



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 06:36 AM GMT

PDB ID : 2XKB
Title : CRYSTAL STRUCTURE OF GDP-FORM PROTOFILAMENTS OF
BACILLUS THURINGIENSIS SEROVAR ISRAELENIS TUBZ
Authors : Aylett, C.H.S.; Lowe, J.
Deposited on : 2010-07-07
Resolution : 3.00 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

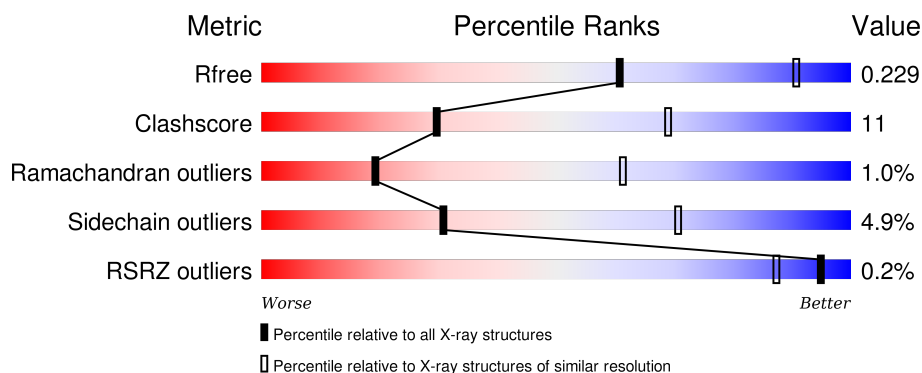
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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}	91344	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (3.00-3.00)

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 $\leq 5\%$. 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	427	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, green 62%, yellow 27%, orange 8%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 62% 27% • 8% </div> </div>
1	B	427	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 71%, yellow 22%, orange 5%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 71% 22% • 5% </div> </div>
1	C	427	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 68%, yellow 22%, orange 9%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 68% 22% • 9% </div> </div>
1	D	427	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 70%, yellow 20%, orange 8%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 70% 20% • 8% </div> </div>
1	E	427	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, green 71%, yellow 19%, orange 7%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 71% 19% • 7% </div> </div>

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Mol	Chain	Length	Quality of chain
1	F	427	 68% 21% • 8%
1	G	427	 70% 22% • 5%
1	H	427	 68% 22% • 8%
1	I	427	 67% 24% • 5%
1	J	427	 68% 22% • 8%
1	K	427	 69% 22% • 6%
1	L	427	 66% 22% • 11%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	MG	I	999	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 37877 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 FTSZ/TUBULIN-RELATED PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	391	Total	C	N	O	S	0	0	0
			3095	1952	526	604	13			
1	B	405	Total	C	N	O	S	0	0	0
			3209	2022	544	630	13			
1	C	389	Total	C	N	O	S	0	0	0
			3095	1949	532	601	13			
1	D	391	Total	C	N	O	S	0	0	0
			3094	1949	528	604	13			
1	E	395	Total	C	N	O	S	0	0	0
			3137	1976	534	614	13			
1	F	391	Total	C	N	O	S	0	0	0
			3095	1949	529	605	12			
1	G	404	Total	C	N	O	S	0	0	0
			3198	2016	543	626	13			
1	H	394	Total	C	N	O	S	0	0	0
			3143	1983	533	614	13			
1	I	404	Total	C	N	O	S	0	0	0
			3202	2018	543	628	13			
1	J	393	Total	C	N	O	S	0	0	0
			3114	1963	531	608	12			
1	K	400	Total	C	N	O	S	0	0	0
			3182	2003	545	622	12			
1	L	379	Total	C	N	O	S	0	0	0
			3001	1897	507	585	12			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	422	HIS	-	EXPRESSION TAG	UNP Q8KNP3
A	423	HIS	-	EXPRESSION TAG	UNP Q8KNP3
A	424	HIS	-	EXPRESSION TAG	UNP Q8KNP3
A	425	HIS	-	EXPRESSION TAG	UNP Q8KNP3
A	426	HIS	-	EXPRESSION TAG	UNP Q8KNP3

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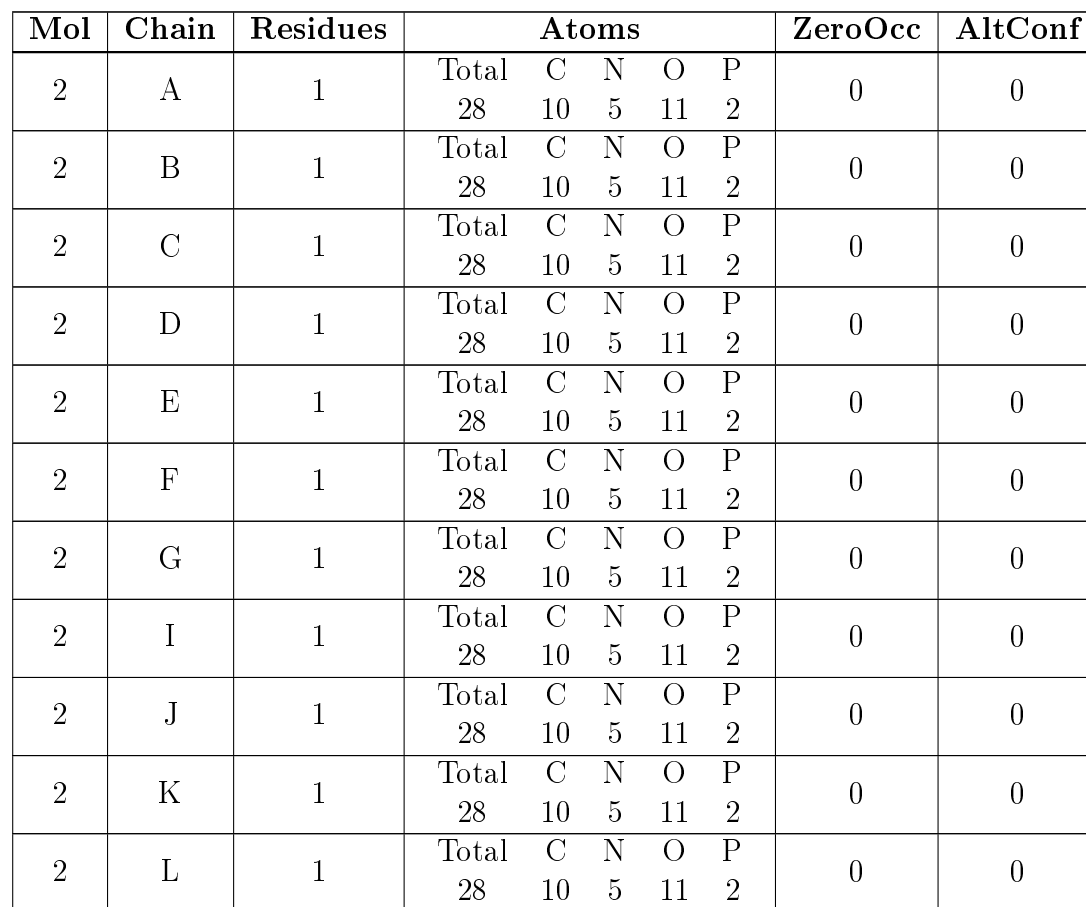
Chain	Residue	Modelled	Actual	Comment	Reference
A	427	HIS	-	EXPRESSION TAG	UNP Q8KNP3
A	2	VAL	LEU	ENGINEERED MUTATION	UNP Q8KNP3
B	422	HIS	-	EXPRESSION TAG	UNP Q8KNP3
B	423	HIS	-	EXPRESSION TAG	UNP Q8KNP3
B	424	HIS	-	EXPRESSION TAG	UNP Q8KNP3
B	425	HIS	-	EXPRESSION TAG	UNP Q8KNP3
B	426	HIS	-	EXPRESSION TAG	UNP Q8KNP3
B	427	HIS	-	EXPRESSION TAG	UNP Q8KNP3
B	2	VAL	LEU	ENGINEERED MUTATION	UNP Q8KNP3
C	422	HIS	-	EXPRESSION TAG	UNP Q8KNP3
C	423	HIS	-	EXPRESSION TAG	UNP Q8KNP3
C	424	HIS	-	EXPRESSION TAG	UNP Q8KNP3
C	425	HIS	-	EXPRESSION TAG	UNP Q8KNP3
C	426	HIS	-	EXPRESSION TAG	UNP Q8KNP3
C	427	HIS	-	EXPRESSION TAG	UNP Q8KNP3
C	2	VAL	LEU	ENGINEERED MUTATION	UNP Q8KNP3
D	422	HIS	-	EXPRESSION TAG	UNP Q8KNP3
D	423	HIS	-	EXPRESSION TAG	UNP Q8KNP3
D	424	HIS	-	EXPRESSION TAG	UNP Q8KNP3
D	425	HIS	-	EXPRESSION TAG	UNP Q8KNP3
D	426	HIS	-	EXPRESSION TAG	UNP Q8KNP3
D	427	HIS	-	EXPRESSION TAG	UNP Q8KNP3
D	2	VAL	LEU	ENGINEERED MUTATION	UNP Q8KNP3
E	422	HIS	-	EXPRESSION TAG	UNP Q8KNP3
E	423	HIS	-	EXPRESSION TAG	UNP Q8KNP3
E	424	HIS	-	EXPRESSION TAG	UNP Q8KNP3
E	425	HIS	-	EXPRESSION TAG	UNP Q8KNP3
E	426	HIS	-	EXPRESSION TAG	UNP Q8KNP3
E	427	HIS	-	EXPRESSION TAG	UNP Q8KNP3
E	2	VAL	LEU	ENGINEERED MUTATION	UNP Q8KNP3
F	422	HIS	-	EXPRESSION TAG	UNP Q8KNP3
F	423	HIS	-	EXPRESSION TAG	UNP Q8KNP3
F	424	HIS	-	EXPRESSION TAG	UNP Q8KNP3
F	425	HIS	-	EXPRESSION TAG	UNP Q8KNP3
F	426	HIS	-	EXPRESSION TAG	UNP Q8KNP3
F	427	HIS	-	EXPRESSION TAG	UNP Q8KNP3
F	2	VAL	LEU	ENGINEERED MUTATION	UNP Q8KNP3
G	422	HIS	-	EXPRESSION TAG	UNP Q8KNP3
G	423	HIS	-	EXPRESSION TAG	UNP Q8KNP3
G	424	HIS	-	EXPRESSION TAG	UNP Q8KNP3
G	425	HIS	-	EXPRESSION TAG	UNP Q8KNP3
G	426	HIS	-	EXPRESSION TAG	UNP Q8KNP3

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Chain	Residue	Modelled	Actual	Comment	Reference
G	427	HIS	-	EXPRESSION TAG	UNP Q8KNP3
G	2	VAL	LEU	ENGINEERED MUTATION	UNP Q8KNP3
H	422	HIS	-	EXPRESSION TAG	UNP Q8KNP3
H	423	HIS	-	EXPRESSION TAG	UNP Q8KNP3
H	424	HIS	-	EXPRESSION TAG	UNP Q8KNP3
H	425	HIS	-	EXPRESSION TAG	UNP Q8KNP3
H	426	HIS	-	EXPRESSION TAG	UNP Q8KNP3
H	427	HIS	-	EXPRESSION TAG	UNP Q8KNP3
H	2	VAL	LEU	ENGINEERED MUTATION	UNP Q8KNP3
I	422	HIS	-	EXPRESSION TAG	UNP Q8KNP3
I	423	HIS	-	EXPRESSION TAG	UNP Q8KNP3
I	424	HIS	-	EXPRESSION TAG	UNP Q8KNP3
I	425	HIS	-	EXPRESSION TAG	UNP Q8KNP3
I	426	HIS	-	EXPRESSION TAG	UNP Q8KNP3
I	427	HIS	-	EXPRESSION TAG	UNP Q8KNP3
I	2	VAL	LEU	ENGINEERED MUTATION	UNP Q8KNP3
J	422	HIS	-	EXPRESSION TAG	UNP Q8KNP3
J	423	HIS	-	EXPRESSION TAG	UNP Q8KNP3
J	424	HIS	-	EXPRESSION TAG	UNP Q8KNP3
J	425	HIS	-	EXPRESSION TAG	UNP Q8KNP3
J	426	HIS	-	EXPRESSION TAG	UNP Q8KNP3
J	427	HIS	-	EXPRESSION TAG	UNP Q8KNP3
J	2	VAL	LEU	ENGINEERED MUTATION	UNP Q8KNP3
K	422	HIS	-	EXPRESSION TAG	UNP Q8KNP3
K	423	HIS	-	EXPRESSION TAG	UNP Q8KNP3
K	424	HIS	-	EXPRESSION TAG	UNP Q8KNP3
K	425	HIS	-	EXPRESSION TAG	UNP Q8KNP3
K	426	HIS	-	EXPRESSION TAG	UNP Q8KNP3
K	427	HIS	-	EXPRESSION TAG	UNP Q8KNP3
K	2	VAL	LEU	ENGINEERED MUTATION	UNP Q8KNP3
L	422	HIS	-	EXPRESSION TAG	UNP Q8KNP3
L	423	HIS	-	EXPRESSION TAG	UNP Q8KNP3
L	424	HIS	-	EXPRESSION TAG	UNP Q8KNP3
L	425	HIS	-	EXPRESSION TAG	UNP Q8KNP3
L	426	HIS	-	EXPRESSION TAG	UNP Q8KNP3
L	427	HIS	-	EXPRESSION TAG	UNP Q8KNP3
L	2	VAL	LEU	ENGINEERED MUTATION	UNP Q8KNP3

- Molecule 2 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



- | Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|-----|-------|----------|-----------------|---------|---------|
| 3 | G | 1 | Total Mg
1 1 | 0 | 0 |

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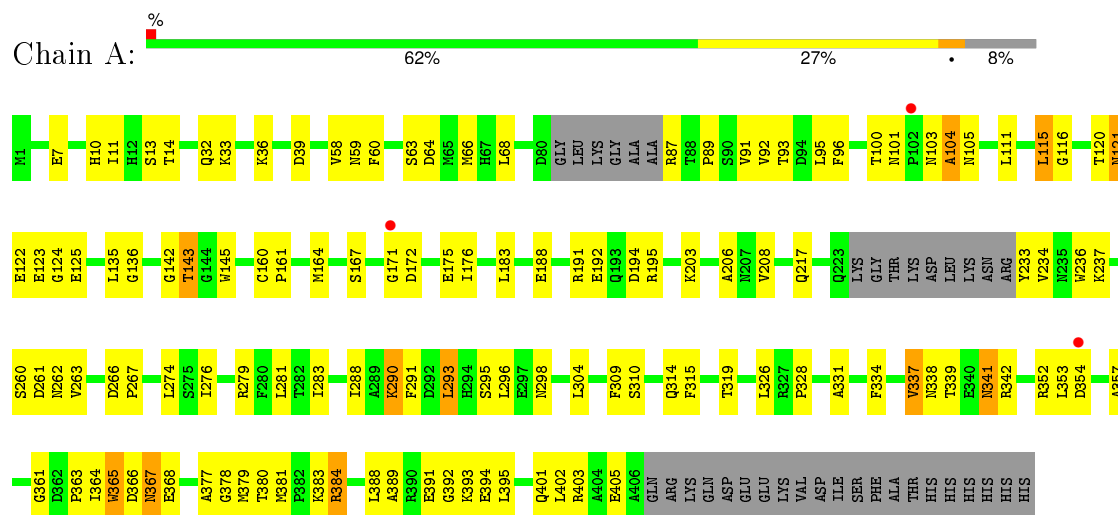
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total 1	Mg 1	0	0
3	A	1	Total 1	Mg 1	0	0
3	I	1	Total 1	Mg 1	0	0

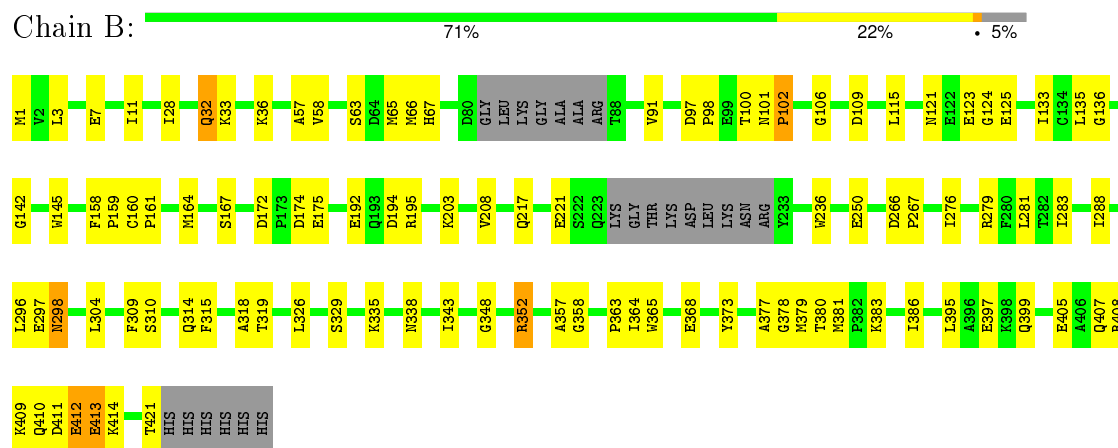
3 Residue-property plots

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.

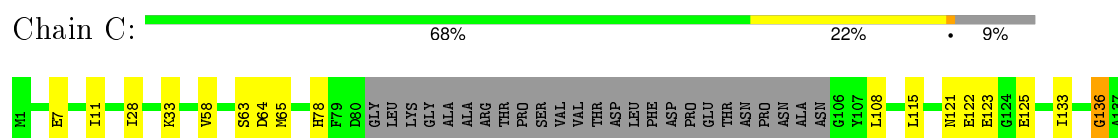
• Molecule 1: FTSZ/TUBULIN-RELATED PROTEIN

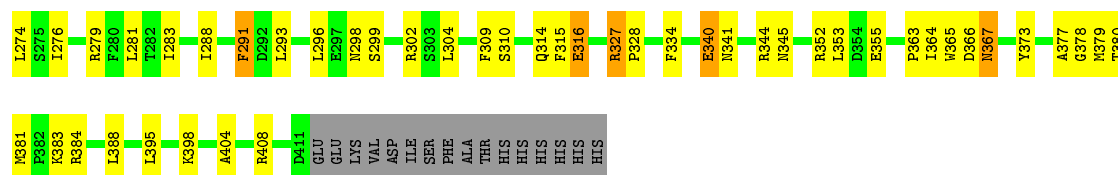


• Molecule 1: FTSZ/TUBULIN-RELATED PROTEIN



• Molecule 1: FTSZ/TUBULIN-RELATED PROTEIN





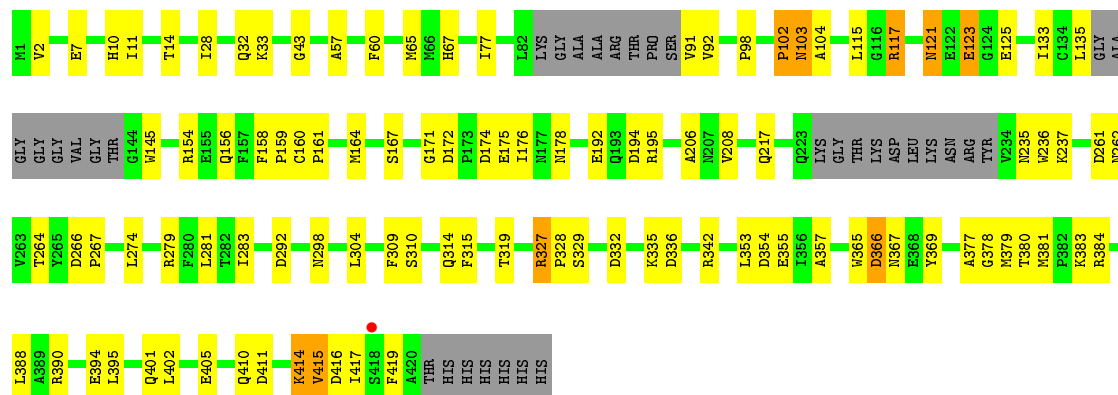
• Molecule 1: FTSZ/TUBULIN-RELATED PROTEIN

Chain G: 70% 22% 5%



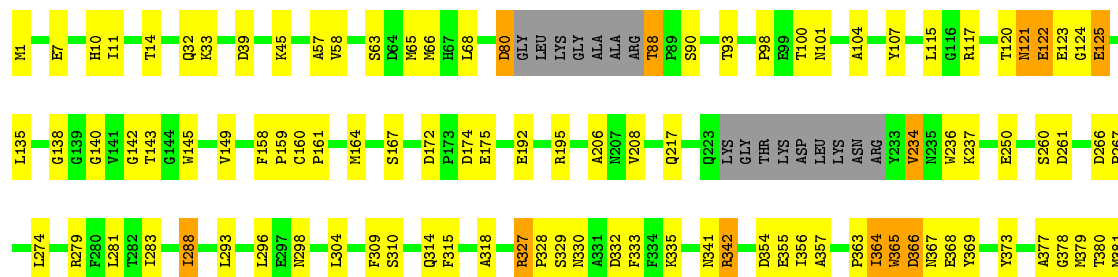
• Molecule 1: FTSZ/TUBULIN-RELATED PROTEIN

Chain H: 68% 22% 8%



• Molecule 1: FTSZ/TUBULIN-RELATED PROTEIN

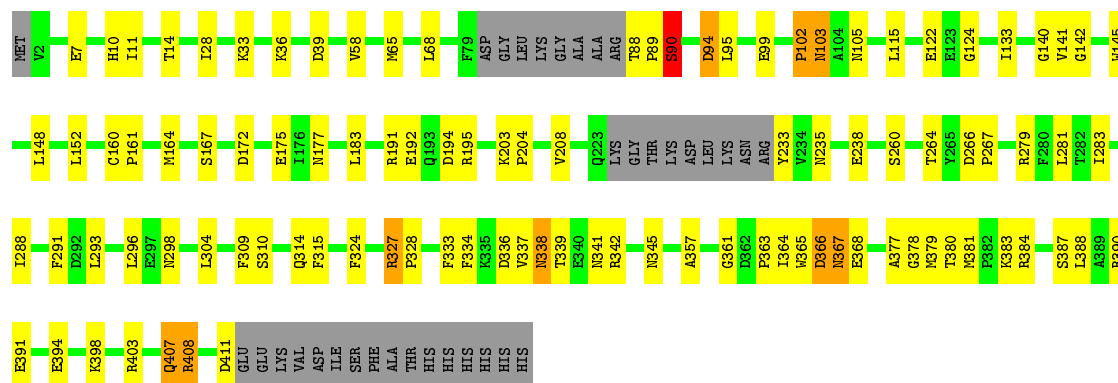
Chain I: 67% 24% 5%





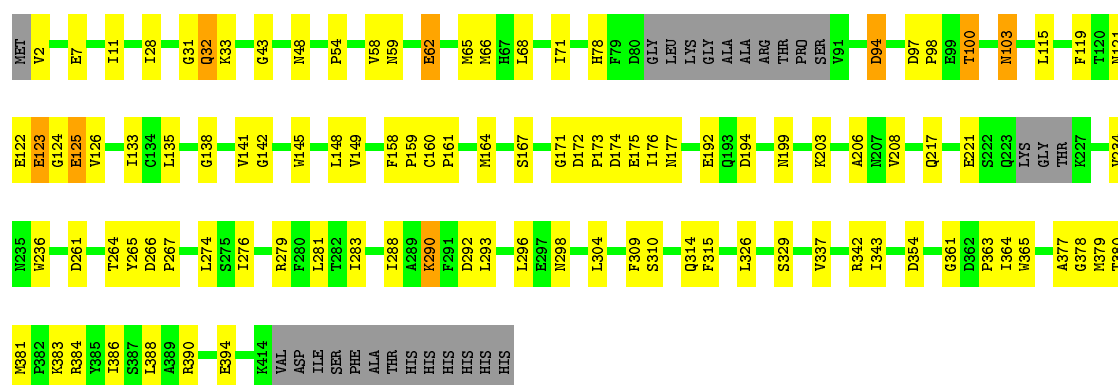
• Molecule 1: FTSZ/TUBULIN-RELATED PROTEIN

Chain J: 68% 22% 8%



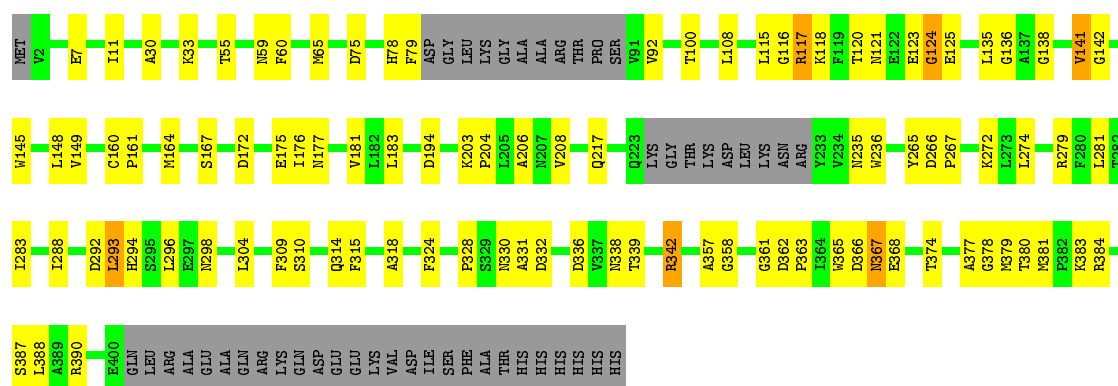
• Molecule 1: FTSZ/TUBULIN-RELATED PROTEIN

Chain K: 69% 22% 6%



• Molecule 1: FTSZ/TUBULIN-RELATED PROTEIN

Chain L: 66% 22% 11%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	52.95Å 541.10Å 86.13Å 90.00° 92.51° 90.00°	Depositor
Resolution (Å)	50.00 – 3.00 77.66 – 3.00	Depositor EDS
% Data completeness (in resolution range)	92.9 (50.00-3.00) 92.9 (77.66-3.00)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.44 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.234 , 0.294 0.231 , 0.229	Depositor DCC
R_{free} test set	4465 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	59.4	Xtriage
Anisotropy	0.870	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 38.7	EDS
Estimated twinning fraction	0.044 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 89209 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	37877	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.23% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: GDP, 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	0.49	0/3155	0.60	1/4268 (0.0%)
1	B	0.50	0/3270	0.60	0/4422
1	C	0.52	0/3152	0.61	1/4252 (0.0%)
1	D	0.57	3/3153 (0.1%)	0.72	5/4263 (0.1%)
1	E	0.48	0/3196	0.58	1/4319 (0.0%)
1	F	0.50	0/3154	0.64	2/4265 (0.0%)
1	G	0.53	0/3258	0.59	0/4405
1	H	0.52	0/3201	0.62	0/4325
1	I	0.50	0/3263	0.61	0/4412
1	J	0.52	0/3174	0.60	0/4293
1	K	0.50	0/3241	0.59	0/4378
1	L	0.50	0/3060	0.60	0/4140
All	All	0.51	3/38277 (0.0%)	0.61	10/51742 (0.0%)

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

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	154	ARG	CZ-NH1	11.48	1.48	1.33
1	D	154	ARG	NE-CZ	9.18	1.45	1.33
1	D	154	ARG	CD-NE	7.03	1.58	1.46

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	154	ARG	NE-CZ-NH1	-17.22	111.69	120.30
1	D	154	ARG	NH1-CZ-NH2	11.91	132.50	119.40
1	D	154	ARG	NE-CZ-NH2	-10.45	115.08	120.30
1	D	154	ARG	CD-NE-CZ	-10.31	109.17	123.60
1	F	316	GLU	CA-CB-CG	9.45	134.18	113.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	223	GLN	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	3095	0	3006	92	0
1	B	3209	0	3114	72	0
1	C	3095	0	3026	68	1
1	D	3094	0	3009	63	0
1	E	3137	0	3045	60	1
1	F	3095	0	3005	67	0
1	G	3198	0	3108	77	0
1	H	3143	0	3056	74	0
1	I	3202	0	3107	88	1
1	J	3114	0	3023	77	0
1	K	3182	0	3093	78	1
1	L	3001	0	2910	75	0
2	A	28	0	12	2	0
2	B	28	0	12	1	0
2	C	28	0	12	0	0
2	D	28	0	12	3	0
2	E	28	0	12	0	0
2	F	28	0	12	0	0
2	G	28	0	12	0	0
2	I	28	0	12	1	0
2	J	28	0	12	0	0
2	K	28	0	12	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	L	28	0	12	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	G	1	0	0	0	0
3	I	1	0	0	0	0
All	All	37877	0	36634	836	2

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 11.

The worst 5 of 836 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:L:117:ARG:HH11	1:L:117:ARG:HG2	1.04	1.12
1:H:117:ARG:HG2	1:H:117:ARG:HH11	1.14	1.10
1:D:176:ILE:HD12	1:D:388:LEU:HD11	1.34	1.09
1:D:141:VAL:O	1:D:145:TRP:HD1	1.37	1.07
1:H:10:HIS:HB3	1:H:367:ASN:ND2	1.70	1.05

All (2) 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:73:LYS:NZ	1:K:48:ASN:O[1_655]	1.73	0.47
1:C:232:ARG:NH2	1:I:124:GLY:O[1_655]	2.09	0.11

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	385/427 (90%)	355 (92%)	24 (6%)	6 (2%)	12 48

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	399/427 (93%)	371 (93%)	25 (6%)	3 (1%)	24	66
1	C	385/427 (90%)	357 (93%)	26 (7%)	2 (0%)	34	76
1	D	385/427 (90%)	356 (92%)	28 (7%)	1 (0%)	46	84
1	E	389/427 (91%)	364 (94%)	22 (6%)	3 (1%)	24	66
1	F	385/427 (90%)	347 (90%)	33 (9%)	5 (1%)	15	53
1	G	396/427 (93%)	356 (90%)	35 (9%)	5 (1%)	15	53
1	H	386/427 (90%)	349 (90%)	32 (8%)	5 (1%)	15	53
1	I	398/427 (93%)	365 (92%)	30 (8%)	3 (1%)	24	66
1	J	387/427 (91%)	353 (91%)	28 (7%)	6 (2%)	12	48
1	K	394/427 (92%)	368 (93%)	24 (6%)	2 (0%)	34	76
1	L	373/427 (87%)	342 (92%)	26 (7%)	5 (1%)	15	53
All	All	4662/5124 (91%)	4283 (92%)	333 (7%)	46 (1%)	19	61

5 of 46 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	121	ASN
1	B	102	PRO
1	B	413	GLU
1	E	60	PHE
1	F	121	ASN

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	339/369 (92%)	322 (95%)	17 (5%)	30	70
1	B	352/369 (95%)	337 (96%)	15 (4%)	35	75
1	C	337/369 (91%)	323 (96%)	14 (4%)	36	76
1	D	339/369 (92%)	325 (96%)	14 (4%)	37	76
1	E	343/369 (93%)	329 (96%)	14 (4%)	37	76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	339/369 (92%)	323 (95%)	16 (5%)	32	72
1	G	351/369 (95%)	334 (95%)	17 (5%)	31	71
1	H	346/369 (94%)	325 (94%)	21 (6%)	23	61
1	I	351/369 (95%)	329 (94%)	22 (6%)	22	60
1	J	341/369 (92%)	322 (94%)	19 (6%)	26	65
1	K	348/369 (94%)	329 (94%)	19 (6%)	27	65
1	L	329/369 (89%)	315 (96%)	14 (4%)	35	75
All	All	4115/4428 (93%)	3913 (95%)	202 (5%)	31	71

5 of 202 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	64	ASP
1	H	194	ASP
1	K	364	ILE
1	G	115	LEU
1	G	365	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 76 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	298	ASN
1	G	67	HIS
1	K	341	ASN
1	F	70	ASN
1	F	298	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 15 ligands modelled in this entry, 4 are monoatomic - leaving 11 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
2	GDP	A	900	3	23,30,30	1.14	2 (8%)	30,47,47	1.77	6 (20%)
2	GDP	B	900	3	23,30,30	1.37	2 (8%)	30,47,47	1.61	7 (23%)
2	GDP	C	900	-	23,30,30	1.25	2 (8%)	30,47,47	2.15	10 (33%)
2	GDP	D	900	-	23,30,30	1.24	3 (13%)	30,47,47	1.97	8 (26%)
2	GDP	E	900	-	23,30,30	1.34	3 (13%)	30,47,47	1.83	8 (26%)
2	GDP	F	900	-	23,30,30	1.22	2 (8%)	30,47,47	1.72	6 (20%)
2	GDP	G	900	3	23,30,30	1.22	3 (13%)	30,47,47	1.75	6 (20%)
2	GDP	I	900	3	23,30,30	1.34	2 (8%)	30,47,47	1.96	9 (30%)
2	GDP	J	900	-	23,30,30	1.33	3 (13%)	30,47,47	1.78	6 (20%)
2	GDP	K	900	-	23,30,30	1.34	3 (13%)	30,47,47	1.86	7 (23%)
2	GDP	L	900	-	23,30,30	1.62	5 (21%)	30,47,47	2.07	9 (30%)

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
2	GDP	A	900	3	-	0/12/32/32	0/3/3/3
2	GDP	B	900	3	-	0/12/32/32	0/3/3/3
2	GDP	C	900	-	-	0/12/32/32	0/3/3/3
2	GDP	D	900	-	-	0/12/32/32	0/3/3/3
2	GDP	E	900	-	-	0/12/32/32	0/3/3/3
2	GDP	F	900	-	-	0/12/32/32	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GDP	G	900	3	-	0/12/32/32	0/3/3/3
2	GDP	I	900	3	-	0/12/32/32	0/3/3/3
2	GDP	J	900	-	-	0/12/32/32	0/3/3/3
2	GDP	K	900	-	-	0/12/32/32	0/3/3/3
2	GDP	L	900	-	-	0/12/32/32	0/3/3/3

The worst 5 of 30 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	900	GDP	O4'-C1'	2.07	1.43	1.41
2	K	900	GDP	O4'-C1'	2.11	1.43	1.41
2	L	900	GDP	O4'-C1'	2.12	1.43	1.41
2	G	900	GDP	O4'-C1'	2.18	1.44	1.41
2	J	900	GDP	O4'-C1'	2.24	1.44	1.41

The worst 5 of 82 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	900	GDP	C2'-C1'-N9	-5.13	106.45	114.29
2	I	900	GDP	C5-C6-N1	-4.46	117.49	123.59
2	E	900	GDP	C5-C6-N1	-4.17	117.89	123.59
2	C	900	GDP	C6-C5-C4	-4.13	115.96	120.90
2	L	900	GDP	C6-C5-C4	-4.10	116.00	120.90

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	900	GDP	2	0
2	B	900	GDP	1	0
2	D	900	GDP	3	0
2	I	900	GDP	1	0
2	L	900	GDP	1	0

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	391/427 (91%)	-0.23	3 (0%) 87 67	35, 54, 77, 83	0
1	B	405/427 (94%)	-0.25	0 100 100	18, 53, 84, 92	0
1	C	389/427 (91%)	-0.28	0 100 100	35, 54, 68, 85	0
1	D	391/427 (91%)	-0.24	0 100 100	35, 56, 87, 95	0
1	E	395/427 (92%)	-0.24	2 (0%) 91 76	35, 54, 72, 103	0
1	F	391/427 (91%)	-0.23	1 (0%) 94 84	35, 55, 78, 87	0
1	G	404/427 (94%)	-0.07	1 (0%) 95 87	35, 56, 82, 88	0
1	H	394/427 (92%)	-0.23	1 (0%) 94 84	35, 53, 71, 82	0
1	I	404/427 (94%)	-0.21	0 100 100	35, 55, 91, 105	0
1	J	393/427 (92%)	-0.31	0 100 100	35, 55, 79, 108	0
1	K	400/427 (93%)	-0.30	0 100 100	35, 55, 75, 115	0
1	L	379/427 (88%)	-0.21	0 100 100	35, 55, 78, 104	0
All	All	4736/5124 (92%)	-0.23	8 (0%) 95 87	18, 55, 79, 115	0

The worst 5 of 8 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	418	SER	3.6
1	E	99	GLU	3.1
1	F	122	GLU	3.1
1	A	171	GLY	2.3
1	E	103	ASN	2.2

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 [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. 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	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	MG	I	999	1/1	0.99	0.28	3.20	17,17,17,17	0
2	GDP	D	900	28/28	0.90	0.26	1.34	107,110,111,111	0
2	GDP	L	900	28/28	0.84	0.23	1.18	110,112,115,115	0
2	GDP	F	900	28/28	0.90	0.27	1.05	107,107,110,110	0
3	MG	A	999	1/1	0.93	0.20	0.54	12,12,12,12	0
3	MG	B	999	1/1	0.95	0.17	0.15	13,13,13,13	0
3	MG	G	999	1/1	0.93	0.18	0.14	17,17,17,17	0
2	GDP	J	900	28/28	0.90	0.19	-0.30	89,91,92,93	0
2	GDP	K	900	28/28	0.94	0.18	-0.48	67,70,70,70	0
2	GDP	A	900	28/28	0.97	0.14	-0.74	47,49,50,51	0
2	GDP	B	900	28/28	0.96	0.14	-0.95	36,37,39,40	0
2	GDP	G	900	28/28	0.97	0.14	-1.09	35,39,44,44	0
2	GDP	C	900	28/28	0.95	0.16	-1.15	37,42,43,43	0
2	GDP	I	900	28/28	0.97	0.14	-1.43	26,30,34,34	0
2	GDP	E	900	28/28	0.96	0.13	-1.81	36,45,52,52	0

6.5 Other polymers [i](#)

There are no such residues in this entry.