



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 21, 2021 – 01:03 PM EDT

PDB ID : 5S5J
Title : Tubulin-Z1148747945-complex
Authors : Muehlethaler, T.; Gioia, D.; Protá, A.E.; Sharpe, M.E.; Cavalli, A.; Steinmetz, M.O.
Deposited on : 2020-11-08
Resolution : 2.25 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 ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.20
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.20

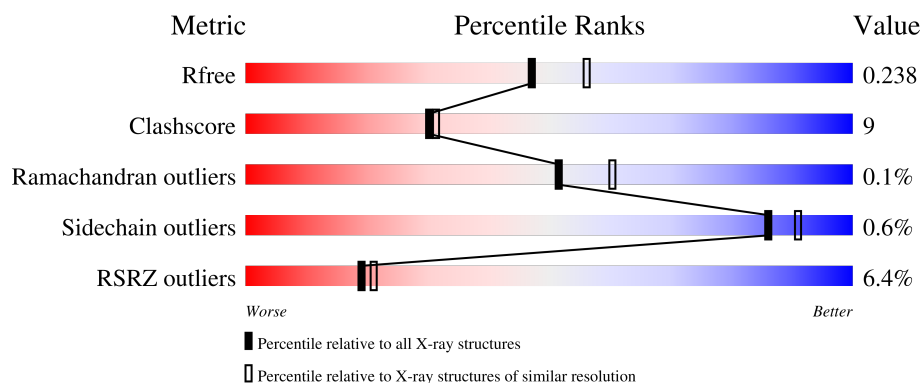
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.




Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (2.26-2.26)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	451	<div> <div>3%</div> <div>77%</div> <div>20%</div> <div>.</div> </div>
1	C	451	<div> <div>81%</div> <div>16%</div> <div>.</div> </div>
2	B	445	<div> <div>3%</div> <div>74%</div> <div>21%</div> <div>.</div> </div>
2	D	445	<div> <div>4%</div> <div>75%</div> <div>21%</div> <div>.</div> </div>
3	E	143	<div> <div>7%</div> <div>72%</div> <div>14%</div> <div>14%</div> </div>

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Mol	Chain	Length	Quality of chain
4	F	384	 A horizontal bar chart showing the quality of chain F. The bar is divided into four segments: red (22%), green (71%), yellow (21%), and grey (8%). The percentages are labeled above or below the segments. The red segment is at the top left, followed by green, then yellow, and finally grey at the bottom right.

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 18056 atoms, of which 10 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	438	Total	C	N	O	S	0	0	0
			3424	2167	582	653	22			
1	C	440	Total	C	N	O	S	0	1	0
			3443	2178	585	657	23			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	425	Total	C	N	O	S	1	1	0
			3359	2109	577	646	27			
2	D	426	Total	C	N	O	S	5	0	0
			3343	2098	570	648	27			

- 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
			1014	625	183	201	5			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	3	MET	-	initiating methionine	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	352	Total	C	N	O	S	0	0	0
			2877	1843	495	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	A	1	Total	Mg	0	0
			1	1		
6	B	1	Total	Mg	0	0
			1	1		
6	C	1	Total	Mg	0	0
			1	1		
6	D	1	Total	Mg	0	0
			1	1		

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

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

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- The image displays the chemical structure of GDP (Guanosine Diphosphate). It consists of a guanine base (a purine derivative) linked to a ribose sugar, which is in turn linked to two phosphate groups. The guanine base is shown with its characteristic fused ring system, including atoms N1, N2, N3, N7, C2, C4, C5, C6, and C8. The ribose sugar is a five-membered ring with carbons C1', C2', C3', C4', and C5'. The two phosphate groups are represented by phosphorus (P) atoms, with the first phosphate (PA(S)) linked to the ribose and the second phosphate (PB(S)) linked to the first. The structure is color-coded: blue for nitrogen atoms, red for oxygen atoms, and purple for phosphorus atoms. Stereochemistry is indicated with wedges and dashes at the C1' and C4' positions of the ribose ring.

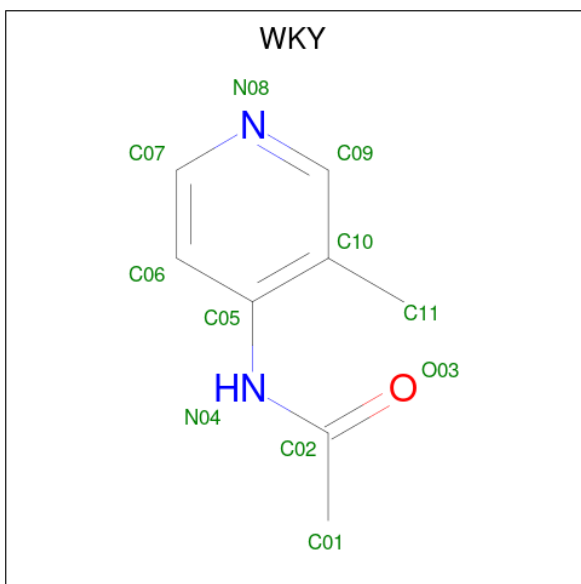
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
8	B	1	Total 28	C 10	N 5	O 11	P 2	0	0
8	D	1	Total 28	C 10	N 5	O 11	P 2	0	0

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- WORLD WIDE
PDB
PROTEIN DATA BANK



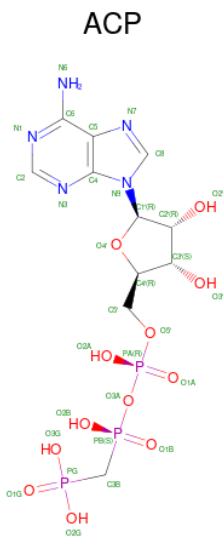
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 10 is N-(3-methylpyridin-4-yl)acetamide (three-letter code: WKY) (formula: $C_8H_{10}N_2O$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
10	B	1	Total	C	H	N	O	0	0
			21	8	10	2	1		

- 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 31	C 11	N 5	O 12	P 3	0	0

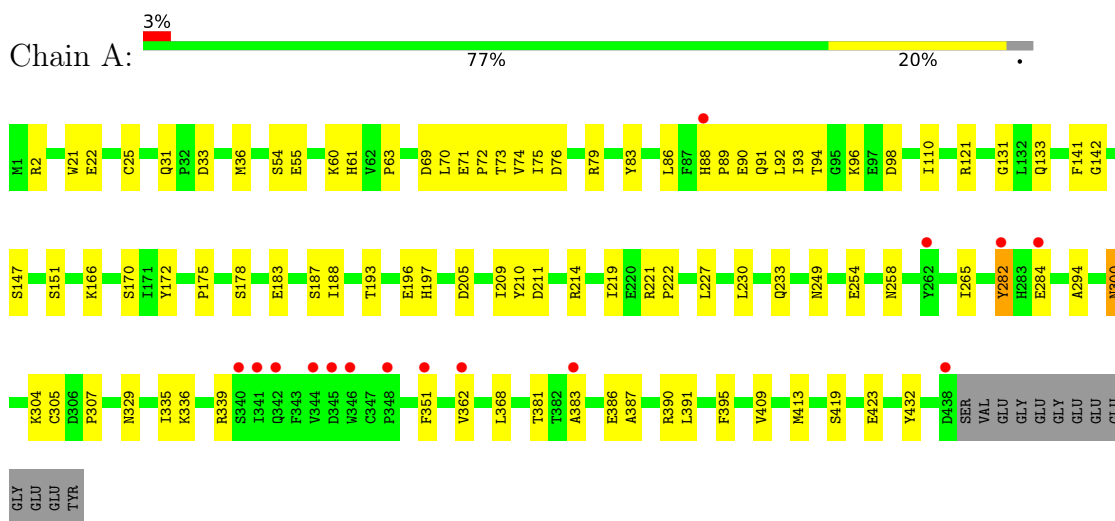
- Molecule 12 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
12	A	65	Total O 65 65	0	0
12	B	86	Total O 86 86	0	0
12	C	199	Total O 199 199	0	0
12	D	31	Total O 31 31	0	0
12	E	9	Total O 9 9	0	0
12	F	13	Total O 13 13	0	0

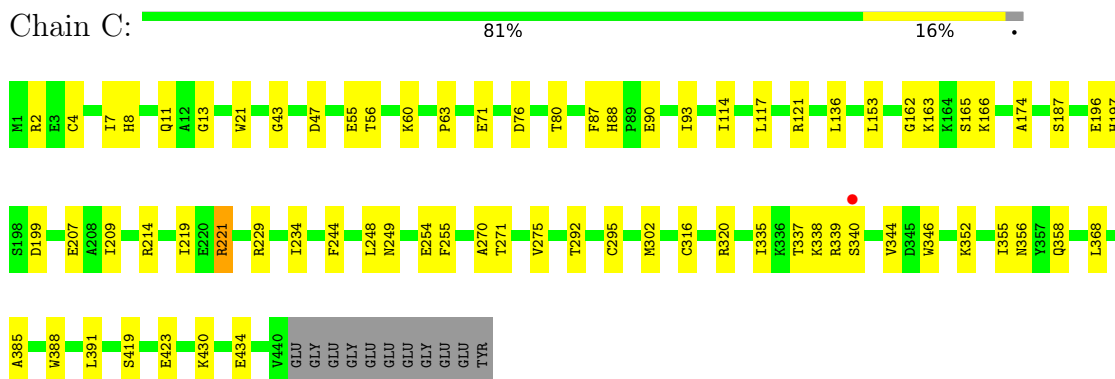
3 Residue-property plots [i](#)

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

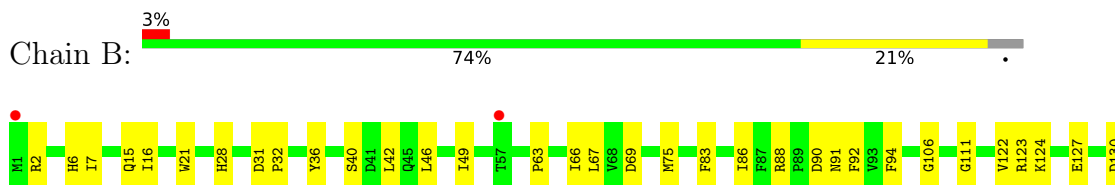
- Molecule 1: Tubulin alpha-1B chain

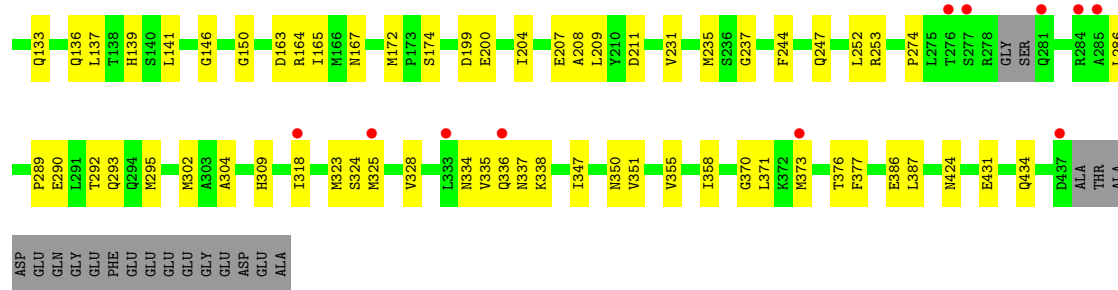


- Molecule 1: Tubulin alpha-1B chain

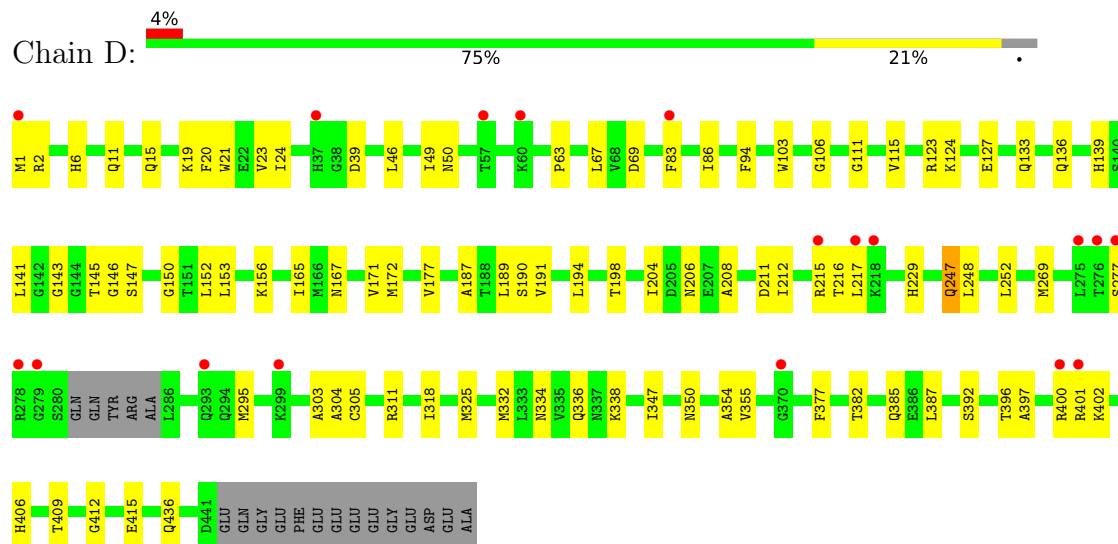


- Molecule 2: Tubulin beta-2B chain

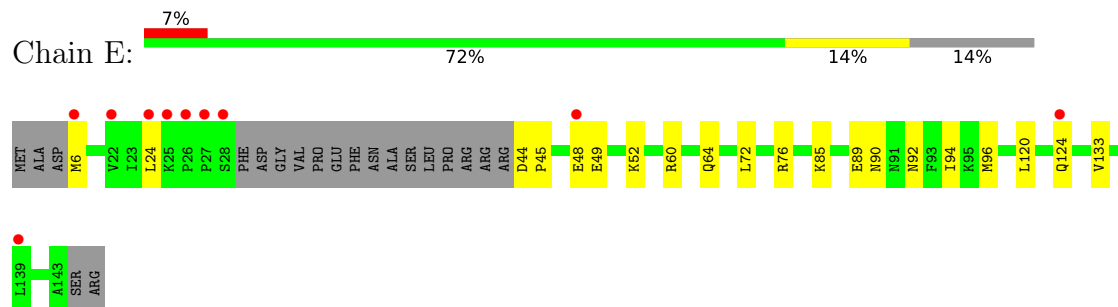




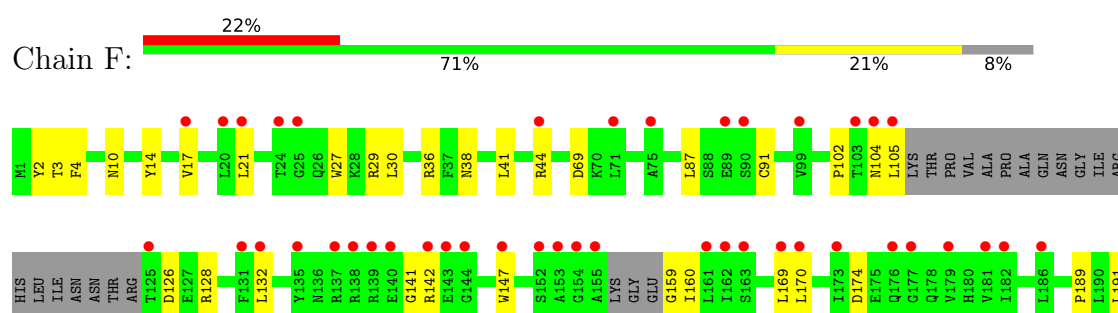
• Molecule 2: Tubulin beta-2B chain

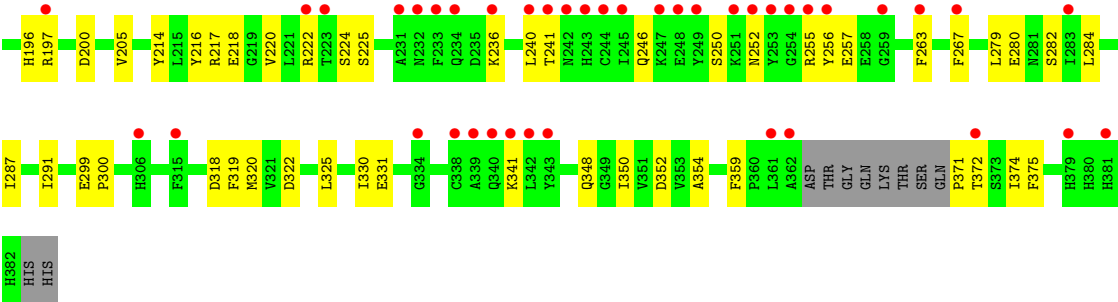


• Molecule 3: Stathmin-4



• 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	104.77Å 159.73Å 179.63Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	62.71 – 2.25 90.50 – 2.25	Depositor EDS
% Data completeness (in resolution range)	99.0 (62.71-2.25) 99.0 (90.50-2.25)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.99 (at 2.25Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.205 , 0.238 0.205 , 0.238	Depositor DCC
R_{free} test set	7005 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	54.6	Xtriage
Anisotropy	0.347	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 46.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	18056	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.24% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.25	0/3502	0.42	0/4754
1	C	0.26	0/3521	0.43	0/4780
2	B	0.25	0/3433	0.42	0/4647
2	D	0.25	0/3416	0.41	0/4626
3	E	0.24	0/1022	0.35	0/1356
4	F	0.24	0/2944	0.40	0/3978
All	All	0.25	0/17838	0.41	0/24141

There are no bond length outliers.

There are no bond angle outliers.

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	3424	0	3334	67	0
1	C	3443	0	3352	51	0
2	B	3359	0	3235	73	0
2	D	3343	0	3222	60	0
3	E	1014	0	1029	16	0
4	F	2877	0	2839	64	0
5	A	32	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	2	0	0	0	0
7	B	1	0	0	0	0
7	C	1	0	0	0	0
8	B	28	0	12	1	0
8	D	28	0	12	2	0
9	B	12	0	12	4	0
10	B	11	10	0	0	0
11	F	31	0	14	5	0
12	A	65	0	0	4	1
12	B	86	0	0	3	0
12	C	199	0	0	5	1
12	D	31	0	0	1	0
12	E	9	0	0	0	0
12	F	13	0	0	1	0
All	All	18046	10	17085	323	1

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 9.

All (323) 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:C:221:ARG:HG3	2:D:325:MET:HG2	1.41	1.00
1:A:381:THR:HG22	1:A:383:ALA:H	1.31	0.95
2:D:217:LEU:HA	2:D:277:SER:HB3	1.48	0.95
1:A:335:ILE:HG23	1:A:339:ARG:HG3	1.57	0.87
2:D:295:MET:HE2	2:D:377:PHE:HB2	1.58	0.85
4:F:241:THR:HG1	11:F:401:ACP:HO3'	1.23	0.84
1:A:2:ARG:HB2	1:A:133:GLN:HE21	1.43	0.81
4:F:102:PRO:HG2	4:F:105:LEU:HD13	1.63	0.79
1:C:209:ILE:HD11	1:C:302:MET:HE3	1.63	0.78
1:A:211:ASP:OD2	1:A:304:LYS:NZ	2.17	0.78
4:F:241:THR:OG1	11:F:401:ACP:O3'	2.00	0.75
1:C:335:ILE:HG23	1:C:339:ARG:HG3	1.68	0.75
4:F:10:ASN:HB2	4:F:44:ARG:HH22	1.51	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:136:GLN:HA	2:D:167:ASN:O	1.88	0.74
1:C:76:ASP:O	1:C:80:THR:HG22	1.89	0.72
2:B:16:ILE:HD13	2:B:231:VAL:HG11	1.72	0.72
2:D:269:MET:HG3	2:D:303:ALA:HB3	1.71	0.72
4:F:236:LYS:HB3	4:F:240:LEU:HD13	1.73	0.71
2:D:248:LEU:HD23	2:D:354:ALA:HB2	1.73	0.69
2:D:334:ASN:HD21	2:D:338:LYS:HE3	1.58	0.69
2:D:83:PHE:O	2:D:86:ILE:HG22	1.93	0.68
4:F:102:PRO:HG2	4:F:105:LEU:CD1	2.22	0.68
2:B:83:PHE:O	2:B:86:ILE:HG22	1.94	0.68
1:C:162:GLY:HA2	3:E:94:ILE:HD11	1.76	0.68
1:C:339:ARG:O	12:C:601:HOH:O	2.12	0.67
4:F:331:GLU:OE2	11:F:401:ACP:O3G	2.13	0.67
2:B:274:PRO:HB3	2:B:286:LEU:HD22	1.77	0.66
2:B:424:ASN:HB3	12:B:609:HOH:O	1.94	0.66
2:B:164:ARG:O	9:B:504:MES:H31	1.95	0.66
4:F:91:CYS:HA	12:F:513:HOH:O	1.97	0.65
2:B:211:ASP:OD2	12:B:601:HOH:O	2.15	0.65
1:C:430:LYS:HE2	1:C:434:GLU:OE2	1.98	0.64
1:C:209:ILE:HD11	1:C:302:MET:CE	2.27	0.64
1:A:142:GLY:HA3	1:A:183:GLU:OE2	1.98	0.63
4:F:371:PRO:HA	4:F:372:THR:C	2.19	0.63
4:F:197:ARG:NH1	4:F:257:GLU:OE2	2.27	0.63
4:F:205:VAL:HG21	4:F:291:ILE:HD13	1.82	0.62
4:F:214:TYR:HB3	4:F:375:PHE:HB3	1.80	0.62
4:F:371:PRO:HA	4:F:372:THR:O	2.00	0.61
2:D:334:ASN:ND2	2:D:338:LYS:HE3	2.15	0.61
3:E:85:LYS:O	3:E:89:GLU:HG3	2.01	0.61
2:B:274:PRO:HB3	2:B:286:LEU:CD2	2.30	0.61
2:D:106:GLY:O	2:D:111:GLY:HA3	2.01	0.61
1:A:336:LYS:HG3	3:E:24:LEU:HD13	1.82	0.61
1:C:4[A]:CYS:SG	1:C:136:LEU:HG	2.40	0.61
2:B:208:ALA:HB2	2:B:304:ALA:HB2	1.83	0.60
2:D:21:TRP:CZ3	2:D:63:PRO:HB3	2.36	0.60
2:B:67:LEU:HD22	2:B:92:PHE:CE2	2.37	0.60
4:F:280:GLU:OE1	4:F:284:LEU:HD23	2.02	0.60
2:D:152:LEU:O	2:D:156:LYS:HG2	2.02	0.59
1:A:71:GLU:OE2	1:A:73:THR:OG1	2.16	0.59
2:B:324:SER:O	2:B:328:VAL:HG23	2.02	0.59
2:B:309:HIS:ND1	2:B:386:GLU:OE2	2.33	0.59
2:B:337:ASN:OD1	4:F:36:ARG:HD3	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:21:TRP:CZ3	2:B:63:PRO:HB3	2.38	0.59
2:B:163:ASP:O	2:B:253[A]:ARG:NH2	2.33	0.59
2:B:295:MET:CG	2:B:377:PHE:HB2	2.33	0.59
2:D:397:ALA:HA	2:D:400:ARG:NH1	2.17	0.59
2:D:347:ILE:HG22	2:D:350:ASN:HB3	1.85	0.59
1:C:244:PHE:CD1	1:C:358:GLN:HG2	2.38	0.58
1:C:270:ALA:O	1:C:302:MET:HG2	2.03	0.58
2:D:171:VAL:HA	2:D:204:ILE:O	2.03	0.58
2:B:253[A]:ARG:NH1	9:B:504:MES:O2S	2.37	0.58
1:C:174:ALA:CB	1:C:207:GLU:HB2	2.34	0.58
1:A:300:ASN:HB3	12:A:601:HOH:O	2.04	0.57
1:A:21:TRP:CZ3	1:A:63:PRO:HB3	2.39	0.57
1:A:141:PHE:HB3	1:A:187:SER:OG	2.04	0.57
2:B:69:ASP:O	2:B:94:PHE:HA	2.04	0.57
2:B:88:ARG:NH1	2:B:90:ASP:HB2	2.19	0.57
4:F:246:GLN:O	4:F:250:SER:HB3	2.04	0.57
1:A:294:ALA:O	1:A:300:ASN:ND2	2.37	0.57
1:A:96:LYS:NZ	2:B:130:ASP:OD1	2.37	0.56
3:E:92:ASN:O	3:E:96:MET:HG2	2.04	0.56
4:F:147:TRP:HB2	4:F:169:LEU:HD11	1.86	0.56
4:F:159:GLY:C	4:F:160:ILE:HD12	2.26	0.56
1:A:210:TYR:CE1	1:A:222:PRO:HD2	2.41	0.56
1:A:36:MET:HB3	1:A:61:HIS:CE1	2.40	0.56
2:B:334:ASN:HD21	2:B:338:LYS:HD2	1.70	0.56
4:F:320:MET:HG3	4:F:330:ILE:HD11	1.87	0.56
1:C:254:GLU:HG2	1:C:352:LYS:HE2	1.87	0.56
1:A:172:TYR:HB3	1:A:205:ASP:HA	1.88	0.55
4:F:10:ASN:CB	4:F:44:ARG:HH22	2.18	0.55
3:E:60:ARG:O	3:E:64:GLN:HG3	2.07	0.55
2:B:289:PRO:O	2:B:293:GLN:HG3	2.07	0.55
2:B:347:ILE:HG22	2:B:350:ASN:HB3	1.88	0.55
4:F:17:VAL:O	4:F:21:LEU:HG	2.07	0.55
1:C:320:ARG:HA	1:C:356:ASN:O	2.07	0.54
1:A:98:ASP:HB2	5:A:501:GTP:O2G	2.07	0.54
2:B:136:GLN:HA	2:B:167:ASN:O	2.06	0.54
1:A:93:ILE:HD11	1:A:121:ARG:HG3	1.89	0.54
1:A:175:PRO:HA	1:A:178:SER:CB	2.37	0.54
2:D:143:GLY:HA3	8:D:501:GDP:O3A	2.07	0.54
2:D:1:MET:HG3	2:D:50:ASN:HB2	1.89	0.54
4:F:371:PRO:CA	4:F:372:THR:HB	2.37	0.54
2:B:172:MET:HG3	2:B:387:LEU:HD11	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:370:GLY:O	2:B:371:LEU:HD23	2.08	0.54
2:B:36:TYR:CD1	2:B:46:LEU:HD21	2.43	0.53
2:D:20:PHE:CZ	2:D:24:ILE:HD13	2.43	0.53
2:B:244:PHE:CE1	2:B:358:ILE:HD12	2.43	0.53
2:B:292:THR:HG22	2:B:335:VAL:HG21	1.90	0.53
1:C:292:THR:HG22	1:C:335:ILE:CD1	2.38	0.53
1:A:254:GLU:HG2	1:A:258:ASN:ND2	2.24	0.53
1:A:265:ILE:HG23	1:A:432:TYR:CE1	2.44	0.53
1:A:419:SER:O	1:A:423:GLU:HG3	2.09	0.53
4:F:205:VAL:CG2	4:F:291:ILE:HD13	2.39	0.53
1:A:88:HIS:HB2	1:A:89:PRO:HD2	1.91	0.53
1:A:175:PRO:HA	1:A:178:SER:HB3	1.90	0.53
2:D:147:SER:HB2	2:D:190:SER:OG	2.08	0.53
11:F:401:ACP:O3G	11:F:401:ACP:O1B	2.27	0.52
2:D:382:THR:O	2:D:385:GLN:HG2	2.09	0.52
4:F:128:ARG:HH12	4:F:170:LEU:HB3	1.74	0.52
1:A:196:GLU:OE1	1:A:196:GLU:HA	2.08	0.52
1:C:174:ALA:HB1	1:C:207:GLU:HB2	1.91	0.52
1:A:209:ILE:HG23	1:A:230:LEU:HD23	1.91	0.52
1:A:71:GLU:HG2	1:A:72:PRO:HD2	1.91	0.52
4:F:191:LEU:HD12	4:F:196:HIS:CE1	2.45	0.52
3:E:72:LEU:O	3:E:76:ARG:HG2	2.10	0.52
2:B:141:LEU:HD12	2:B:172:MET:SD	2.49	0.52
2:B:2:ARG:HB2	2:B:133:GLN:CG	2.40	0.52
2:D:21:TRP:CE3	2:D:63:PRO:HB3	2.44	0.52
1:C:11:GLN:HE22	2:D:247:GLN:NE2	2.09	0.51
4:F:200:ASP:OD1	4:F:222:ARG:HB2	2.10	0.51
1:C:234:ILE:HG12	1:C:302:MET:HE2	1.93	0.51
1:A:2:ARG:HB2	1:A:133:GLN:NE2	2.18	0.51
1:A:193:THR:HG23	12:A:631:HOH:O	2.10	0.51
4:F:132:LEU:HD21	4:F:170:LEU:HD11	1.92	0.51
2:B:209:LEU:HD23	2:B:302:MET:HG2	1.92	0.51
1:A:214:ARG:HG2	1:A:219:ILE:O	2.11	0.51
2:B:204:ILE:CG2	2:B:209:LEU:HD11	2.41	0.51
4:F:10:ASN:HB2	4:F:44:ARG:NH2	2.24	0.51
2:B:124:LYS:HD3	2:B:124:LYS:C	2.31	0.50
1:C:340:SER:HA	12:C:691:HOH:O	2.10	0.50
2:D:397:ALA:O	2:D:401:ARG:NH1	2.45	0.50
1:C:93:ILE:HD11	1:C:121:ARG:HG3	1.93	0.50
2:B:295:MET:HG2	2:B:377:PHE:HB2	1.93	0.50
2:D:318:ILE:HG12	12:D:607:HOH:O	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:75:ILE:HD12	1:A:94:THR:HG22	1.91	0.50
2:B:146:GLY:O	2:B:150:GLY:HA3	2.12	0.50
1:C:93:ILE:HG22	1:C:114:ILE:HD11	1.94	0.50
2:D:172:MET:HG3	2:D:387:LEU:HD11	1.94	0.50
1:C:335:ILE:HG23	1:C:339:ARG:CG	2.40	0.50
2:D:11:GLN:O	2:D:15:GLN:HG2	2.11	0.50
1:A:351:PHE:HE1	3:E:24:LEU:HD11	1.75	0.50
2:D:318:ILE:N	2:D:318:ILE:HD12	2.27	0.50
4:F:128:ARG:NH2	4:F:174:ASP:OD1	2.45	0.50
2:B:286:LEU:HD12	2:B:290:GLU:OE1	2.12	0.49
2:D:6:HIS:CD2	2:D:21:TRP:HE1	2.30	0.49
2:D:402:LYS:HE2	2:D:415:GLU:OE1	2.12	0.49
2:B:323:MET:HE2	2:B:373:MET:HB2	1.95	0.49
4:F:350:ILE:O	4:F:354:ALA:HB3	2.13	0.49
2:B:2:ARG:HB2	2:B:133:GLN:HG3	1.94	0.49
2:B:199:ASP:OD1	9:B:504:MES:H62	2.12	0.49
1:C:419:SER:O	1:C:423:GLU:HG3	2.12	0.49
3:E:48:GLU:HG2	3:E:52:LYS:HE3	1.94	0.49
2:B:123:ARG:O	2:B:127:GLU:HG3	2.13	0.49
2:D:124:LYS:C	2:D:124:LYS:HD3	2.33	0.49
3:E:45:PRO:HA	3:E:49:GLU:OE1	2.13	0.48
1:A:25:CYS:SG	1:A:86:LEU:HD11	2.53	0.48
4:F:14:TYR:HB3	4:F:41:LEU:HD13	1.94	0.48
2:B:323:MET:HB3	2:B:373:MET:CE	2.44	0.48
1:A:79:ARG:HG2	1:A:92:LEU:HD12	1.96	0.48
2:D:303:ALA:O	2:D:305:CYS:N	2.42	0.48
2:B:66:ILE:HD12	2:B:122:VAL:HG22	1.95	0.48
2:B:167:ASN:HD22	2:B:252:LEU:HD22	1.79	0.48
4:F:320:MET:CG	4:F:330:ILE:HD11	2.44	0.48
1:A:141:PHE:CE1	1:A:170:SER:HB3	2.48	0.48
4:F:87:LEU:O	4:F:91:CYS:HB2	2.14	0.48
2:B:325:MET:HE2	2:B:355:VAL:HG21	1.96	0.48
4:F:102:PRO:HB2	4:F:104:ASN:OD1	2.13	0.48
2:B:6:HIS:CD2	2:B:21:TRP:HE1	2.32	0.48
4:F:267:PHE:CE2	4:F:279:LEU:HD13	2.48	0.48
4:F:287:ILE:HG23	4:F:319:PHE:CE2	2.49	0.48
4:F:348:GLN:NE2	4:F:352:ASP:OD1	2.47	0.48
4:F:371:PRO:N	4:F:372:THR:HB	2.29	0.48
1:A:335:ILE:CG2	1:A:339:ARG:HG3	2.37	0.47
2:B:75:MET:HE3	2:B:92:PHE:HD2	1.78	0.47
2:B:42:LEU:H	2:B:42:LEU:HD12	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:248:LEU:HD13	1:C:355:ILE:HD12	1.96	0.47
4:F:220:VAL:HG12	4:F:263:PHE:CE1	2.49	0.47
1:C:163:LYS:HG3	3:E:90:ASN:OD1	2.14	0.47
2:D:208:ALA:O	2:D:212:ILE:HG13	2.14	0.47
1:A:151:SER:HB2	1:A:193:THR:OG1	2.15	0.47
1:C:88:HIS:HE1	1:C:90:GLU:HG3	1.79	0.47
1:C:187:SER:HB3	1:C:391:LEU:HD21	1.95	0.47
4:F:2:TYR:CE1	4:F:359:PHE:HB3	2.49	0.47
1:A:69:ASP:O	1:A:94:THR:HA	2.14	0.47
2:B:31:ASP:HB2	2:B:32:PRO:CD	2.45	0.47
1:C:271:THR:HG21	1:C:295:CYS:O	2.14	0.47
2:B:46:LEU:HA	2:B:49:ILE:HB	1.96	0.46
3:E:120:LEU:O	3:E:124:GLN:HG3	2.14	0.46
1:C:21:TRP:CZ3	1:C:63:PRO:HB3	2.50	0.46
2:D:194:LEU:HD22	2:D:198:THR:HG21	1.97	0.46
2:B:318:ILE:N	2:B:318:ILE:HD12	2.30	0.46
12:B:606:HOH:O	3:E:85:LYS:NZ	2.48	0.46
1:C:7:ILE:HG21	1:C:153:LEU:HD21	1.96	0.46
2:D:19:LYS:O	2:D:23:VAL:HG23	2.16	0.46
2:B:67:LEU:N	2:B:67:LEU:HD12	2.31	0.46
1:A:188:ILE:HD12	1:A:395:PHE:HB2	1.97	0.46
1:A:386:GLU:O	1:A:390:ARG:HG3	2.15	0.46
1:A:88:HIS:HD2	1:A:90:GLU:HB2	1.81	0.46
1:A:362:VAL:HG22	12:A:602:HOH:O	2.16	0.46
1:C:166:LYS:HE2	1:C:197:HIS:O	2.16	0.46
2:B:231:VAL:O	2:B:235:MET:HG3	2.16	0.46
2:D:115:VAL:HG23	2:D:153:LEU:HD23	1.98	0.46
1:A:76:ASP:OD1	1:A:79:ARG:NH1	2.48	0.45
1:A:75:ILE:HB	1:A:94:THR:CG2	2.46	0.45
2:B:334:ASN:ND2	2:B:338:LYS:HD2	2.31	0.45
2:B:336:GLN:OE1	2:B:351:VAL:HB	2.16	0.45
2:D:69:ASP:O	2:D:94:PHE:HA	2.16	0.45
2:D:211:ASP:O	2:D:215:ARG:HB2	2.17	0.45
2:D:412:GLY:C	3:E:133:VAL:HG13	2.37	0.45
1:A:141:PHE:O	1:A:147:SER:HB3	2.17	0.45
2:B:323:MET:HB3	2:B:373:MET:HE2	1.98	0.45
1:C:385:ALA:HA	1:C:388:TRP:CD1	2.52	0.45
1:A:305:CYS:O	1:A:307:PRO:HD3	2.17	0.45
4:F:141:GLY:O	4:F:142:ARG:HB2	2.17	0.44
1:A:54:SER:O	1:A:61:HIS:HA	2.17	0.44
1:C:337:THR:O	1:C:338:LYS:HG3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:344:VAL:HG21	1:C:346:TRP:CE2	2.52	0.44
1:A:71:GLU:HG2	1:A:72:PRO:CD	2.47	0.44
1:C:63:PRO:HG2	1:C:87:PHE:CE1	2.53	0.44
1:A:74:VAL:HB	12:A:603:HOH:O	2.16	0.44
1:A:209:ILE:HG22	1:A:227:LEU:HD22	1.98	0.44
1:A:409:VAL:HA	1:A:413:MET:O	2.18	0.44
1:A:387:ALA:HA	1:A:390:ARG:HD3	1.99	0.44
2:B:15:GLN:NE2	8:B:501:GDP:O6	2.51	0.44
2:D:325:MET:HE2	2:D:355:VAL:HG21	2.00	0.44
1:A:71:GLU:HG2	1:A:72:PRO:N	2.32	0.44
2:D:392:SER:O	2:D:396:THR:HG22	2.18	0.44
2:D:141:LEU:HA	2:D:147:SER:HB3	2.00	0.44
2:B:88:ARG:HH11	2:B:90:ASP:HB2	1.81	0.44
1:C:165:SER:HA	1:C:199:ASP:OD2	2.18	0.44
1:C:229:ARG:NH1	12:C:620:HOH:O	2.51	0.44
4:F:217:ARG:NH2	4:F:374:ILE:HG22	2.33	0.44
2:B:75:MET:HE3	2:B:92:PHE:CD2	2.51	0.43
1:A:2:ARG:HB3	1:A:131:GLY:O	2.18	0.43
1:A:284:GLU:CD	1:A:284:GLU:H	2.21	0.43
1:A:329:ASN:HB3	3:E:6:MET:CE	2.48	0.43
2:D:141:LEU:HD12	2:D:172:MET:SD	2.58	0.43
1:A:22:GLU:HG3	1:A:83:TYR:CE1	2.53	0.43
2:B:2:ARG:HB2	2:B:133:GLN:HE21	1.83	0.43
1:A:249:ASN:HA	1:A:254:GLU:HB3	2.01	0.43
1:C:196:GLU:HG2	12:C:661:HOH:O	2.19	0.43
4:F:287:ILE:HG23	4:F:319:PHE:CZ	2.54	0.43
1:C:55:GLU:HA	1:C:60:LYS:O	2.19	0.43
2:D:46:LEU:HA	2:D:49:ILE:HB	2.00	0.43
4:F:216:TYR:CE2	4:F:218:GLU:HB2	2.53	0.43
4:F:341:LYS:HG2	4:F:341:LYS:O	2.18	0.43
4:F:371:PRO:HA	4:F:372:THR:HB	1.99	0.43
2:B:21:TRP:CE3	2:B:63:PRO:HB3	2.54	0.43
2:B:167:ASN:OD1	2:B:200:GLU:HB2	2.18	0.43
2:D:67:LEU:N	2:D:67:LEU:HD12	2.33	0.43
2:B:7:ILE:O	2:B:137:LEU:HA	2.19	0.43
4:F:318:ASP:OD2	11:F:401:ACP:O2G	2.36	0.43
1:C:174:ALA:HB2	1:C:207:GLU:HB2	1.99	0.43
2:D:332:MET:O	2:D:336:GLN:HG3	2.19	0.43
1:A:70:LEU:HD13	1:A:110:ILE:HG21	2.01	0.43
2:B:28:HIS:HB3	2:B:49:ILE:HD13	2.00	0.42
2:B:42:LEU:HB2	2:B:358:ILE:HD11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:106:GLY:O	2:B:111:GLY:HA3	2.18	0.42
2:D:103:TRP:CE3	2:D:189:LEU:HD13	2.53	0.42
2:D:165:ILE:HG21	2:D:252:LEU:HB3	2.00	0.42
3:E:44:ASP:HB3	3:E:45:PRO:HD2	2.01	0.42
4:F:3:THR:HB	4:F:30:LEU:HD11	2.01	0.42
2:D:2:ARG:HB3	2:D:133:GLN:CG	2.49	0.42
4:F:217:ARG:HG3	4:F:218:GLU:HG2	2.01	0.42
1:C:8:HIS:HB3	1:C:13:GLY:O	2.19	0.42
2:D:115:VAL:HG23	2:D:153:LEU:CD2	2.49	0.42
4:F:282:SER:HB2	4:F:325:LEU:HD13	2.02	0.42
2:D:20:PHE:CE2	2:D:24:ILE:HD13	2.54	0.42
1:A:187:SER:HB3	1:A:391:LEU:HD21	2.02	0.42
4:F:147:TRP:HB2	4:F:169:LEU:CD1	2.47	0.42
4:F:299:GLU:HB3	4:F:300:PRO:HD3	2.01	0.42
3:E:48:GLU:CG	3:E:52:LYS:HE3	2.49	0.42
1:A:88:HIS:CD2	1:A:91:GLN:HG3	2.55	0.42
1:C:117:LEU:O	1:C:121:ARG:HG2	2.19	0.42
1:C:214:ARG:HG2	1:C:219:ILE:O	2.19	0.42
4:F:189:PRO:HA	4:F:322:ASP:HA	2.02	0.42
1:A:175:PRO:HA	1:A:178:SER:HB2	2.01	0.41
2:B:42:LEU:HD12	2:B:42:LEU:N	2.34	0.41
1:C:187:SER:CB	1:C:391:LEU:HD21	2.49	0.41
1:A:31:GLN:HB2	1:A:33:ASP:OD1	2.20	0.41
1:A:55:GLU:HA	1:A:60:LYS:O	2.20	0.41
2:B:165:ILE:HG21	2:B:252:LEU:HB3	2.02	0.41
4:F:69:ASP:N	4:F:69:ASP:OD1	2.53	0.41
4:F:197:ARG:HB2	4:F:224:SER:O	2.19	0.41
4:F:217:ARG:NH2	4:F:374:ILE:HA	2.35	0.41
2:D:187:ALA:O	2:D:191:VAL:HG23	2.20	0.41
1:A:210:TYR:CZ	1:A:222:PRO:HD2	2.55	0.41
1:A:166:LYS:HE2	1:A:197:HIS:O	2.20	0.41
2:D:406:HIS:HA	2:D:409:THR:OG1	2.20	0.41
2:B:431:GLU:O	2:B:434:GLN:HG2	2.21	0.41
2:B:40:SER:OG	2:B:42:LEU:HD13	2.20	0.41
1:C:292:THR:HG22	1:C:335:ILE:HD12	2.02	0.41
2:D:212:ILE:O	2:D:216:THR:HB	2.20	0.41
4:F:2:TYR:HB2	4:F:27:TRP:CD2	2.55	0.41
4:F:126:ASP:OD2	4:F:128:ARG:HG3	2.20	0.41
1:C:275:VAL:HG13	1:C:368:LEU:HD21	2.02	0.41
2:D:123:ARG:O	2:D:127:GLU:HG3	2.20	0.41
2:B:88:ARG:HD3	2:B:91:ASN:OD1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:216:TYR:CZ	4:F:218:GLU:HB2	2.56	0.41
4:F:255:ARG:HD3	4:F:256:TYR:CE2	2.56	0.41
1:A:233:GLN:HG3	1:A:368:LEU:HD12	2.03	0.41
2:B:237:GLY:HA3	2:B:376:THR:OG1	2.21	0.41
1:C:43:GLY:HA2	1:C:56:THR:O	2.21	0.41
1:C:47:ASP:OD2	12:C:602:HOH:O	2.22	0.41
4:F:4:PHE:CZ	4:F:29:ARG:HB2	2.56	0.41
4:F:225:SER:HB2	4:F:252:ASN:O	2.20	0.41
1:C:234:ILE:H	1:C:234:ILE:HD12	1.86	0.40
2:D:145:THR:HB	8:D:501:GDP:O2B	2.22	0.40
2:D:311:ARG:NH1	2:D:436:GLN:O	2.53	0.40
9:B:504:MES:H81	9:B:504:MES:H51	1.69	0.40
1:C:249:ASN:OD1	1:C:356:ASN:ND2	2.44	0.40
4:F:372:THR:O	4:F:372:THR:HG22	2.20	0.40
2:B:174:SER:OG	2:B:207:GLU:HB2	2.21	0.40
1:A:75:ILE:HB	1:A:94:THR:HG21	2.03	0.40
2:B:387:LEU:HD23	2:B:387:LEU:C	2.41	0.40
1:C:255:PHE:CD1	1:C:316:CYS:HB3	2.56	0.40
2:D:1:MET:HG3	2:D:50:ASN:CB	2.51	0.40
2:D:146:GLY:O	2:D:150:GLY:HA3	2.21	0.40
2:D:177:VAL:HG21	2:D:206:ASN:HB3	2.02	0.40
2:D:387:LEU:C	2:D:387:LEU:HD23	2.42	0.40
4:F:38:ASN:HB3	4:F:359:PHE:CE1	2.57	0.40

All (1) 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)
12:A:645:HOH:O	12:C:704:HOH:O[3_555]	2.08	0.12

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	436/451 (97%)	428 (98%)	7 (2%)	1 (0%)	47	55
1	C	439/451 (97%)	428 (98%)	11 (2%)	0	100	100
2	B	422/445 (95%)	410 (97%)	12 (3%)	0	100	100
2	D	422/445 (95%)	410 (97%)	11 (3%)	1 (0%)	47	55
3	E	119/143 (83%)	118 (99%)	1 (1%)	0	100	100
4	F	344/384 (90%)	332 (96%)	12 (4%)	0	100	100
All	All	2182/2319 (94%)	2126 (97%)	54 (2%)	2 (0%)	51	60

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	304	ALA
1	A	282	TYR

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	369/379 (97%)	366 (99%)	3 (1%)	81	88
1	C	372/379 (98%)	369 (99%)	3 (1%)	81	88
2	B	368/383 (96%)	366 (100%)	2 (0%)	88	92
2	D	368/383 (96%)	364 (99%)	4 (1%)	73	82
3	E	110/127 (87%)	110 (100%)	0	100	100
4	F	315/342 (92%)	315 (100%)	0	100	100
All	All	1902/1993 (95%)	1890 (99%)	12 (1%)	86	91

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	221	ARG
1	A	282	TYR
1	A	300	ASN

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Mol	Chain	Res	Type
2	B	139	HIS
2	B	247	GLN
1	C	2	ARG
1	C	71	GLU
1	C	221	ARG
2	D	39	ASP
2	D	139	HIS
2	D	229	HIS
2	D	247	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	88	HIS
2	B	15	GLN
2	B	167	ASN
2	B	282	GLN
2	B	294	GLN
2	B	424	ASN
1	C	11	GLN
1	C	300	ASN
2	D	167	ASN
2	D	294	GLN
4	F	269	GLN
4	F	333	ASN
4	F	380	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry

Of 16 ligands modelled in this entry, 9 are monoatomic - leaving 7 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
11	ACP	F	401	6	27,33,33	1.40	5 (18%)	32,52,52	1.50	4 (12%)
8	GDP	D	501	6	24,30,30	1.14	2 (8%)	31,47,47	1.91	7 (22%)
8	GDP	B	501	6	24,30,30	1.20	3 (12%)	31,47,47	1.95	7 (22%)
5	GTP	A	501	6	26,34,34	0.97	1 (3%)	33,54,54	1.74	6 (18%)
5	GTP	C	501	6	26,34,34	0.96	1 (3%)	33,54,54	1.64	6 (18%)
9	MES	B	504	-	12,12,12	2.30	1 (8%)	14,16,16	2.01	7 (50%)
10	WKY	B	505	-	11,11,11	0.32	0	13,14,14	0.57	0

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
11	ACP	F	401	6	-	11/15/38/38	0/3/3/3
8	GDP	D	501	6	-	6/12/32/32	0/3/3/3
8	GDP	B	501	6	-	3/12/32/32	0/3/3/3
5	GTP	A	501	6	-	8/18/38/38	0/3/3/3
5	GTP	C	501	6	-	8/18/38/38	0/3/3/3
9	MES	B	504	-	-	4/6/14/14	0/1/1/1
10	WKY	B	505	-	-	1/4/4/4	0/1/1/1

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	B	504	MES	C8-S	-7.69	1.66	1.77
8	B	501	GDP	C6-C5	4.09	1.48	1.41
8	D	501	GDP	C6-C5	3.96	1.48	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	501	GTP	C6-N1	3.11	1.38	1.33
5	C	501	GTP	C6-N1	3.04	1.38	1.33
11	F	401	ACP	PG-O3G	2.96	1.61	1.54
11	F	401	ACP	PG-O2G	2.94	1.61	1.54
11	F	401	ACP	PB-O3A	2.83	1.61	1.58
11	F	401	ACP	C5-C4	2.55	1.47	1.40
8	B	501	GDP	C5-C4	2.36	1.47	1.40
8	D	501	GDP	C5-C4	2.35	1.47	1.40
11	F	401	ACP	PB-O2B	2.24	1.61	1.56
8	B	501	GDP	O4'-C1'	2.04	1.43	1.41

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	501	GTP	N3-C2-N1	-5.35	120.09	127.22
5	C	501	GTP	N3-C2-N1	-5.16	120.34	127.22
8	B	501	GDP	C2-N3-C4	5.07	121.15	115.36
8	D	501	GDP	C2-N3-C4	4.75	120.78	115.36
8	B	501	GDP	C6-C5-C4	-4.37	116.63	120.80
5	A	501	GTP	C2-N3-C4	4.29	120.26	115.36
8	B	501	GDP	C6-N1-C2	4.25	122.68	115.93
11	F	401	ACP	PA-O3A-PB	-4.25	119.09	132.56
8	D	501	GDP	C6-N1-C2	4.14	122.51	115.93
8	D	501	GDP	C5-C6-N1	-4.10	117.82	123.43
8	B	501	GDP	C5-C6-N1	-3.82	118.20	123.43
8	D	501	GDP	C6-C5-C4	-3.81	117.16	120.80
5	C	501	GTP	C2-N3-C4	3.80	119.69	115.36
9	B	504	MES	C5-N4-C3	3.75	117.28	108.83
8	B	501	GDP	N3-C2-N1	-3.72	122.27	127.22
11	F	401	ACP	C3'-C2'-C1'	3.59	106.38	100.98
8	D	501	GDP	N3-C2-N1	-3.40	122.69	127.22
9	B	504	MES	C6-C5-N4	-3.35	105.02	110.10
5	C	501	GTP	C5-C6-N1	-3.15	119.13	123.43
11	F	401	ACP	N3-C2-N1	-3.13	123.78	128.68
5	A	501	GTP	C5-C6-N1	-2.91	119.44	123.43
8	D	501	GDP	PA-O3A-PB	-2.91	122.85	132.83
8	B	501	GDP	PA-O3A-PB	-2.79	123.26	132.83
8	D	501	GDP	C4-C5-N7	-2.76	106.52	109.40
5	A	501	GTP	PB-O3B-PG	-2.75	123.38	132.83
5	C	501	GTP	C6-N1-C2	2.73	120.27	115.93
8	B	501	GDP	C4-C5-N7	-2.69	106.60	109.40
5	A	501	GTP	PA-O3A-PB	-2.65	123.72	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	501	GTP	C6-N1-C2	2.64	120.13	115.93
5	C	501	GTP	PA-O3A-PB	-2.57	124.02	132.83
11	F	401	ACP	C4-C5-N7	-2.52	106.77	109.40
5	C	501	GTP	PB-O3B-PG	-2.52	124.18	132.83
9	B	504	MES	O1S-S-C8	2.33	109.72	106.92
9	B	504	MES	C7-N4-C5	2.21	116.89	111.23
9	B	504	MES	O3S-S-C8	2.18	109.29	105.77
9	B	504	MES	O2S-S-C8	2.12	109.47	106.92
9	B	504	MES	C7-N4-C3	2.02	116.39	111.23

There are no chirality outliers.

All (41) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	501	GTP	C5'-O5'-PA-O1A
5	A	501	GTP	C5'-O5'-PA-O2A
5	C	501	GTP	C5'-O5'-PA-O1A
5	C	501	GTP	C5'-O5'-PA-O2A
8	B	501	GDP	C5'-O5'-PA-O1A
8	B	501	GDP	C5'-O5'-PA-O2A
8	D	501	GDP	C5'-O5'-PA-O1A
8	D	501	GDP	C5'-O5'-PA-O2A
9	B	504	MES	C8-C7-N4-C5
9	B	504	MES	C7-C8-S-O2S
9	B	504	MES	C7-C8-S-O3S
11	F	401	ACP	PB-C3B-PG-O1G
11	F	401	ACP	PB-C3B-PG-O2G
11	F	401	ACP	PB-C3B-PG-O3G
11	F	401	ACP	PG-C3B-PB-O1B
11	F	401	ACP	PG-C3B-PB-O2B
11	F	401	ACP	PG-C3B-PB-O3A
11	F	401	ACP	C5'-O5'-PA-O1A
11	F	401	ACP	C5'-O5'-PA-O2A
5	C	501	GTP	PB-O3B-PG-O1G
8	D	501	GDP	C5'-O5'-PA-O3A
11	F	401	ACP	C5'-O5'-PA-O3A
9	B	504	MES	C7-C8-S-O1S
5	A	501	GTP	PB-O3B-PG-O1G
5	A	501	GTP	PB-O3B-PG-O2G
5	A	501	GTP	PB-O3B-PG-O3G
5	C	501	GTP	PB-O3B-PG-O2G
5	C	501	GTP	PB-O3B-PG-O3G

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Mol	Chain	Res	Type	Atoms
8	D	501	GDP	PA-O3A-PB-O2B
8	D	501	GDP	PA-O3A-PB-O3B
11	F	401	ACP	PB-O3A-PA-O1A
11	F	401	ACP	PB-O3A-PA-O2A
5	A	501	GTP	C5'-O5'-PA-O3A
5	C	501	GTP	C5'-O5'-PA-O3A
8	B	501	GDP	C5'-O5'-PA-O3A
5	A	501	GTP	PB-O3A-PA-O1A
5	A	501	GTP	PB-O3A-PA-O2A
5	C	501	GTP	PB-O3A-PA-O1A
5	C	501	GTP	PB-O3A-PA-O2A
8	D	501	GDP	PA-O3A-PB-O1B
10	B	505	WKY	C01-C02-N04-C05

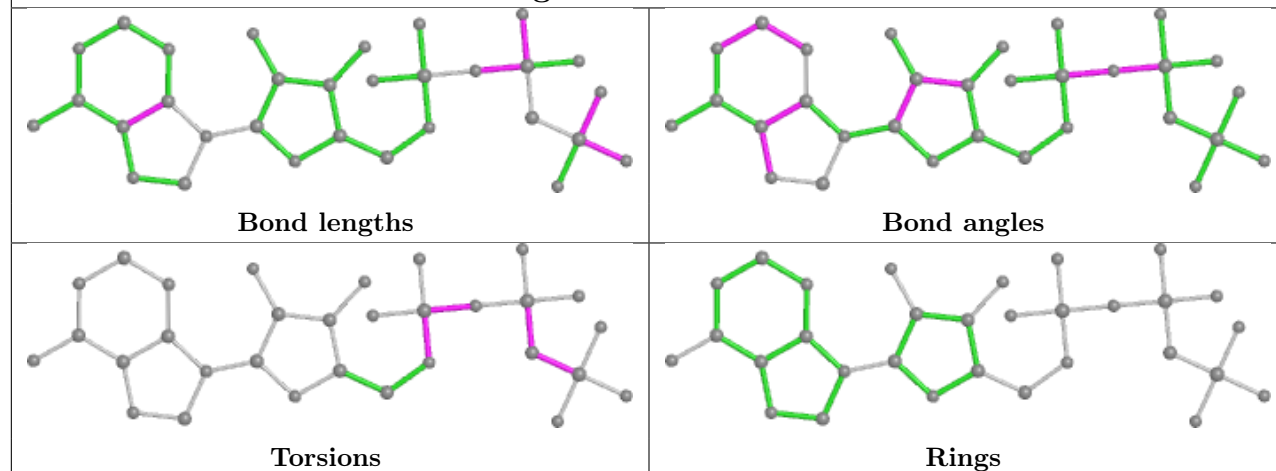
There are no ring outliers.

5 monomers are involved in 13 short contacts:

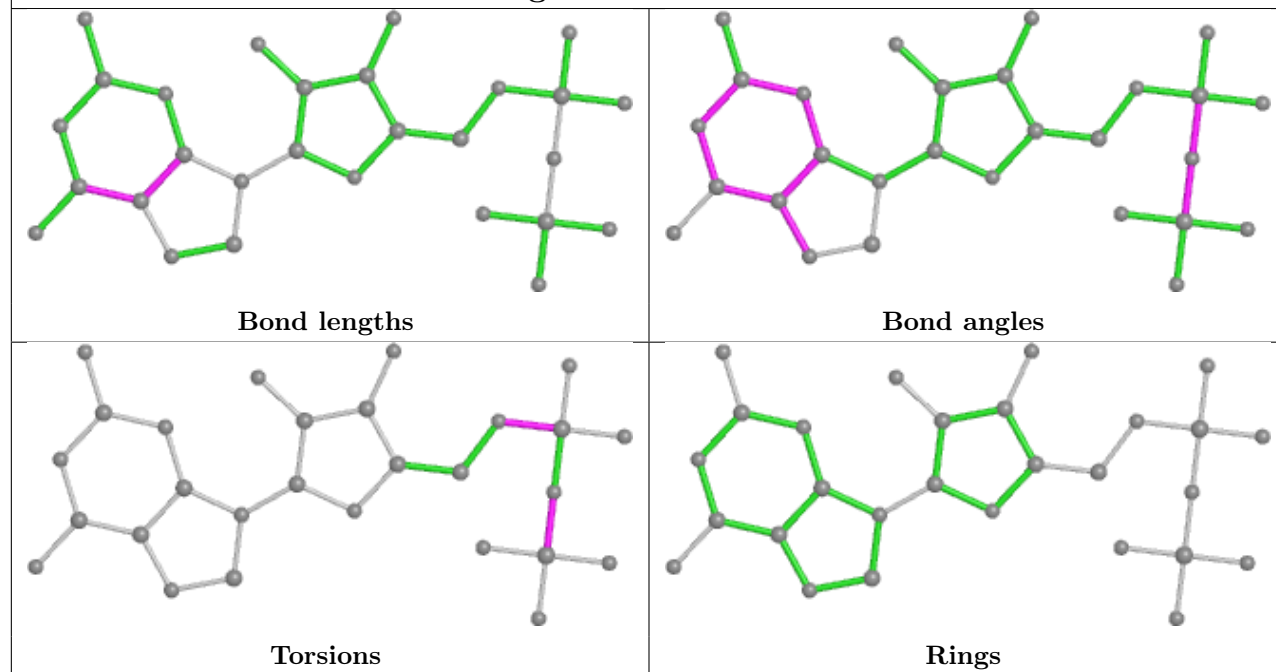
Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	F	401	ACP	5	0
8	D	501	GDP	2	0
8	B	501	GDP	1	0
5	A	501	GTP	1	0
9	B	504	MES	4	0

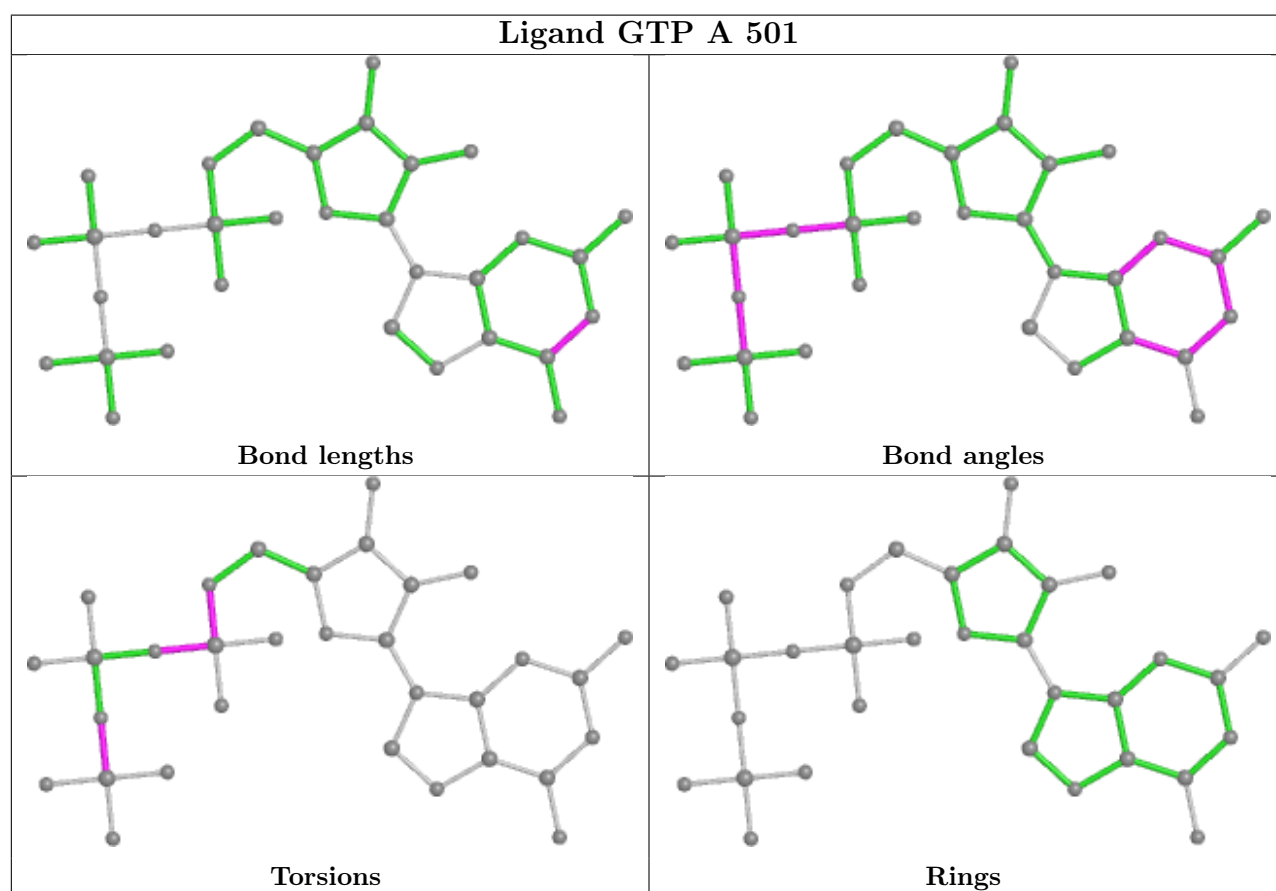
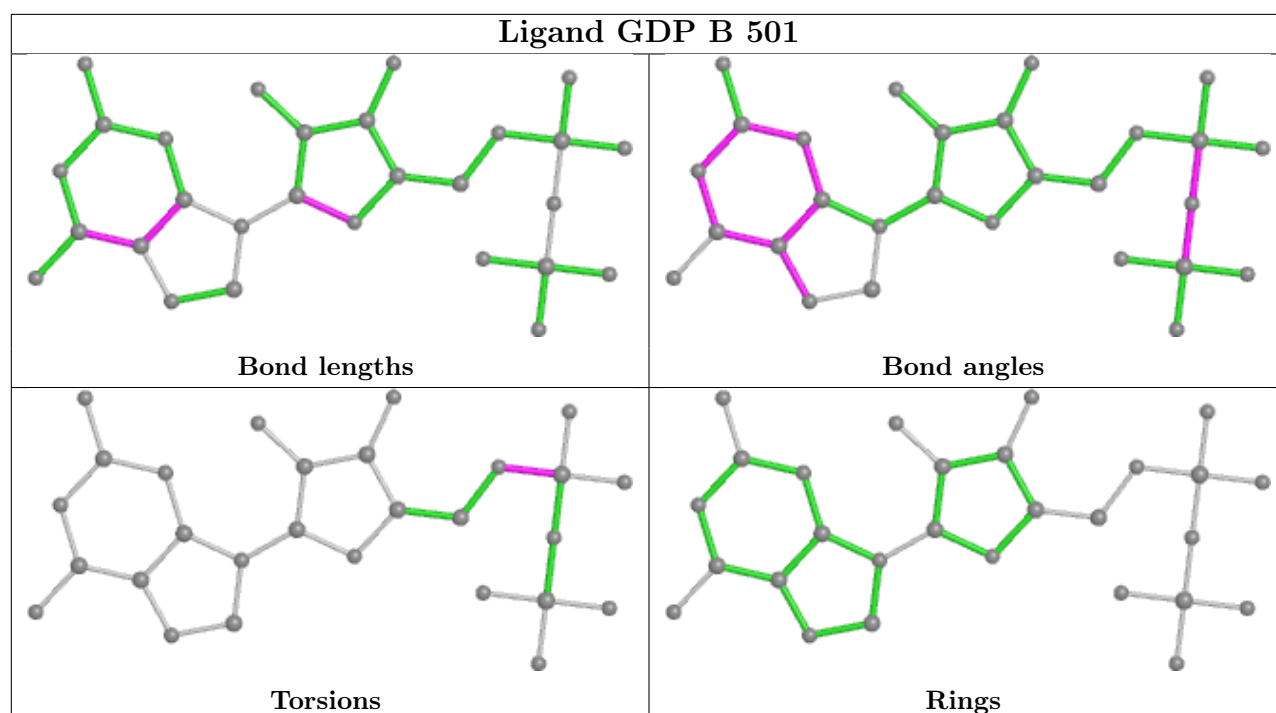
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

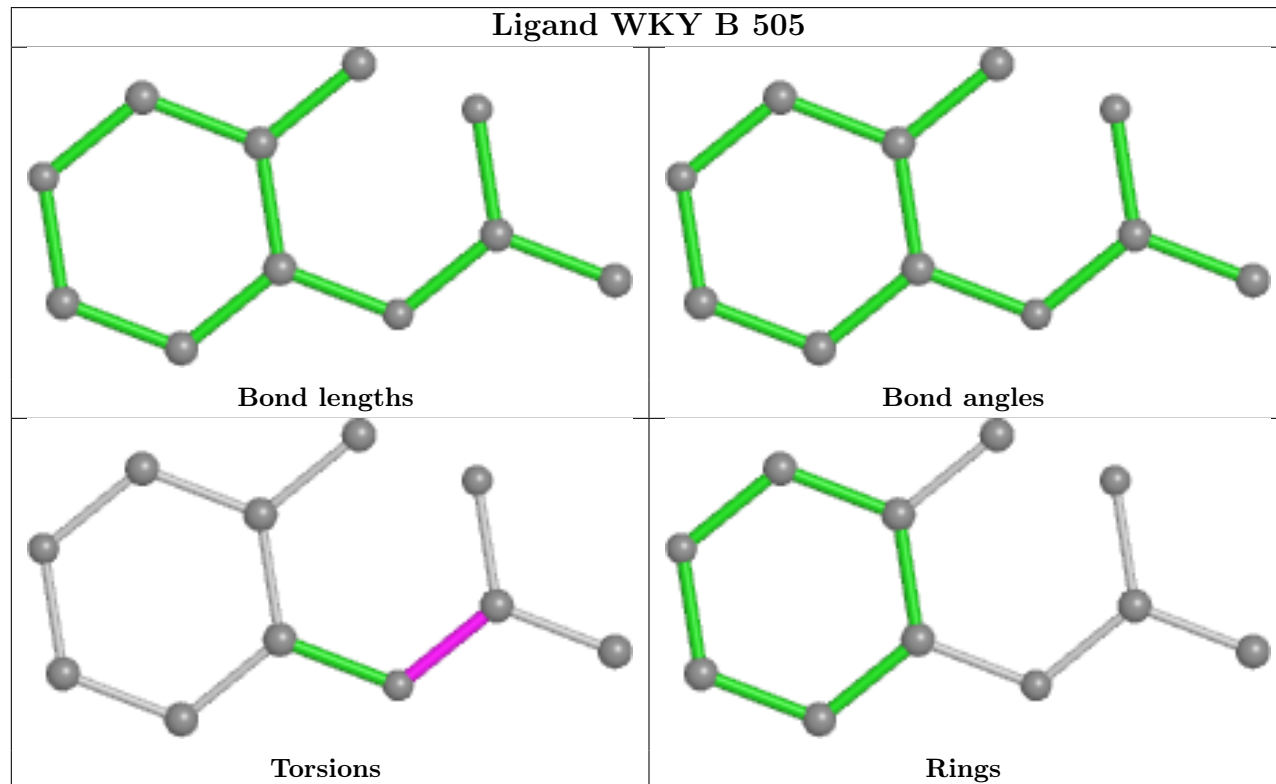
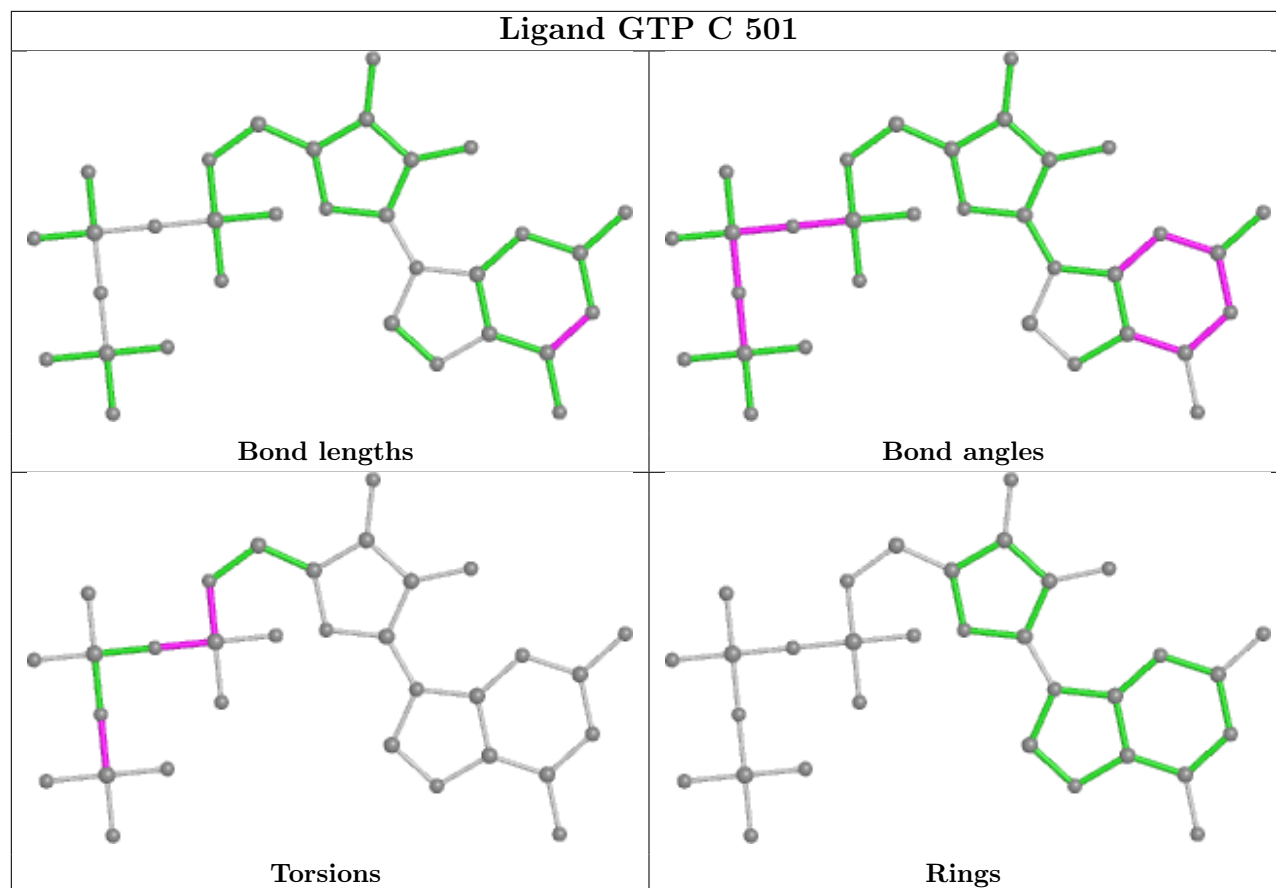
Ligand ACP F 401



Ligand GDP D 501







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	438/451 (97%)	0.24	15 (3%)	45	47	45, 64, 101, 161	0
1	C	440/451 (97%)	0.42	1 (0%)	95	96	37, 50, 73, 126	0
2	B	425/445 (95%)	0.39	13 (3%)	49	52	39, 63, 106, 146	2 (0%)
2	D	426/445 (95%)	0.23	18 (4%)	36	38	46, 70, 107, 149	4 (0%)
3	E	123/143 (86%)	0.84	10 (8%)	12	13	55, 75, 120, 146	0
4	F	352/384 (91%)	1.08	83 (23%)	0	0	58, 93, 155, 187	0
All	All	2204/2319 (95%)	0.47	140 (6%)	19	21	37, 66, 122, 187	6 (0%)

All (140) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	E	28	SER	11.8
3	E	27	PRO	10.5
3	E	24	LEU	7.9
3	E	26	PRO	7.7
2	D	277	SER	7.7
2	D	276	THR	7.6
2	D	278	ARG	7.3
3	E	25	LYS	6.2
4	F	142	ARG	6.0
1	A	346	TRP	5.9
4	F	103	THR	5.4
4	F	240	LEU	4.8
2	B	281	GLN	4.8
1	C	340	SER	4.8
4	F	381	HIS	4.8
3	E	6	MET	4.8
4	F	243	HIS	4.7
2	D	279	GLY	4.5
4	F	143	GLU	4.4

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Mol	Chain	Res	Type	RSRZ
4	F	169	LEU	4.3
4	F	259	GLY	4.3
2	D	57	THR	4.3
1	A	262	TYR	4.2
4	F	90	SER	4.2
1	A	340	SER	4.1
1	A	282	TYR	4.0
4	F	231	ALA	4.0
4	F	248	GLU	3.9
2	D	215	ARG	3.9
4	F	244	CYS	3.9
2	B	1	MET	3.9
4	F	342	LEU	3.9
4	F	135	TYR	3.8
4	F	173	ILE	3.8
4	F	182	ILE	3.7
4	F	236	LYS	3.7
4	F	138	ARG	3.7
4	F	233	PHE	3.7
1	A	438	ASP	3.7
1	A	88	HIS	3.7
4	F	249	TYR	3.7
4	F	253	TYR	3.6
1	A	348	PRO	3.6
2	D	401	ARG	3.6
2	D	275	LEU	3.5
4	F	245	ILE	3.5
2	D	217	LEU	3.5
4	F	153	ALA	3.4
4	F	361	LEU	3.4
4	F	163	SER	3.3
4	F	247	LYS	3.3
4	F	137	ARG	3.3
2	B	285	ALA	3.2
2	D	218	LYS	3.2
4	F	131	PHE	3.2
4	F	181	VAL	3.2
4	F	362	ALA	3.2
4	F	338	CYS	3.2
2	B	284	ARG	3.1
2	D	1	MET	3.1
4	F	20	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
4	F	125	THR	3.1
4	F	170	LEU	3.1
3	E	48	GLU	3.1
2	D	37	HIS	3.0
4	F	372	THR	3.0
4	F	17	VAL	3.0
4	F	254	GLY	3.0
1	A	341	ILE	3.0
1	A	362	VAL	2.9
4	F	89	GLU	2.9
4	F	105	LEU	2.9
2	B	336	GLN	2.9
2	B	57	THR	2.8
4	F	263	PHE	2.8
4	F	379	HIS	2.8
1	A	351	PHE	2.7
4	F	161	LEU	2.7
4	F	177	GLY	2.7
4	F	154	GLY	2.7
4	F	251	LYS	2.7
4	F	104	ASN	2.7
4	F	241	THR	2.7
4	F	306	HIS	2.7
4	F	152	SER	2.7
1	A	342	GLN	2.7
4	F	21	LEU	2.6
4	F	162	ILE	2.6
4	F	267	PHE	2.6
2	D	299	LYS	2.5
4	F	44	ARG	2.5
2	B	276	THR	2.5
2	B	437	ASP	2.5
4	F	25	GLY	2.5
4	F	132	LEU	2.5
4	F	186	LEU	2.5
4	F	197	ARG	2.5
4	F	71	LEU	2.5
4	F	144	GLY	2.5
2	B	333	LEU	2.5
4	F	99	VAL	2.5
4	F	140	GLU	2.4
2	B	325	MET	2.4

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Mol	Chain	Res	Type	RSRZ
4	F	252	ASN	2.4
1	A	284	GLU	2.4
4	F	223	THR	2.4
3	E	22	VAL	2.4
4	F	339	ALA	2.3
4	F	139	ARG	2.3
4	F	341	LYS	2.3
1	A	383	ALA	2.3
2	D	293	GLN	2.3
4	F	334	GLY	2.3
2	B	277	SER	2.3
4	F	255	ARG	2.2
4	F	256	TYR	2.2
4	F	176	GLN	2.2
4	F	234	GLN	2.2
4	F	242	ASN	2.2
2	D	83	PHE	2.2
4	F	179	VAL	2.2
4	F	147	TRP	2.2
4	F	155	ALA	2.1
4	F	222	ARG	2.1
2	D	400	ARG	2.1
4	F	24	THR	2.1
4	F	232	ASN	2.1
2	D	370	GLY	2.1
4	F	340	GLN	2.1
4	F	343	TYR	2.1
2	B	373	MET	2.1
2	D	60	LYS	2.1
4	F	75	ALA	2.1
2	B	318	ILE	2.0
1	A	344	VAL	2.0
1	A	345	ASP	2.0
4	F	283	ILE	2.0
3	E	124	GLN	2.0
4	F	315	PHE	2.0
3	E	139	LEU	2.0

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 monosaccharides in this entry.

6.4 Ligands ⓘ

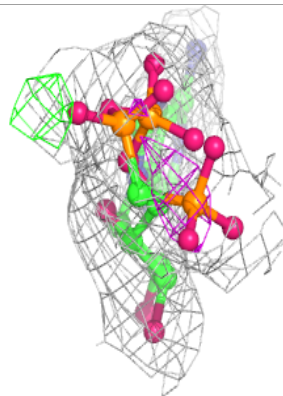
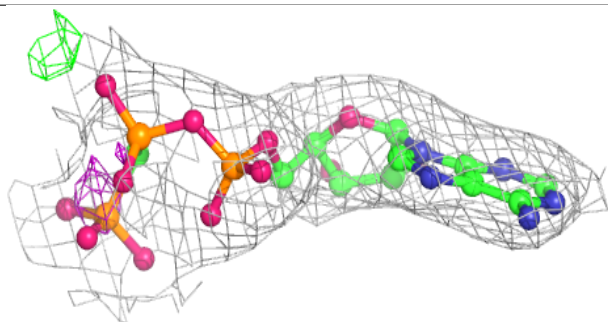
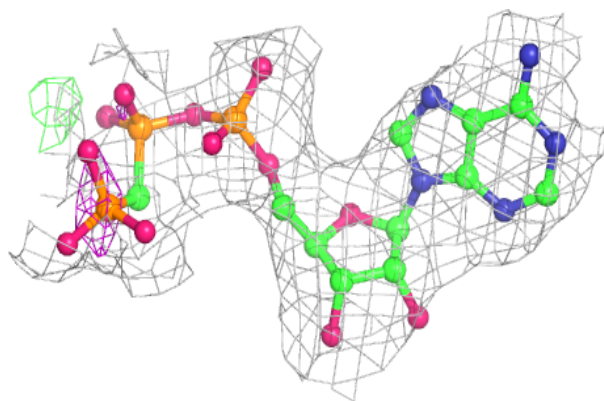
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
9	MES	B	504	12/12	0.73	0.30	124,129,139,142	0
6	MG	D	502	1/1	0.84	0.13	73,73,73,73	0
11	ACP	F	401	31/31	0.85	0.14	91,102,111,118	0
7	CA	A	503	1/1	0.86	0.12	92,92,92,92	0
10	WKY	B	505	11/11	0.89	0.18	43,52,59,64	21
6	MG	F	402	1/1	0.89	0.06	94,94,94,94	0
7	CA	B	503	1/1	0.93	0.24	113,113,113,113	0
6	MG	C	502	1/1	0.93	0.18	42,42,42,42	0
8	GDP	D	501	28/28	0.95	0.17	61,66,79,82	0
7	CA	A	504	1/1	0.95	0.14	92,92,92,92	0
5	GTP	A	501	32/32	0.97	0.14	40,49,56,59	0
6	MG	B	502	1/1	0.97	0.21	39,39,39,39	0
5	GTP	C	501	32/32	0.98	0.17	37,43,45,47	0
7	CA	C	503	1/1	0.98	0.12	65,65,65,65	0
6	MG	A	502	1/1	0.99	0.13	46,46,46,46	0
8	GDP	B	501	28/28	0.99	0.17	38,44,51,53	0

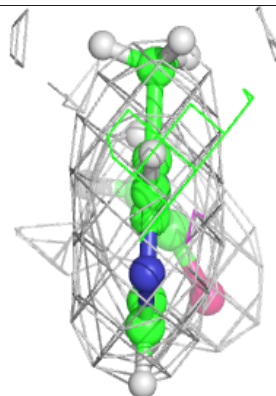
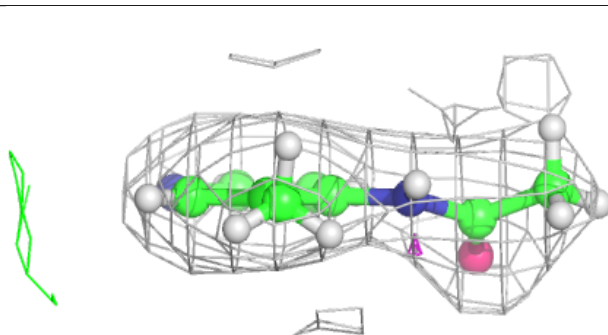
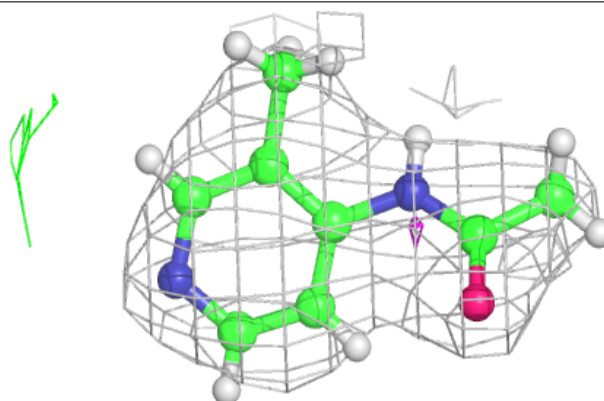
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around ACP F 401:

$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)

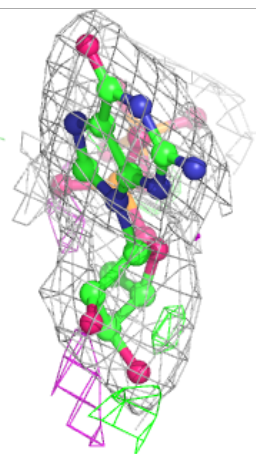
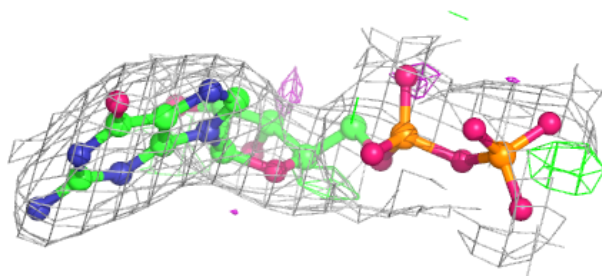
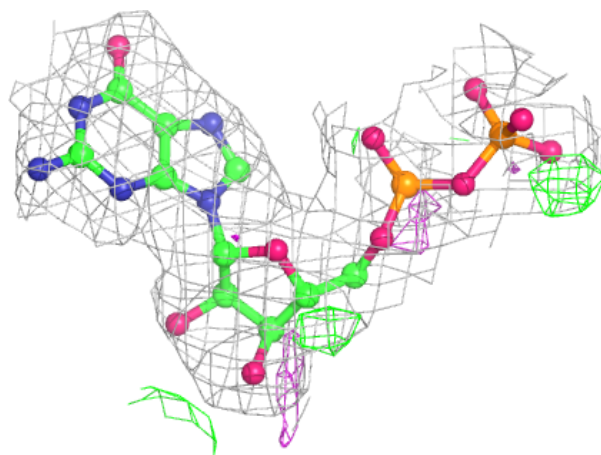
**Electron density around WKY B 505:**

$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)

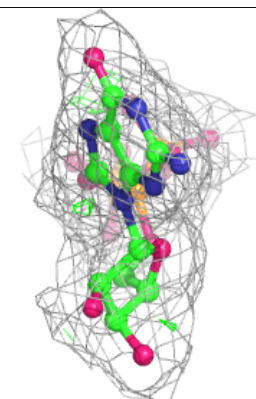
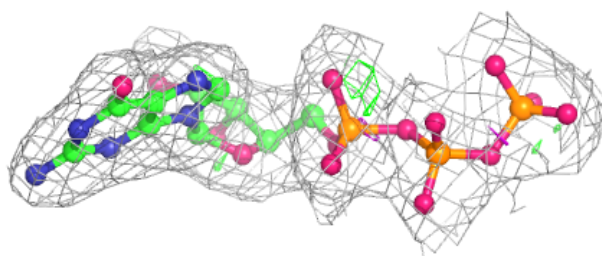
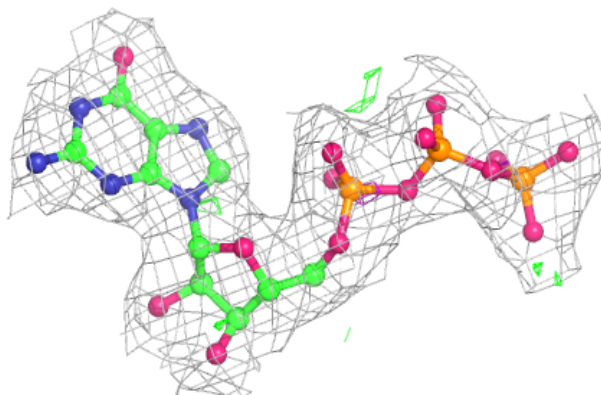


Electron density around GDP D 501:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

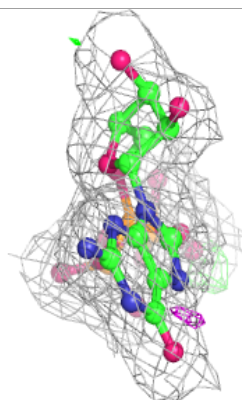
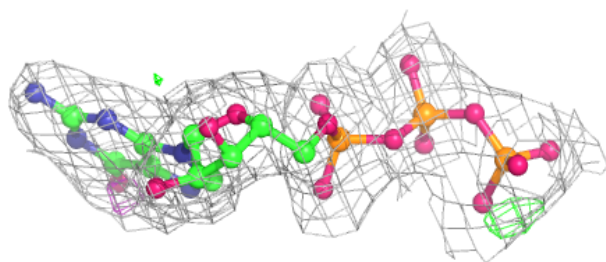
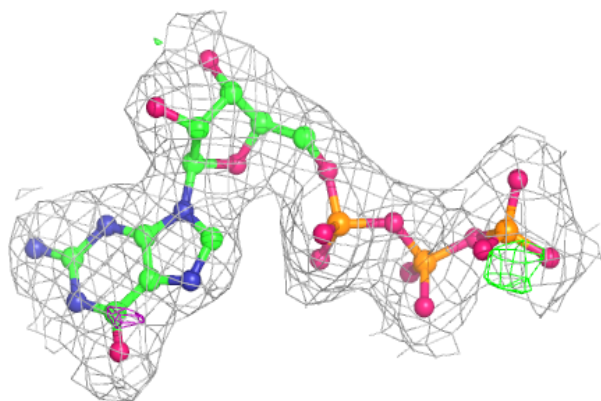
**Electron density around GTP A 501:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



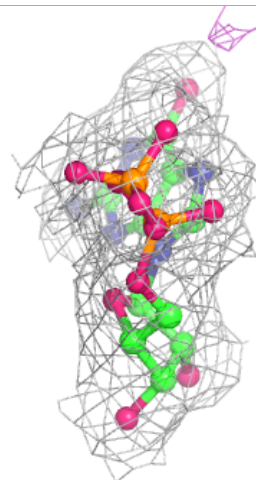
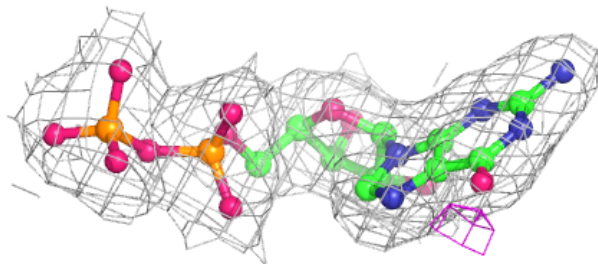
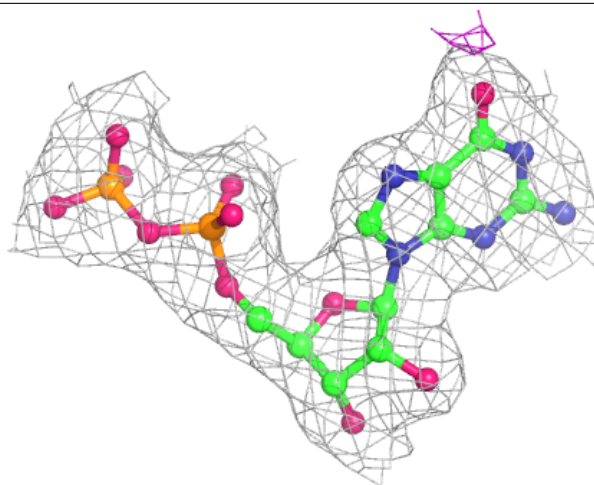
Electron density around GTP C 501:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around GDP B 501:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.