



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 13, 2018 – 07:21 pm GMT

PDB ID : 3N2G
Title : TUBULIN-NSC 613863: RB3 Stathmin-like domain complex
Authors : Barbier, P.; Dorleans, A.; Devred, F.; Sanz, L.; Allegro, D.; Alfonso, C.;
Knossow, M.; Peyrot, V.; Andreu, J.M.
Deposited on : 2010-05-18
Resolution : 4.00 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

<https://www.wwpdb.org/validation/2017/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 : 1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix) : 1.13
EDS : trunk31020
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) : trunk31020

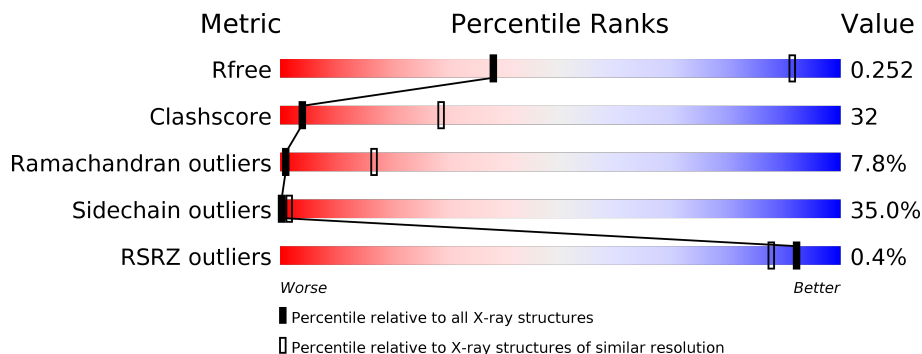
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.00 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}	111664	1008 (4.38-3.62)
Clashscore	122126	1012 (4.34-3.66)
Ramachandran outliers	120053	1000 (4.36-3.64)
Sidechain outliers	120020	1023 (4.38-3.62)
RSRZ outliers	108989	1107 (4.40-3.60)

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	451	<div> <div></div> <div>41% 37% 14% 5%</div> </div>
1	C	451	<div> <div></div> <div>45% 33% 14% 5%</div> </div>
2	B	445	<div> <div></div> <div>29% 43% 18% 6%</div> </div>
2	D	445	<div> <div>%</div> <div>27% 43% 22% . .</div> </div>
3	E	142	<div> <div>%</div> <div>36% 32% 17% . 13%</div> </div>

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
6	GDP	D	600	-	-	X	-
7	G2N	D	700	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 14220 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 chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	428	Total	C	N	O	S	0	0	0
			3300	2097	557	625	21			
1	C	429	Total	C	N	O	S	0	0	0
			3286	2084	554	627	21			

- Molecule 2 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	419	Total	C	N	O	S	0	0	0
			3246	2043	546	632	25			
2	D	427	Total	C	N	O	S	0	0	0
			3297	2071	559	643	24			

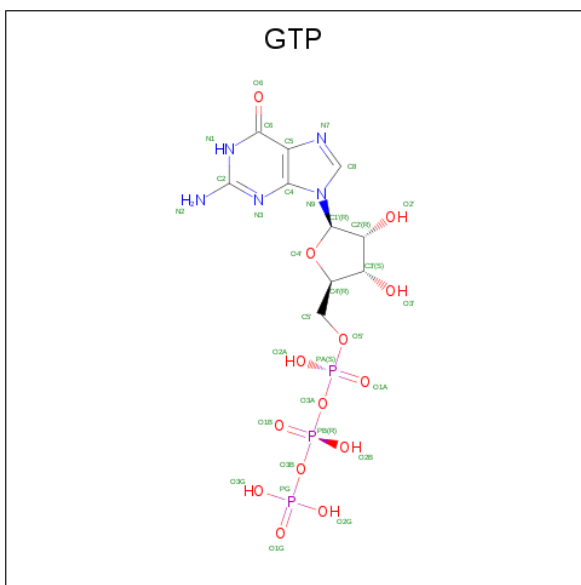
- Molecule 3 is a protein called Stathmin-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	123	Total	C	N	O	S	0	0	0
			920	557	174	184	5			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	4	ALA	-	EXPRESSION TAG	UNP P63043

- Molecule 4 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).

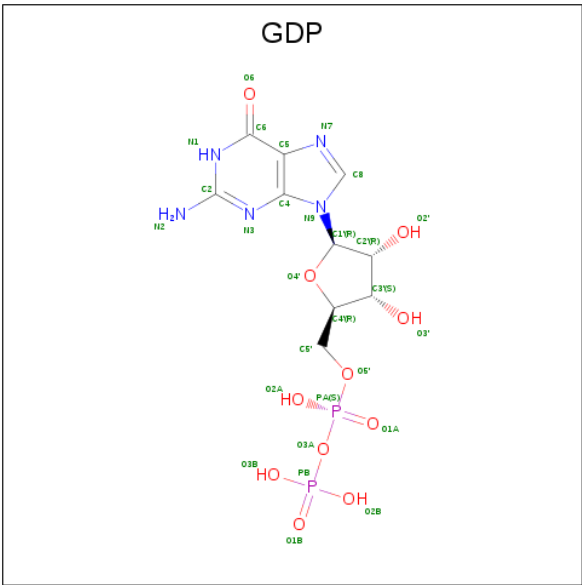


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	
			32	10	5	14	3	0
4	C	1	Total	C	N	O	P	
			32	10	5	14	3	0

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

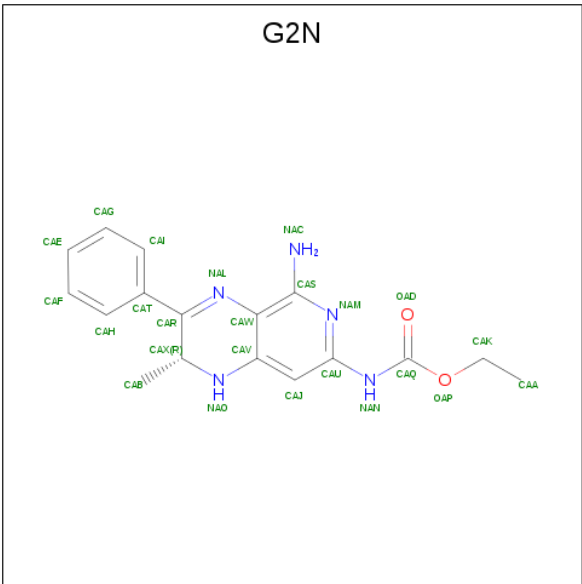
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Mg	0	0
			1	1		
5	A	1	Total	Mg	0	0
			1	1		
5	C	1	Total	Mg	0	0
			1	1		

- Molecule 6 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



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

- Molecule 7 is ethyl [(2R)-5-amino-2-methyl-3-phenyl-1,2-dihydropyrido[3,4-b]pyrazin-7-yl]carbamate (three-letter code: G2N) (formula: C₁₇H₁₉N₅O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	B	1	Total	C	N	O	0	0
			24	17	5	2		

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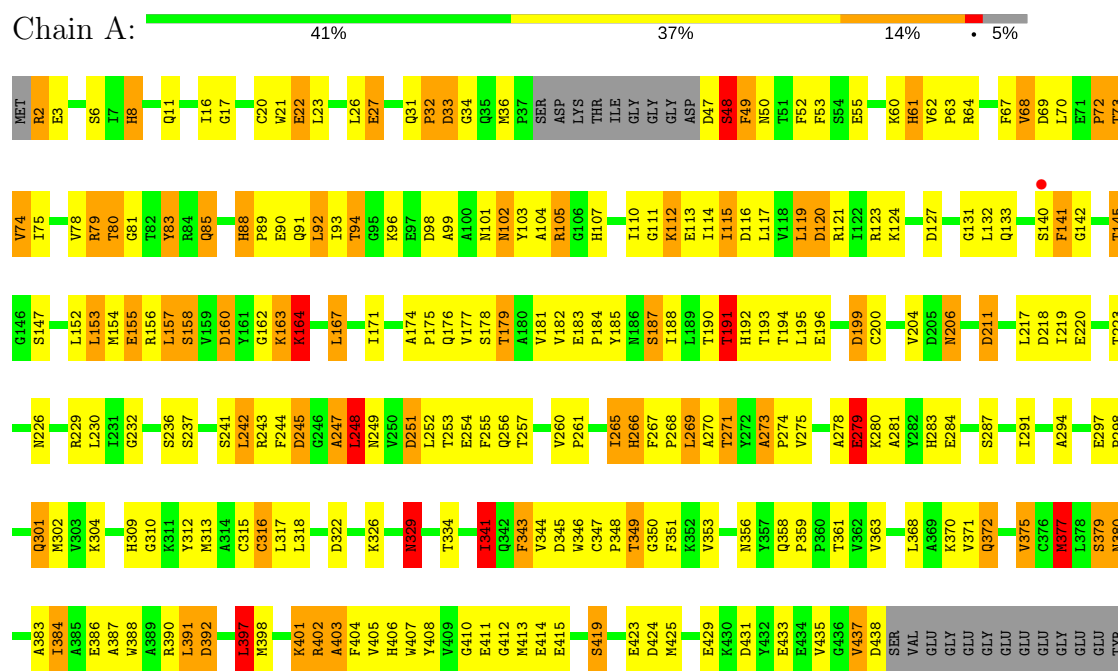
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	D	1	Total	C	N	O	0	0
			24	17	5	2		

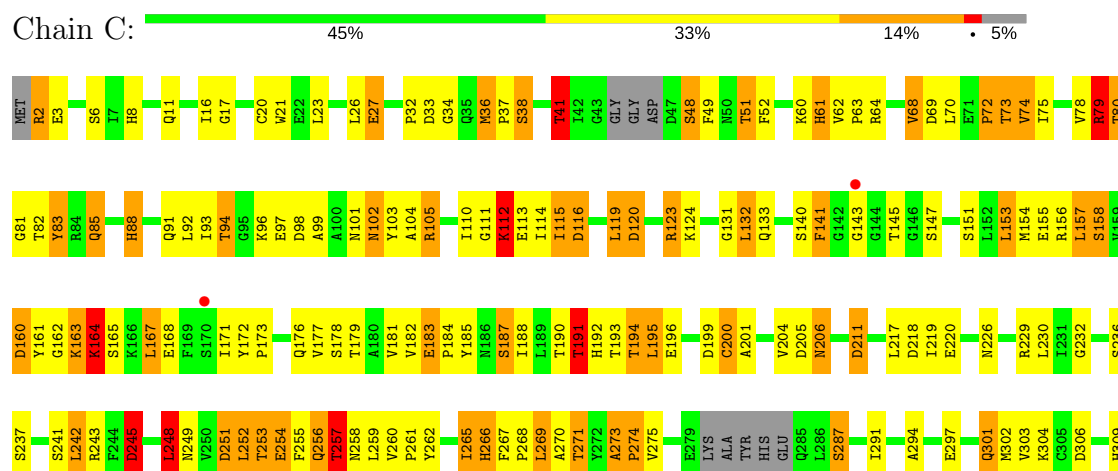
3 Residue-property plots

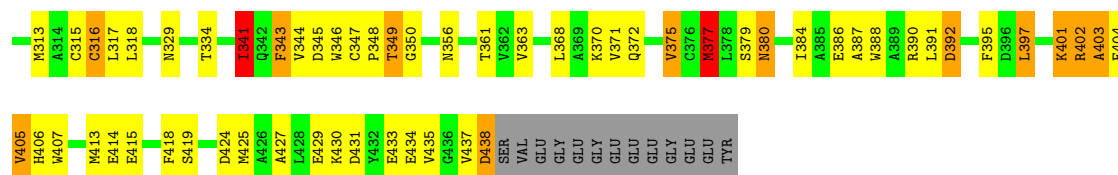
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Tubulin alpha chain



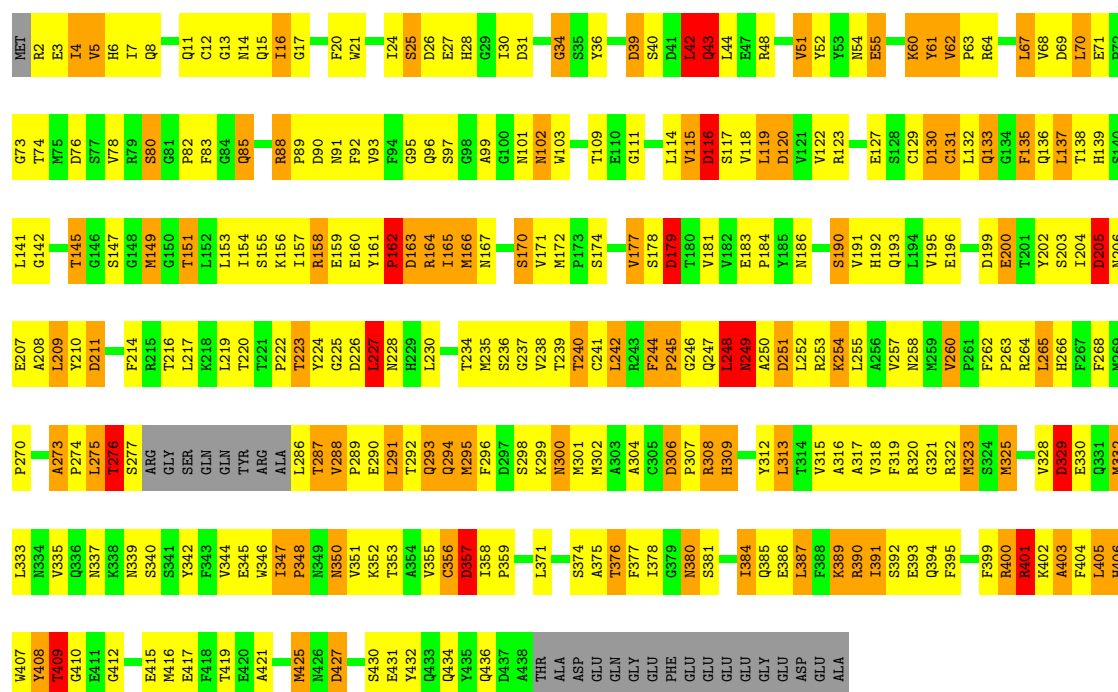
• Molecule 1: Tubulin alpha chain





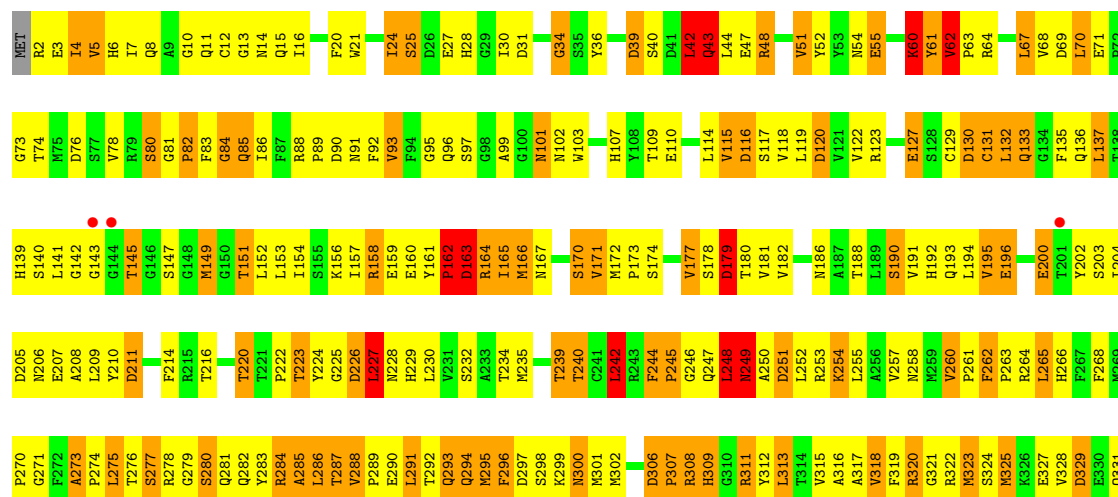
• Molecule 2: Tubulin beta chain

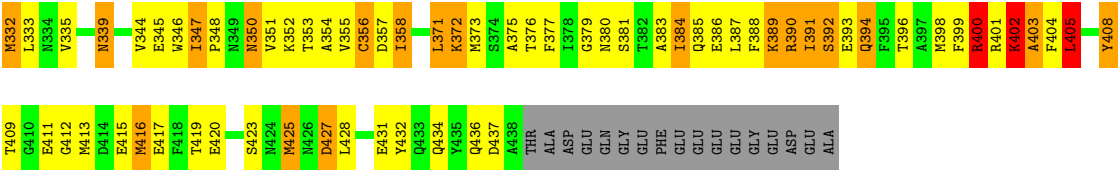
Chain B: 29% 43% 18% 6%



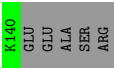
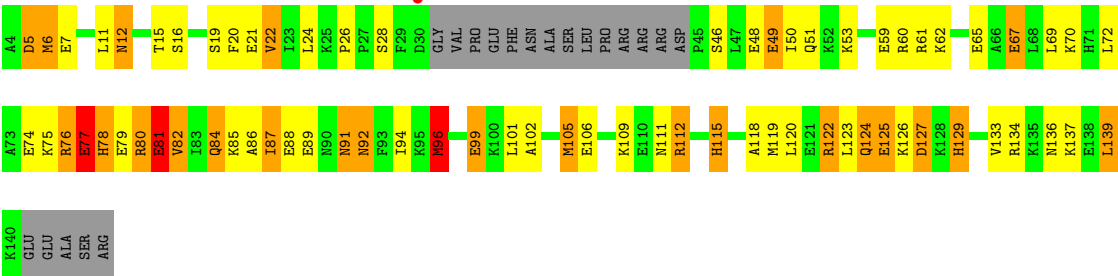
• Molecule 2: Tubulin beta chain

Chain D: 27% 43% 22%





● Molecule 3: Stathmin-4



4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	328.55Å 328.55Å 54.74Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 4.00 29.83 – 4.00	Depositor EDS
% Data completeness (in resolution range)	98.5 (20.00-4.00) 98.3 (29.83-4.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.59 (at 3.98Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.209 , 0.241 0.238 , 0.252	Depositor DCC
R_{free} test set	1472 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	168.5	Xtriage
Anisotropy	0.192	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 173.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.038 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	14220	wwPDB-VP
Average B, all atoms (Å ²)	79.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.96% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GDP, GTP, MG, G2N

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	0.79	0/3377	0.98	18/4593 (0.4%)
1	C	0.69	0/3360	0.94	15/4572 (0.3%)
2	B	0.78	0/3318	0.98	16/4505 (0.4%)
2	D	0.73	1/3370 (0.0%)	0.96	14/4574 (0.3%)
3	E	0.79	1/928 (0.1%)	0.90	2/1243 (0.2%)
All	All	0.75	2/14353 (0.0%)	0.96	65/19487 (0.3%)

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	2
2	B	0	3
2	D	0	4
3	E	0	1
All	All	0	10

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	127	GLU	CD-OE2	5.89	1.32	1.25
3	E	96	MET	SD-CE	5.26	2.07	1.77

The worst 5 of 65 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	427	ASP	CB-CG-OD2	8.53	125.98	118.30
1	A	397	LEU	CA-CB-CG	8.00	133.71	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	69	ASP	CB-CG-OD2	7.82	125.34	118.30
1	C	397	LEU	CA-CB-CG	7.41	132.34	115.30
1	C	160	ASP	CB-CG-OD2	7.33	124.89	118.30

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	162	PRO	Peptide
2	B	248	LEU	Peptide
2	B	249	ASN	Peptide
1	C	266	HIS	Peptide
1	C	41	THR	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	3300	0	3162	166	0
1	C	3286	0	3133	164	0
2	B	3246	0	3072	255	0
2	D	3297	0	3116	285	0
3	E	920	0	816	56	0
4	A	32	0	12	3	0
4	C	32	0	12	4	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
6	B	28	0	12	8	0
6	D	28	0	12	15	0
7	B	24	0	19	7	0
7	D	24	0	19	11	0
All	All	14220	0	13385	890	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 32.

The worst 5 of 890 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:B:325:MET:SD	2:B:325:MET:CE	2.04	1.45
3:E:105:MET:SD	3:E:105:MET:CE	2.04	1.43
3:E:96:MET:CE	3:E:96:MET:SD	2.07	1.42
2:B:308:ARG:HH11	2:B:308:ARG:HG3	1.09	1.17
2:B:273:ALA:HB3	2:B:274:PRO:HD3	1.16	1.14

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	424/451 (94%)	330 (78%)	68 (16%)	26 (6%)	1	22
1	C	423/451 (94%)	337 (80%)	61 (14%)	25 (6%)	2	23
2	B	415/445 (93%)	301 (72%)	80 (19%)	34 (8%)	1	15
2	D	425/445 (96%)	298 (70%)	85 (20%)	42 (10%)	1	11
3	E	119/142 (84%)	81 (68%)	24 (20%)	14 (12%)	0	7
All	All	1806/1934 (93%)	1347 (75%)	318 (18%)	141 (8%)	1	17

5 of 141 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	48	SER
1	A	72	PRO
1	A	73	THR
1	A	112	LYS
1	A	265	ILE

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	346/378 (92%)	236 (68%)	110 (32%)	0	2
1	C	344/378 (91%)	234 (68%)	110 (32%)	0	2
2	B	350/383 (91%)	228 (65%)	122 (35%)	0	1
2	D	353/383 (92%)	218 (62%)	135 (38%)	0	1
3	E	82/126 (65%)	43 (52%)	39 (48%)	0	0
All	All	1475/1648 (90%)	959 (65%)	516 (35%)	0	1

5 of 516 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	11	GLN
1	C	200	CYS
2	D	436	GLN
1	C	41	THR
1	C	116	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 69 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	350	ASN
1	C	102	ASN
2	D	385	GLN
2	B	380	ASN
1	C	50	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 9 ligands modelled in this entry, 3 are monoatomic - leaving 6 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$
4	GTP	A	600	5	27,34,34	0.94	2 (7%)	29,54,54	1.95	8 (27%)
6	GDP	B	600	-	25,30,30	1.09	1 (4%)	27,47,47	1.84	6 (22%)
7	G2N	B	700	-	25,26,26	1.95	3 (12%)	26,36,36	3.55	13 (50%)
4	GTP	C	600	5	27,34,34	1.03	3 (11%)	29,54,54	2.38	9 (31%)
6	GDP	D	600	-	25,30,30	1.09	2 (8%)	27,47,47	2.26	6 (22%)
7	G2N	D	700	-	25,26,26	1.90	3 (12%)	26,36,36	2.97	11 (42%)

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
4	GTP	A	600	5	-	0/18/38/38	0/3/3/3
6	GDP	B	600	-	-	0/12/32/32	0/3/3/3
7	G2N	B	700	-	-	0/11/23/23	0/3/3/3
4	GTP	C	600	5	-	0/18/38/38	0/3/3/3
6	GDP	D	600	-	-	0/12/32/32	0/3/3/3
7	G2N	D	700	-	-	0/11/23/23	0/3/3/3

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	700	G2N	CAT-CAR	-7.07	1.37	1.48
7	D	700	G2N	CAT-CAR	-5.37	1.40	1.48
7	B	700	G2N	CAU-NAN	-4.11	1.31	1.40
7	B	700	G2N	CAW-NAL	-3.43	1.30	1.38
4	C	600	GTP	O4'-C4'	-2.43	1.39	1.45

The worst 5 of 53 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	700	G2N	CAT-CAR-NAL	-9.85	105.60	118.13
4	C	600	GTP	N3-C2-N1	-6.68	117.61	127.41
6	D	600	GDP	N3-C2-N1	-6.39	118.05	127.41
7	B	700	G2N	CAH-CAT-CAR	-6.14	113.55	120.76
4	C	600	GTP	PB-O3B-PG	-5.44	114.36	132.63

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 48 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	600	GTP	3	0
6	B	600	GDP	8	0
7	B	700	G2N	7	0
4	C	600	GTP	4	0
6	D	600	GDP	15	0
7	D	700	G2N	11	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 [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	428/451 (94%)	-0.42	1 (0%) 94 93	78, 79, 80, 82	0
1	C	429/451 (95%)	-0.28	2 (0%) 90 85	79, 80, 80, 85	0
2	B	419/445 (94%)	-0.36	0 100 100	74, 79, 81, 86	0
2	D	427/445 (95%)	-0.27	3 (0%) 87 81	78, 80, 81, 83	0
3	E	123/142 (86%)	-0.29	1 (0%) 86 79	75, 80, 82, 84	0
All	All	1826/1934 (94%)	-0.33	7 (0%) 92 87	74, 80, 81, 86	0

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	143	GLY	3.3
2	D	201	THR	2.7
1	C	143	GLY	2.3
2	D	144	GLY	2.2
3	E	30	ASP	2.2

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, 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(Å ²)	Q<0.9
7	G2N	D	700	24/24	0.83	0.38	85,88,91,91	0
5	MG	B	601	1/1	0.86	0.66	81,81,81,81	0
6	GDP	D	600	28/28	0.88	0.25	77,78,80,80	0
4	GTP	C	600	32/32	0.91	0.20	72,75,76,77	0
6	GDP	B	600	28/28	0.92	0.19	76,80,81,81	0
7	G2N	B	700	24/24	0.92	0.27	75,78,79,82	0
4	GTP	A	600	32/32	0.94	0.15	71,75,76,76	0
5	MG	C	601	1/1	0.97	0.09	67,67,67,67	0
5	MG	A	601	1/1	0.98	0.12	46,46,46,46	0

6.5 Other polymers [i](#)

There are no such residues in this entry.