



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 07:13 PM GMT

PDB ID : 4O4H
Title : Tubulin-Laulimalide complex
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Deposited on : 2013-12-18
Resolution : 2.10 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

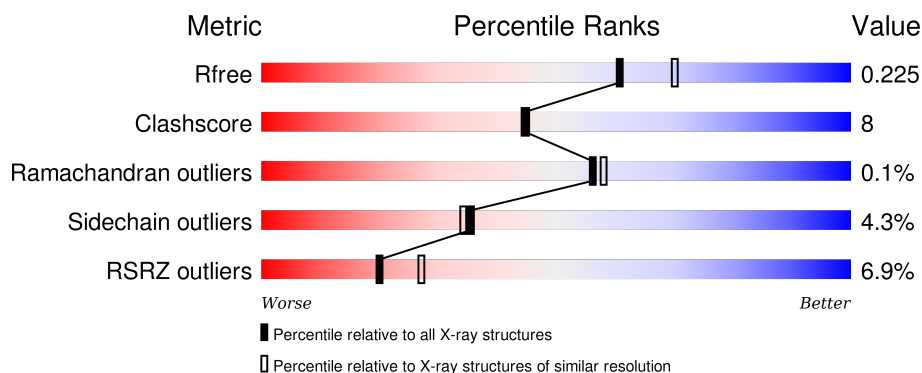
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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>2%</div> <div>82%</div> <div>14%</div> <div>••</div> </div>
1	C	451	<div> <div>%</div> <div>85%</div> <div>12%</div> <div>••</div> </div>
2	B	445	<div> <div>%</div> <div>80%</div> <div>15%</div> <div>••</div> </div>
2	D	445	<div> <div>4%</div> <div>78%</div> <div>16%</div> <div>••</div> </div>
3	E	143	<div> <div>3%</div> <div>78%</div> <div>7%</div> <div>• 14%</div> </div>

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Mol	Chain	Length	Quality of chain
4	F	384	

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
10	GOL	B	504	-	-	X	X
10	GOL	D	503	-	-	-	X
7	CA	A	503	-	-	-	X
9	LLM	B	503	-	-	-	X

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 18548 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	439	Total	C	N	O	S	0	12	0
			3481	2214	584	658	25			
1	C	440	Total	C	N	O	S	0	19	0
			3519	2235	586	672	26			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	426	Total	C	N	O	S	0	10	0
			3397	2137	573	660	27			
2	D	427	Total	C	N	O	S	0	6	0
			3370	2117	571	653	29			

- Molecule 3 is a protein called Stathmin-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	123	Total	C	N	O	S	0	5	0
			1039	642	187	205	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	3	MET	ILE	CLONING ARTIFACT	UNP P63043
E	4	ALA	SER	CLONING ARTIFACT	UNP P63043

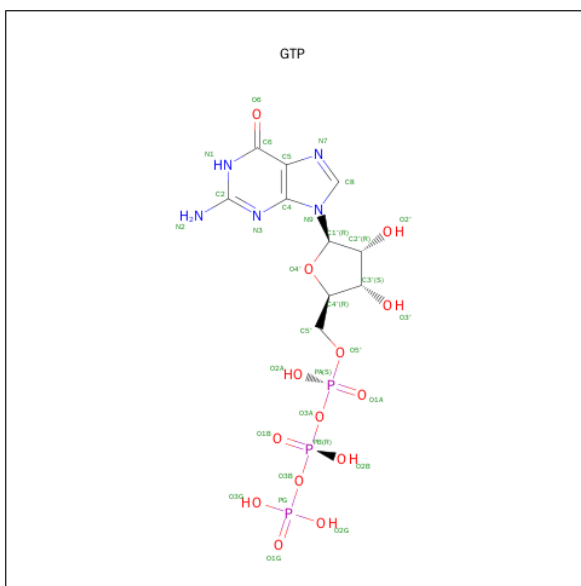
- Molecule 4 is a protein called Tubulin-tyrosine ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	348	Total	C	N	O	S	0	6	0
			2878	1852	487	525	14			

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		

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

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

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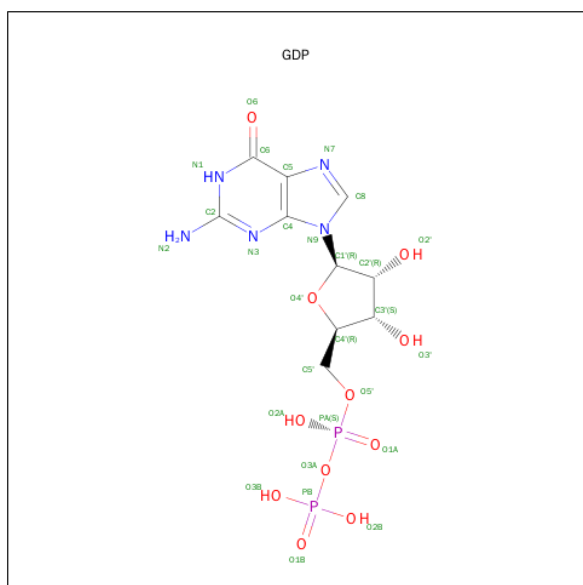
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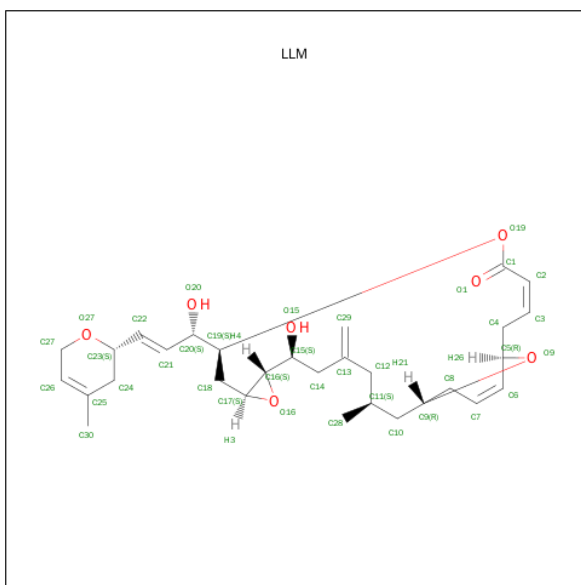
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	F	1	Total	Mg	0	0
			1	1		

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	2	Total	Ca	0	0
			2	2		
7	A	1	Total	Ca	0	0
			1	1		

- Molecule 8 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	B	1	Total	C	O	0	0
			37	30	7		

- Molecule 10 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).

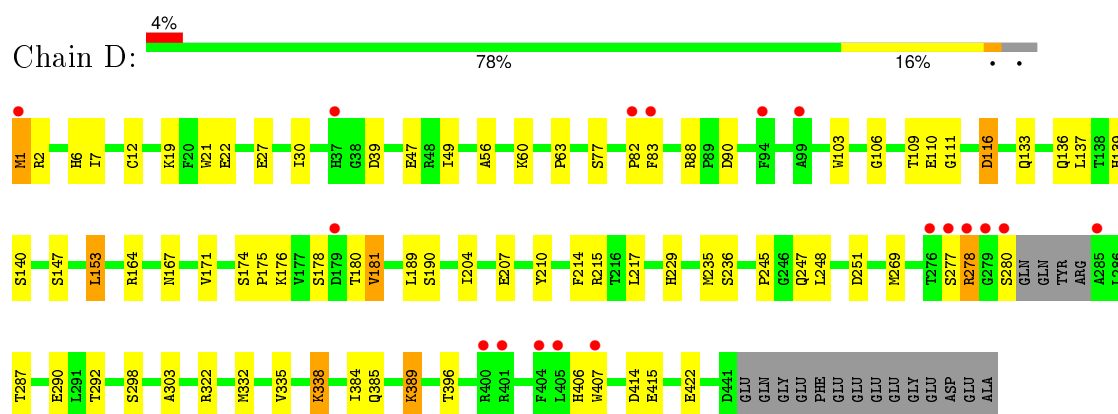


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	B	1	Total	C	O	0	0
			6	3	3		
10	D	1	Total	C	O	0	0
			6	3	3		

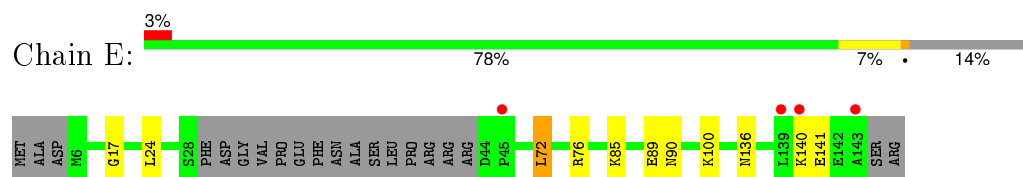
- Molecule 11 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (three-

- Molecule 12 is water.

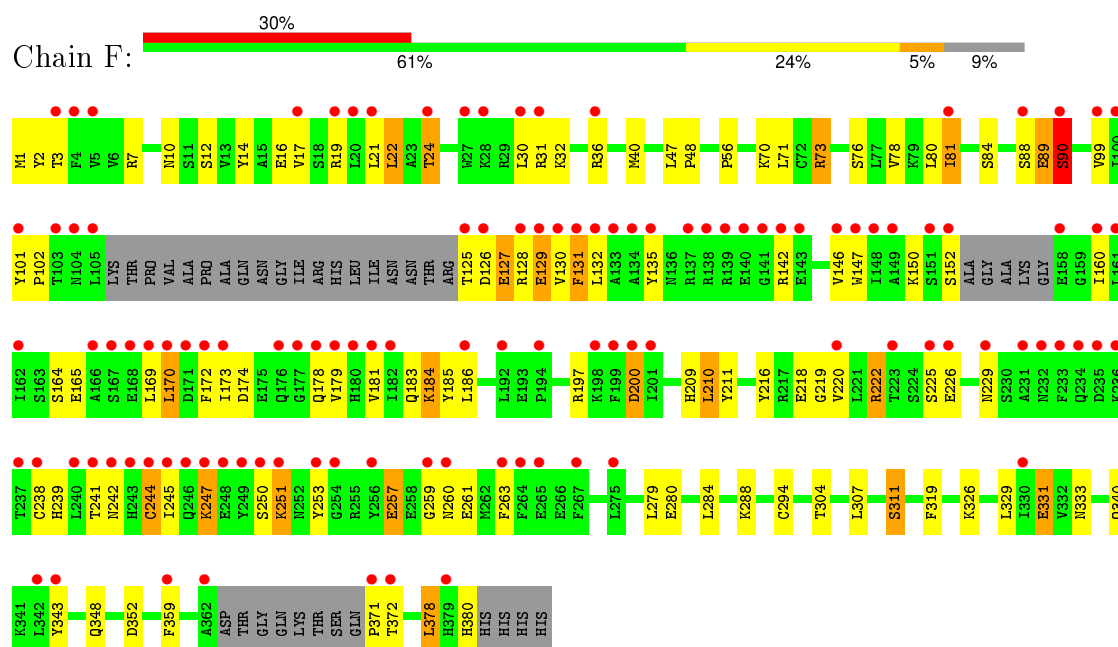




• Molecule 3: Stathmin-4



• Molecule 4: Tubulin-tyrosine ligase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	104.69Å 156.87Å 180.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	71.90 – 2.10 78.43 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (71.90-2.10) 99.8 (78.43-2.10)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.62 (at 2.10Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.192 , 0.224 0.198 , 0.225	Depositor DCC
R_{free} test set	8659 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	33.4	Xtriage
Anisotropy	0.217	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 58.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 172824 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	18548	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.51% 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, GOL, MG, CA, GTP, ACP, LLM

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	0.31	1/3596 (0.0%)	0.51	1/4883 (0.0%)
1	C	0.33	0/3655	0.52	0/4965
2	B	0.31	0/3498	0.50	0/4738
2	D	0.31	0/3461	0.52	1/4689 (0.0%)
3	E	0.30	0/1063	0.42	0/1412
4	F	0.38	1/2961 (0.0%)	0.49	0/4002
All	All	0.33	2/18234 (0.0%)	0.50	2/24689 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	90	SER	CB-OG	-12.87	1.25	1.42
1	A	89	PRO	N-CD	5.28	1.55	1.47

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	338	LYS	CD-CE-NZ	-12.12	83.83	111.70
1	A	88	HIS	C-N-CD	5.62	140.19	128.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	3481	0	3437	51	2
1	C	3519	0	3469	41	0
2	B	3397	0	3291	47	0
2	D	3370	0	3265	44	1
3	E	1039	0	1062	10	0
4	F	2878	0	2872	83	3
5	A	32	0	12	0	0
5	C	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
6	F	1	0	0	0	0
7	A	1	0	0	0	0
7	B	2	0	0	0	0
8	B	28	0	12	0	0
8	D	28	0	12	0	0
9	B	37	0	42	7	0
10	B	6	0	8	5	0
10	D	6	0	8	0	0
11	F	31	0	14	6	0
12	A	110	0	0	6	0
12	B	142	0	0	6	0
12	C	231	0	0	5	0
12	D	102	0	0	6	0
12	E	31	0	0	0	0
12	F	40	0	0	3	0
All	All	18548	0	17516	278	3

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 8.

The worst 5 of 278 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)
9:B:503:LLM:H11	9:B:503:LLM:H18	1.29	1.14
1:A:88:HIS:CD2	1:A:90:GLU:HB2	1.99	0.96
4:F:19:ARG:HA	4:F:22:LEU:HD12	1.53	0.90
1:A:88:HIS:CD2	1:A:90:GLU:H	1.90	0.88
2:B:282:GLN:HG2	2:B:283:TYR:H	1.43	0.84

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the sym-

metry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:HIS:CE1	4:F:142:ARG:NH2[2_564]	1.14	1.06
1:A:88:HIS:ND1	4:F:142:ARG:NH2[2_564]	1.95	0.25
2:D:338:LYS:NZ	4:F:90:SER:OG[3_545]	2.05	0.15

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	449/451 (100%)	440 (98%)	9 (2%)	0	100	100
1	C	457/451 (101%)	447 (98%)	10 (2%)	0	100	100
2	B	432/445 (97%)	417 (96%)	14 (3%)	1 (0%)	52	53
2	D	429/445 (96%)	410 (96%)	18 (4%)	1 (0%)	52	53
3	E	124/143 (87%)	123 (99%)	1 (1%)	0	100	100
4	F	346/384 (90%)	327 (94%)	19 (6%)	0	100	100
All	All	2237/2319 (96%)	2164 (97%)	71 (3%)	2 (0%)	56	58

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	283	TYR
2	D	181	VAL

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	382/379 (101%)	372 (97%)	10 (3%)	54	58
1	C	390/379 (103%)	380 (97%)	10 (3%)	54	58
2	B	378/383 (99%)	365 (97%)	13 (3%)	44	45
2	D	374/383 (98%)	359 (96%)	15 (4%)	38	38
3	E	115/127 (91%)	113 (98%)	2 (2%)	68	74
4	F	320/342 (94%)	286 (89%)	34 (11%)	8	5
All	All	1959/1993 (98%)	1875 (96%)	84 (4%)	35	34

5 of 84 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	139	HIS
2	D	415	GLU
4	F	260	ASN
2	D	247	GLN
2	D	280	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	136	GLN
4	F	178	GLN
4	F	348	GLN

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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 16 ligands modelled in this entry, 8 are monoatomic - leaving 8 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	25,34,34	0.85	1 (4%)	34,54,54	1.65	6 (17%)
8	GDP	B	501	6	23,30,30	1.15	3 (13%)	30,47,47	1.81	6 (20%)
9	LLM	B	503	-	37,40,40	2.29	12 (32%)	33,55,55	1.98	7 (21%)
10	GOL	B	504	-	5,5,5	0.39	0	5,5,5	0.39	0
5	GTP	C	501	6	25,34,34	0.98	2 (8%)	34,54,54	1.63	6 (17%)
8	GDP	D	501	6	23,30,30	1.17	2 (8%)	30,47,47	1.80	6 (20%)
10	GOL	D	503	-	5,5,5	0.40	0	5,5,5	0.37	0
11	ACP	F	401	-	25,33,33	2.35	10 (40%)	31,52,52	5.03	14 (45%)

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	LLM	B	503	-	-	0/39/64/64	0/1/4/4
10	GOL	B	504	-	-	0/4/4/4	0/0/0/0
5	GTP	C	501	6	-	0/18/38/38	0/3/3/3
8	GDP	D	501	6	-	0/12/32/32	0/3/3/3
10	GOL	D	503	-	-	0/4/4/4	0/0/0/0
11	ACP	F	401	-	-	0/15/38/38	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)
9	B	503	LLM	C30-C25	-5.14	1.38	1.50
9	B	503	LLM	C5-C6	-5.02	1.40	1.50
9	B	503	LLM	C2-C1	-3.79	1.39	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	B	503	LLM	C8-C7	-3.65	1.41	1.49
9	B	503	LLM	C27-C26	-3.43	1.40	1.48

The worst 5 of 45 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	F	401	ACP	N3-C2-N1	-14.32	117.93	128.89
11	F	401	ACP	C1'-N9-C4	-10.34	111.34	126.94
11	F	401	ACP	O4'-C4'-C3'	-10.26	84.48	105.15
9	B	503	LLM	C23-C22-C21	-7.27	113.00	125.55
11	F	401	ACP	C5'-C4'-C3'	-5.79	92.23	115.21

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 18 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	B	503	LLM	7	0
10	B	504	GOL	5	0
11	F	401	ACP	6	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, 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	439/451 (97%)	0.22	9 (2%) 67 72	26, 44, 80, 131	0
1	C	440/451 (97%)	0.33	3 (0%) 89 91	22, 34, 58, 99	0
2	B	426/445 (95%)	0.32	5 (1%) 81 85	25, 41, 72, 126	2 (0%)
2	D	427/445 (95%)	0.47	18 (4%) 40 49	28, 47, 78, 123	6 (1%)
3	E	123/143 (86%)	0.64	4 (3%) 50 59	34, 56, 93, 139	0
4	F	348/384 (90%)	1.60	114 (32%) 0 1	34, 69, 131, 174	0
All	All	2203/2319 (94%)	0.55	153 (6%) 20 27	22, 45, 96, 174	8 (0%)

The worst 5 of 153 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	F	105	LEU	12.3
4	F	249	TYR	7.9
2	D	285	ALA	7.4
2	D	277	SER	7.1
2	D	1	MET	6.5

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands [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
10	GOL	D	503	6/6	0.80	0.41	9.51	63,74,92,100	0
10	GOL	B	504	6/6	0.89	0.25	8.33	55,62,66,75	0
7	CA	A	503	1/1	0.77	0.18	3.92	80,80,80,80	0
9	LLM	B	503	37/37	0.80	0.23	2.86	91,93,102,104	0
5	GTP	A	501	32/32	0.99	0.14	0.41	25,30,34,43	0
5	GTP	C	501	32/32	0.99	0.14	0.22	21,26,32,36	0
8	GDP	B	501	28/28	0.99	0.14	-0.30	21,27,33,37	0
8	GDP	D	501	28/28	0.97	0.14	-0.35	34,44,53,59	0
11	ACP	F	401	31/31	0.89	0.16	-1.24	49,73,130,140	0
6	MG	F	402	1/1	0.91	0.25	-	30,30,30,30	0
6	MG	C	502	1/1	0.98	0.21	-	34,34,34,34	0
6	MG	D	502	1/1	0.92	0.07	-	44,44,44,44	0
7	CA	B	505	1/1	0.78	0.20	-	109,109,109,109	0
7	CA	B	506	1/1	0.92	0.11	-	93,93,93,93	0
6	MG	B	502	1/1	0.99	0.23	-	22,22,22,22	0
6	MG	A	502	1/1	0.98	0.21	-	38,38,38,38	0

6.5 Other polymers [i](#)

There are no such residues in this entry.