (96%)	15 (4%)	3 (1%)	24	57
2	D	417/445 (94%)	393 (94%)	20 (5%)	4 (1%)	17	48
3	E	116/143 (81%)	109 (94%)	7 (6%)	0	100	100
4	F	300/384 (78%)	289 (96%)	10 (3%)	1 (0%)	43	75
All	All	2138/2317 (92%)	2058 (96%)	71 (3%)	9 (0%)	36	70

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	243	PRO
2	D	39	ASP
2	D	248	ALA
2	D	392	LYS
2	B	245	GLN
4	F	253	TYR
2	B	39	ASP

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Mol	Chain	Res	Type
1	C	164	LYS
2	D	243	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	372/378 (98%)	362 (97%)	10 (3%)	48	81
1	C	377/378 (100%)	368 (98%)	9 (2%)	52	83
2	B	367/383 (96%)	358 (98%)	9 (2%)	50	82
2	D	362/383 (94%)	356 (98%)	6 (2%)	63	89
3	E	108/127 (85%)	107 (99%)	1 (1%)	81	95
4	F	281/342 (82%)	275 (98%)	6 (2%)	56	86
All	All	1867/1991 (94%)	1826 (98%)	41 (2%)	56	85

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	177	VAL
1	A	179	THR
1	A	229[A]	ARG
1	A	229[B]	ARG
1	A	262	TYR
1	A	316[A]	CYS
1	A	316[B]	CYS
1	A	326	LYS
1	A	402	ARG
2	B	15	GLN
2	B	83	GLN
2	B	88	ASP
2	B	115	SER
2	B	137	HIS
2	B	245	GLN

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Mol	Chain	Res	Type
2	B	280	GLN
2	B	359	ARG
2	B	382	SER
1	C	71	GLU
1	C	177	VAL
1	C	178	SER
1	C	221	ARG
1	C	340	SER
1	C	342	GLN
1	C	361	THR
1	C	379	SER
1	C	440	VAL
2	D	2	ARG
2	D	137	HIS
2	D	153	SER
2	D	162	ARG
2	D	253	LEU
2	D	364	SER
3	E	131	GLU
4	F	1	MET
4	F	12	SER
4	F	87	LEU
4	F	89	GLU
4	F	234	GLN
4	F	238	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	101	ASN
2	B	11	GLN
2	B	52	ASN
2	B	83	GLN
2	B	190	HIS
1	C	101	ASN
1	C	128	GLN
1	C	133	GLN
1	C	249	ASN
1	C	372	GLN
2	D	99	ASN
4	F	252	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 carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 16 ligands modelled in this entry, 7 are monoatomic - leaving 9 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	$\#\|Z\| > 2$
5	GTP	A	501	6	26,34,34	1.30	3 (11%)	29,54,54	2.08	9 (31%)
8	GDP	B	501	6	24,30,30	1.20	2 (8%)	27,47,47	2.27	7 (25%)
9	MES	B	503	-	12,12,12	2.21	1 (8%)	14,16,16	6.68	9 (64%)
9	MES	B	505	-	12,12,12	2.10	1 (8%)	14,16,16	6.37	9 (64%)
10	9LX	B	506	-	26,30,30	2.51	4 (15%)	27,42,42	1.14	2 (7%)
5	GTP	C	501	6	26,34,34	1.16	2 (7%)	29,54,54	2.37	8 (27%)
5	GTP	D	501	6	26,34,34	1.16	2 (7%)	29,54,54	1.98	10 (34%)
10	9LX	D	503	-	26,30,30	2.06	2 (7%)	27,42,42	1.24	1 (3%)
11	ACP	F	401	-	26,33,33	1.81	6 (23%)	30,52,52	1.27	2 (6%)

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
5	GTP	A	501	6	-	0/18/38/38	0/3/3/3
8	GDP	B	501	6	-	0/12/32/32	0/3/3/3
9	MES	B	503	-	-	0/6/14/14	0/1/1/1
9	MES	B	505	-	-	0/6/14/14	0/1/1/1
10	9LX	B	506	-	-	0/8/11/11	0/4/4/4
5	GTP	C	501	6	-	0/18/38/38	0/3/3/3
5	GTP	D	501	6	-	0/18/38/38	0/3/3/3
10	9LX	D	503	-	-	0/8/11/11	0/4/4/4
11	ACP	F	401	-	-	0/15/38/38	0/3/3/3

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	B	506	9LX	C11-C10	-10.92	1.38	1.49
10	D	503	9LX	C11-C10	-8.84	1.40	1.49
9	B	503	MES	C8-S	-7.07	1.67	1.77
9	B	505	MES	C8-S	-6.76	1.67	1.77
10	B	506	9LX	C10-N18	-2.66	1.32	1.37
11	F	401	ACP	PG-O2G	-2.51	1.49	1.54
10	B	506	9LX	O17-C16	2.09	1.40	1.36
11	F	401	ACP	PB-O2B	2.10	1.61	1.56
8	B	501	GDP	C5-C4	2.69	1.46	1.40
11	F	401	ACP	PG-O3G	2.98	1.61	1.54
5	A	501	GTP	C5-C4	2.99	1.47	1.40
5	C	501	GTP	C5-C4	3.03	1.47	1.40
5	A	501	GTP	PG-O3B	3.09	1.64	1.60
11	F	401	ACP	C5-C4	3.10	1.47	1.40
10	D	503	9LX	C19-N18	3.14	1.36	1.33
8	B	501	GDP	C6-C5	3.27	1.47	1.41
11	F	401	ACP	PB-O3A	3.30	1.62	1.58
5	D	501	GTP	C5-C4	3.31	1.48	1.40
5	A	501	GTP	C6-C5	3.70	1.47	1.41
5	C	501	GTP	C6-C5	3.73	1.47	1.41
5	D	501	GTP	C6-C5	3.73	1.47	1.41
10	B	506	9LX	C19-N18	4.27	1.37	1.33
11	F	401	ACP	PG-O1G	5.40	1.61	1.50

All (57) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
9	B	505	MES	O3S-S-O1S	-12.92	79.72	111.27
9	B	503	MES	O3S-S-C8	-12.09	86.22	105.77
9	B	503	MES	O3S-S-O2S	-11.40	83.42	111.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
9	B	503	MES	O3S-S-O1S	-11.13	84.07	111.27
9	B	505	MES	O3S-S-O2S	-11.12	84.11	111.27
9	B	505	MES	O3S-S-C8	-8.70	91.70	105.77
5	C	501	GTP	C5-C6-N1	-4.84	116.73	123.47
8	B	501	GDP	C6-C5-C4	-4.66	116.31	120.79
5	C	501	GTP	C6-C5-C4	-4.57	116.39	120.79
8	B	501	GDP	N3-C2-N1	-4.55	121.10	127.25
8	B	501	GDP	C5-C6-N1	-4.41	117.34	123.47
5	A	501	GTP	C5-C6-N1	-4.33	117.45	123.47
5	D	501	GTP	C6-C5-C4	-4.13	116.82	120.79
5	D	501	GTP	C5-C6-N1	-4.07	117.81	123.47
5	C	501	GTP	N3-C2-N1	-3.98	121.86	127.25
11	F	401	ACP	N3-C2-N1	-3.59	122.89	128.68
5	A	501	GTP	C6-C5-C4	-3.58	117.34	120.79
5	A	501	GTP	PA-O3A-PB	-3.45	121.60	132.57
5	A	501	GTP	C4-C5-N7	-3.20	106.06	109.40
5	C	501	GTP	C4-C5-N7	-2.90	106.38	109.40
11	F	401	ACP	C4-C5-N7	-2.88	106.40	109.40
5	D	501	GTP	N3-C2-N1	-2.75	123.53	127.25
5	D	501	GTP	PA-O3A-PB	-2.69	124.02	132.57
5	A	501	GTP	N3-C2-N1	-2.64	123.68	127.25
5	C	501	GTP	C1'-N9-C4	-2.51	122.30	126.64
5	A	501	GTP	C1'-N9-C4	-2.42	122.45	126.64
9	B	505	MES	C7-N4-C5	-2.40	105.07	111.23
5	C	501	GTP	PB-O3B-PG	-2.37	125.03	132.57
5	D	501	GTP	PB-O3B-PG	-2.23	125.49	132.57
9	B	503	MES	O1-C6-C5	-2.16	107.06	111.78
8	B	501	GDP	C1'-N9-C4	-2.10	123.00	126.64
10	B	506	9LX	C24-C22-C21	-2.09	117.71	122.00
5	D	501	GTP	C4-C5-N7	-2.00	107.31	109.40
10	B	506	9LX	F23-C22-C21	2.16	122.23	118.54
9	B	505	MES	O2S-S-O1S	2.27	121.82	113.95
9	B	505	MES	C6-C5-N4	2.31	113.64	110.09
5	D	501	GTP	O3G-PG-O2G	2.37	116.78	107.57
8	B	501	GDP	O3B-PB-O2B	2.44	117.06	107.57
5	D	501	GTP	O3G-PG-O1G	2.49	120.35	110.53
9	B	503	MES	C6-C5-N4	2.72	114.25	110.09
9	B	503	MES	C5-N4-C3	2.74	114.90	108.86
9	B	505	MES	C2-C3-N4	2.96	114.63	110.09
5	D	501	GTP	C2-N3-C4	3.06	118.86	115.36
5	A	501	GTP	O3G-PG-O2G	3.11	119.66	107.57
5	A	501	GTP	C2-N3-C4	3.48	119.34	115.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
10	D	503	9LX	C01-O02-C03	3.65	125.52	117.51
5	C	501	GTP	C2-N3-C4	4.21	120.16	115.36
9	B	503	MES	C2-C3-N4	4.31	116.69	110.09
5	A	501	GTP	C6-N1-C2	4.37	122.28	116.06
8	B	501	GDP	C2-N3-C4	4.52	120.51	115.36
5	D	501	GTP	C6-N1-C2	4.52	122.50	116.06
5	C	501	GTP	C6-N1-C2	5.66	124.11	116.06
8	B	501	GDP	C6-N1-C2	5.78	124.30	116.06
9	B	505	MES	O2S-S-C8	8.17	116.75	106.92
9	B	503	MES	O1S-S-C8	9.26	118.06	106.92
9	B	503	MES	O2S-S-C8	9.73	118.63	106.92
9	B	505	MES	O1S-S-C8	10.22	119.22	106.92

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	B	503	MES	1	0
11	F	401	ACP	1	0

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, 95^{th} 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	437/450 (97%)	-0.21	2 (0%) 90 88	19, 39, 66, 81	0
1	C	440/450 (97%)	-0.35	0 100 100	13, 29, 55, 73	1 (0%)
2	B	424/445 (95%)	-0.24	5 (1%) 79 72	17, 36, 67, 89	1 (0%)
2	D	421/445 (94%)	0.24	23 (5%) 25 16	22, 55, 89, 113	4 (0%)
3	E	120/143 (83%)	0.26	2 (1%) 70 63	26, 54, 91, 120	0
4	F	309/384 (80%)	0.24	21 (6%) 17 10	27, 59, 100, 118	0
All	All	2151/2317 (92%)	-0.07	53 (2%) 57 47	13, 42, 81, 120	6 (0%)

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	F	233	PHE	5.4
2	B	55	THR	4.0
4	F	161	LEU	3.9
4	F	182	ILE	3.9
4	F	232	ASN	3.7
2	D	389	PHE	3.4
4	F	362	ALA	3.3
2	D	390	ARG	3.3
4	F	25	GLY	3.1
2	D	37	HIS	3.0
4	F	165	GLU	3.0
2	D	73	MET	2.9
2	D	112	LEU	2.9
2	D	115	SER	2.8
4	F	234	GLN	2.8
2	D	406	MET	2.7
2	B	57	ASN	2.7
4	F	361	LEU	2.6
4	F	163	SER	2.6

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Mol	Chain	Res	Type	RSRZ
2	D	95	SER	2.5
2	D	71	GLY	2.5
2	D	395	LEU	2.5
4	F	253	TYR	2.5
2	D	397	TRP	2.5
2	B	37	HIS	2.5
4	F	194	PRO	2.4
2	B	54	ALA	2.3
2	D	94	GLN	2.3
2	D	245	GLN	2.3
2	D	215	LEU	2.3
2	D	398	TYR	2.3
2	D	405	GLU	2.3
4	F	230	SER	2.2
4	F	231	ALA	2.2
4	F	26	GLN	2.2
4	F	254	GLY	2.2
4	F	24	THR	2.2
2	D	396	HIS	2.2
2	D	175	VAL	2.2
2	D	92	PHE	2.2
2	D	177	ASP	2.1
2	D	55	THR	2.1
2	D	391	ARG	2.1
4	F	101	TYR	2.1
3	E	138	GLU	2.1
4	F	147	TRP	2.1
4	F	149	ALA	2.1
3	E	25	LYS	2.1
2	B	427	ASP	2.1
4	F	239	HIS	2.0
2	D	216	LYS	2.0
1	A	279	GLU	2.0
1	A	346	TRP	2.0

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 carbohydrates 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, 95^{th} 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(Å^2)	Q<0.9
6	MG	B	502	1/1	0.82	0.35	37,37,37,37	0
11	ACP	F	401	31/31	0.84	0.29	76,86,136,142	0
7	CA	B	504	1/1	0.89	0.15	82,82,82,82	0
9	MES	B	505	12/12	0.92	0.25	66,72,81,81	0
9	MES	B	503	12/12	0.93	0.18	66,71,73,80	0
6	MG	D	502	1/1	0.93	0.11	42,42,42,42	0
7	CA	C	503	1/1	0.93	0.09	56,56,56,56	0
7	CA	A	503	1/1	0.94	0.05	62,62,62,62	0
10	9LX	D	503	27/27	0.94	0.18	40,52,56,58	0
5	GTP	D	501	32/32	0.95	0.13	39,45,50,58	0
10	9LX	B	506	27/27	0.96	0.17	28,29,33,34	0
8	GDP	B	501	28/28	0.97	0.15	17,22,25,28	0
6	MG	A	502	1/1	0.97	0.14	25,25,25,25	0
5	GTP	A	501	32/32	0.98	0.17	19,22,24,24	0
5	GTP	C	501	32/32	0.98	0.14	18,20,23,24	0
6	MG	C	502	1/1	0.98	0.12	17,17,17,17	0

6.5 Other polymers (i)

There are no such residues in this entry.