



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2024 – 08:58 PM EST

PDB ID : 5S5X
Title : Tubulin-Z45705015-complex
Authors : Muehlethaler, T.; Gioia, D.; Prota, A.E.; Sharpe, M.E.; Cavalli, A.; Steinmetz, M.O.
Deposited on : 2020-11-08
Resolution : 2.32 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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 : 2.36
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) : 2.36

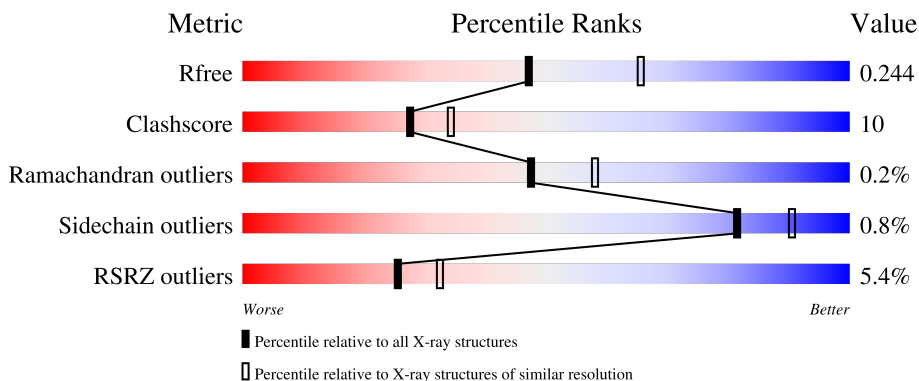
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.32 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.



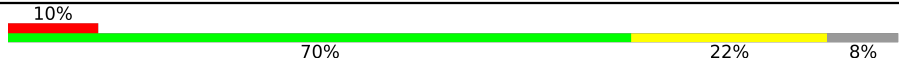
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5974 (2.34-2.30)
Clashscore	141614	6604 (2.34-2.30)
Ramachandran outliers	138981	6523 (2.34-2.30)
Sidechain outliers	138945	6523 (2.34-2.30)
RSRZ outliers	127900	5855 (2.34-2.30)

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	 3% 77% 19%
1	C	451	 2% 79% 18%
2	B	445	 6% 71% 25%
2	D	445	 4% 75% 21%
3	E	143	 8% 72% 14% 14%

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Mol	Chain	Length	Quality of chain
4	F	384	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into four segments: a red segment on the left labeled '10%', a large green segment labeled '70%', a yellow segment labeled '22%', and a small grey segment on the far right labeled '8%'.</p>

2 Entry composition [i](#)

There are 12 unique types of molecules in this entry. The entry contains 18044 atoms, of which 12 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
			Total	C	N	O	S			
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	0	0
			3437	2175	584	656	22			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	425	Total	C	N	O	S	2	1	0
			3359	2109	577	646	27			
2	D	428	Total	C	N	O	S	5	0	0
			3353	2104	572	650	27			

- Molecule 3 is a protein called Stathmin-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
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

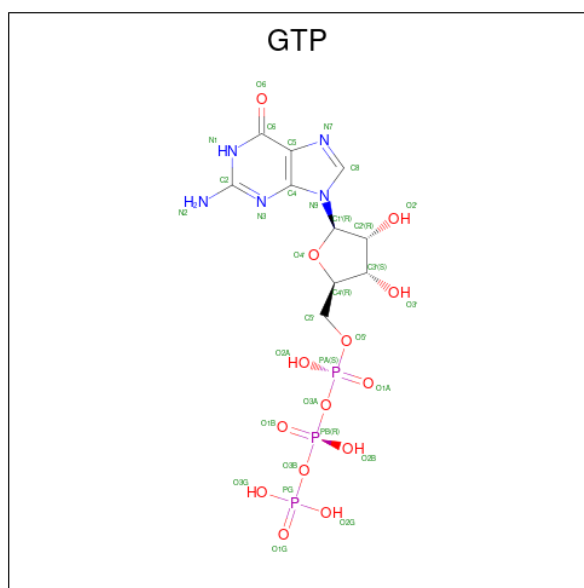
- Molecule 4 is a protein called Tubulin-Tyrosine Ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
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
			Total	C	N	O	P		
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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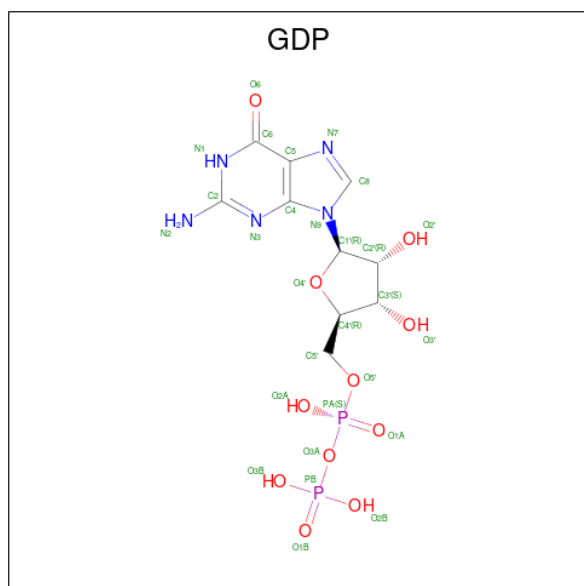
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	F	1	Total	Mg	0	0
			1	1		

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

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

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



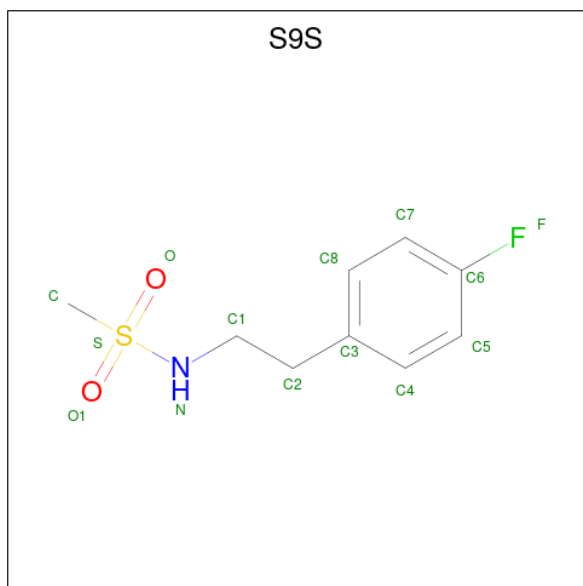
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
8	B	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
8	D	1	Total	C	N	O	P	0	0
			28	10	5	11	2		

- Molecule 9 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C₆H₁₃NO₄S).



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

- Molecule 10 is {N}-[2-(4-fluorophenyl)ethyl]methanesulfonamide (three-letter code: S9S) (formula: $C_9H_{12}FNO_2S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	
			Total	C	F	H	N	O			S
10	B	1	26	9	1	12	1	2	1	0	0

- 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
			Total	C	N	O	P		
11	F	1	31	11	5	12	3	0	0

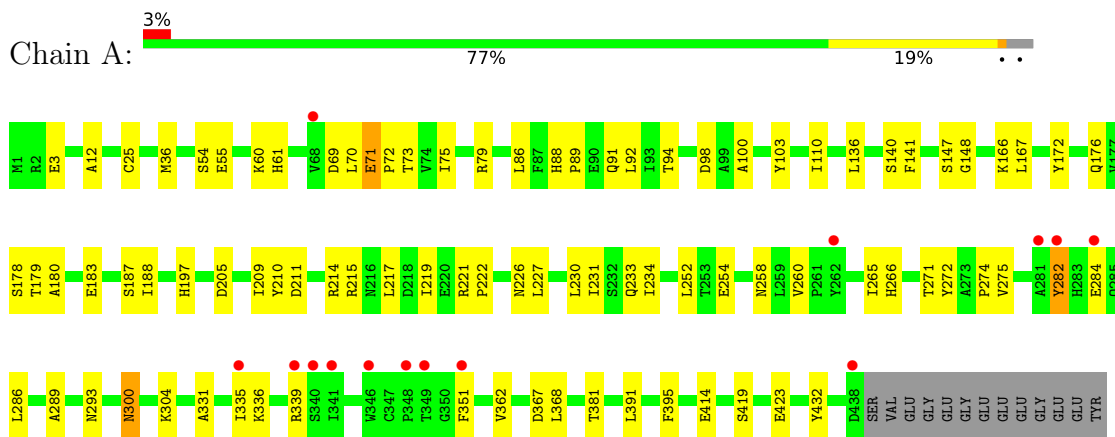
- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	67	Total	O	0	0
			67	67		
12	B	81	Total	O	0	0
			81	81		
12	C	181	Total	O	0	0
			181	181		
12	D	27	Total	O	0	0
			27	27		
12	E	13	Total	O	0	0
			13	13		
12	F	13	Total	O	0	0
			13	13		

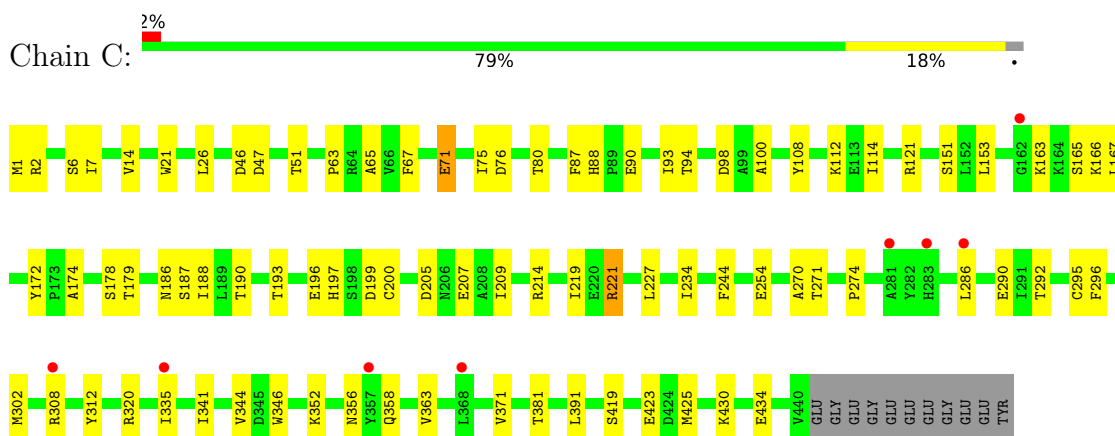
3 Residue-property plots [i](#)

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.

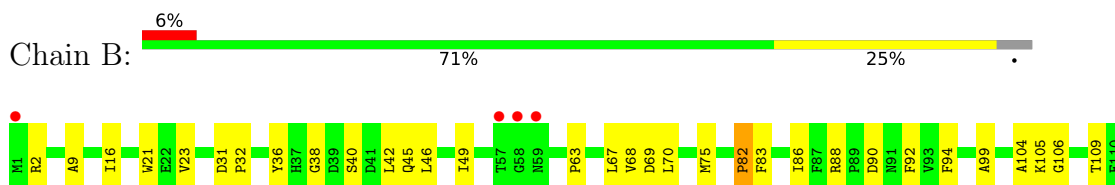
- Molecule 1: Tubulin alpha-1B chain

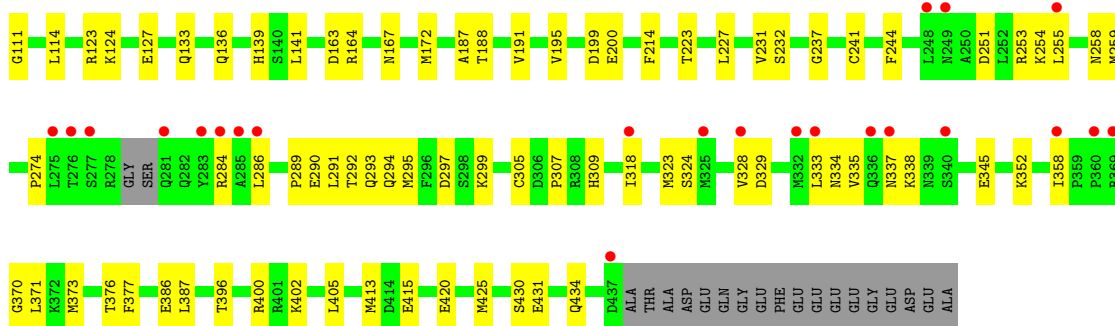


- Molecule 1: Tubulin alpha-1B chain

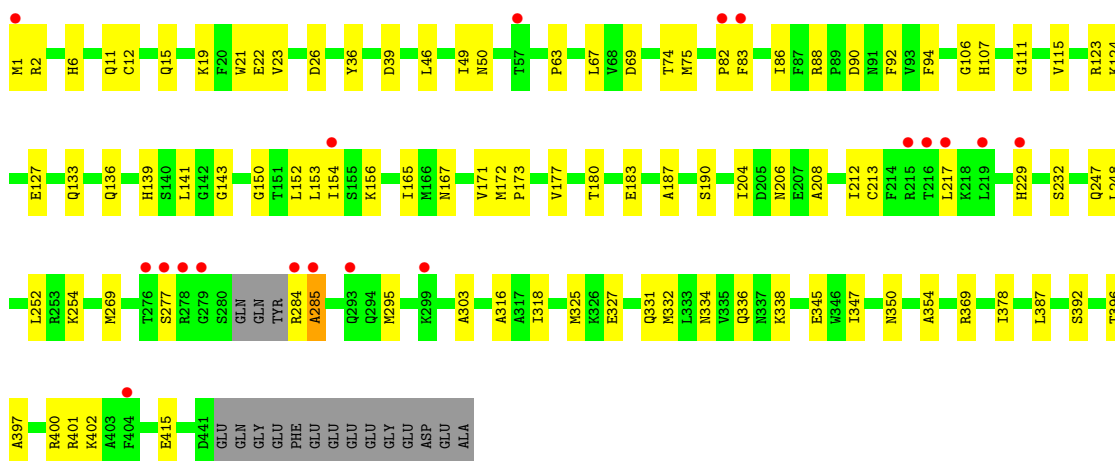
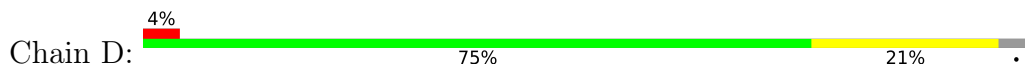


- Molecule 2: Tubulin beta-2B chain

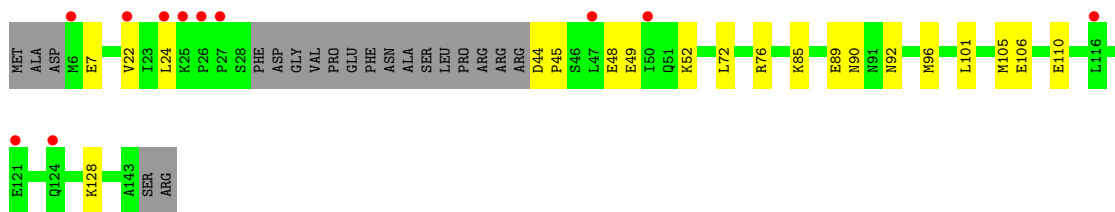
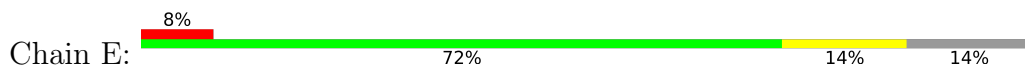




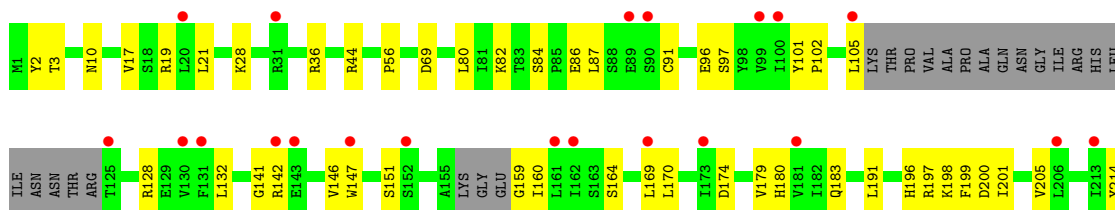
• Molecule 2: Tubulin beta-2B chain

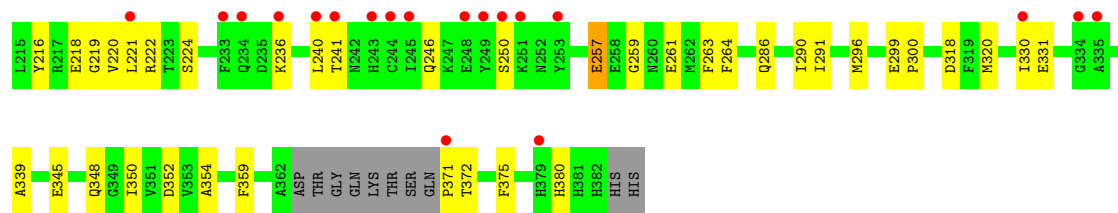


• Molecule 3: Stathmin-4



• 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	104.96Å 159.13Å 178.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	63.41 – 2.32 118.81 – 2.32	Depositor EDS
% Data completeness (in resolution range)	99.3 (63.41-2.32) 99.3 (118.81-2.32)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.20 (at 2.32Å)	Xtrriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.207 , 0.243 0.208 , 0.244	Depositor DCC
R_{free} test set	6541 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	57.3	Xtrriage
Anisotropy	0.247	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 47.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	18044	wwPDB-VP
Average B, all atoms (Å ²)	74.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.54% 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: CA, MG, MES, S9S, GDP, GTP, ACP

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	0/3515	0.42	0/4772
2	B	0.26	0/3433	0.42	0/4647
2	D	0.25	0/3426	0.41	0/4640
3	E	0.24	0/1022	0.35	0/1356
4	F	0.24	0/2944	0.40	0/3978
All	All	0.25	0/17842	0.41	0/24147

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	69	0
1	C	3437	0	3348	61	0
2	B	3359	0	3235	86	0
2	D	3353	0	3229	65	0
3	E	1014	0	1029	13	0
4	F	2877	0	2839	62	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	0	0
8	D	28	0	12	2	0
9	B	12	0	12	3	0
10	B	14	12	0	1	0
11	F	31	0	14	6	0
12	A	67	0	0	4	0
12	B	81	0	0	6	0
12	C	181	0	0	5	0
12	D	27	0	0	1	0
12	E	13	0	0	0	0
12	F	13	0	0	1	0
All	All	18032	12	17088	347	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 10.

All (347) 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:D:217:LEU:HA	2:D:277:SER:HB3	1.49	0.93
1:C:221:ARG:HG3	2:D:325:MET:HG2	1.49	0.92
4:F:236:LYS:HB3	4:F:240:LEU:HD13	1.52	0.92
4:F:102:PRO:HG2	4:F:105:LEU:HD13	1.53	0.90
4:F:331:GLU:OE2	11:F:401:ACP:O3G	1.93	0.85
1:C:209:ILE:HD11	1:C:302:MET:HE3	1.60	0.84
4:F:318:ASP:OD2	11:F:401:ACP:O2G	1.98	0.82
4:F:241:THR:OG1	11:F:401:ACP:O3'	1.98	0.82
2:B:253[A]:ARG:NH1	9:B:504:MES:O3S	2.15	0.80
1:A:335:ILE:HG23	1:A:339:ARG:HG3	1.64	0.78
2:D:334:ASN:HD21	2:D:338:LYS:HE3	1.47	0.78
4:F:10:ASN:HB2	4:F:44:ARG:HH22	1.49	0.78
1:A:71:GLU:OE2	1:A:73:THR:OG1	2.00	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:98:ASP:HB2	5:A:501:GTP:O2G	1.89	0.72
2:B:2:ARG:HB2	2:B:133:GLN:CG	2.21	0.71
2:B:167:ASN:OD1	2:B:200:GLU:HB2	1.91	0.70
4:F:241:THR:HG1	11:F:401:ACP:HO3'	1.33	0.70
1:C:1:MET:O	12:C:601:HOH:O	2.10	0.70
1:C:76:ASP:O	1:C:80:THR:HG22	1.91	0.70
2:D:269:MET:HG3	2:D:303:ALA:HB3	1.73	0.70
1:C:271:THR:HG21	1:C:295:CYS:O	1.91	0.69
2:B:274:PRO:HB3	2:B:286:LEU:HD22	1.74	0.69
4:F:371:PRO:HA	4:F:372:THR:HB	1.75	0.69
1:A:293:ASN:OD1	1:A:339:ARG:NH2	2.22	0.69
1:C:312:TYR:CD1	1:C:341:ILE:HG23	2.28	0.69
2:B:83:PHE:O	2:B:86:ILE:HG22	1.93	0.68
2:D:392:SER:O	2:D:396:THR:HG22	1.94	0.68
1:A:217:LEU:HD21	1:A:368:LEU:HD23	1.76	0.68
4:F:197:ARG:NH1	4:F:257:GLU:OE2	2.23	0.68
2:D:136:GLN:HA	2:D:167:ASN:O	1.94	0.67
2:B:67:LEU:HD22	2:B:92:PHE:CE2	2.30	0.67
1:C:47:ASP:OD2	12:C:602:HOH:O	2.11	0.66
2:B:69:ASP:O	2:B:94:PHE:HA	1.96	0.66
1:C:93:ILE:HD11	1:C:121:ARG:HG3	1.76	0.66
2:D:21:TRP:CZ3	2:D:63:PRO:HB3	2.31	0.66
1:A:100:ALA:HA	2:B:254:LYS:HG3	1.77	0.66
3:E:85:LYS:O	3:E:89:GLU:HG3	1.95	0.65
2:B:2:ARG:HB2	2:B:133:GLN:HG3	1.79	0.65
4:F:128:ARG:NH2	4:F:174:ASP:OD1	2.31	0.64
1:A:88:HIS:HB2	1:A:89:PRO:HD2	1.80	0.64
2:B:337:ASN:OD1	4:F:36:ARG:HD3	1.97	0.64
2:D:83:PHE:O	2:D:86:ILE:HG22	1.97	0.64
1:A:136:LEU:HD21	1:A:252:LEU:HD21	1.81	0.62
2:B:329:ASP:O	2:B:333:LEU:HG	1.99	0.62
1:A:166:LYS:HE2	1:A:197:HIS:O	1.99	0.62
2:D:248:LEU:HD23	2:D:354:ALA:HB2	1.82	0.62
1:C:430:LYS:HE2	1:C:434:GLU:OE2	1.99	0.62
4:F:320:MET:HG3	4:F:330:ILE:HD11	1.81	0.62
4:F:220:VAL:HG11	4:F:339:ALA:HB2	1.82	0.62
2:B:402:LYS:HB3	2:B:405:LEU:HD12	1.82	0.61
2:B:333:LEU:O	2:B:337:ASN:ND2	2.33	0.61
2:B:88:ARG:HH11	2:B:90:ASP:HB2	1.64	0.61
1:A:214:ARG:HG2	1:A:219:ILE:O	2.01	0.61
3:E:92:ASN:O	3:E:96:MET:HG2	1.99	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:234:ILE:HG12	1:C:302:MET:HE2	1.81	0.61
1:A:36:MET:HB3	1:A:61:HIS:CE1	2.36	0.60
4:F:236:LYS:HB3	4:F:240:LEU:CD1	2.28	0.60
2:B:36:TYR:CD1	2:B:46:LEU:HD21	2.37	0.60
2:B:274:PRO:HB3	2:B:286:LEU:CD2	2.32	0.60
2:D:332:MET:O	2:D:336:GLN:HG3	2.01	0.59
1:C:209:ILE:HD11	1:C:302:MET:CE	2.31	0.59
10:B:505:S9S:C	1:C:352:LYS:HG3	2.31	0.59
2:D:21:TRP:CE3	2:D:63:PRO:HB3	2.36	0.59
4:F:216:TYR:OH	4:F:345:GLU:OE1	2.20	0.58
1:A:176:GLN:HB2	12:A:627:HOH:O	2.03	0.58
2:B:106:GLY:O	2:B:111:GLY:HA3	2.02	0.58
2:B:16:ILE:HD13	2:B:231:VAL:HG11	1.85	0.58
1:A:419:SER:O	1:A:423:GLU:HG3	2.04	0.58
2:B:136:GLN:HA	2:B:167:ASN:O	2.03	0.58
2:D:171:VAL:HA	2:D:204:ILE:O	2.04	0.58
2:D:334:ASN:ND2	2:D:338:LYS:HE3	2.17	0.58
4:F:371:PRO:HA	4:F:372:THR:O	2.04	0.58
2:B:415:GLU:HG3	12:B:633:HOH:O	2.04	0.58
1:C:254:GLU:HG2	1:C:352:LYS:HE2	1.86	0.58
1:C:320:ARG:HA	1:C:356:ASN:O	2.04	0.58
4:F:371:PRO:CA	4:F:372:THR:HB	2.34	0.57
2:B:199:ASP:OD1	9:B:504:MES:H62	2.05	0.57
1:C:292:THR:HG22	1:C:335:ILE:CD1	2.34	0.57
2:D:141:LEU:HD12	2:D:172:MET:SD	2.44	0.57
2:D:402:LYS:HE2	2:D:415:GLU:OE1	2.03	0.57
1:C:308:ARG:HD2	12:C:728:HOH:O	2.04	0.57
4:F:216:TYR:CE2	4:F:218:GLU:HB2	2.40	0.57
4:F:320:MET:CG	4:F:330:ILE:HD11	2.35	0.57
2:D:397:ALA:HA	2:D:400:ARG:NH1	2.20	0.56
1:A:210:TYR:CE1	1:A:222:PRO:HD2	2.39	0.56
1:A:336:LYS:HG3	3:E:24:LEU:HD13	1.87	0.56
2:B:123:ARG:O	2:B:127:GLU:HG3	2.06	0.56
1:C:296:PHE:CD1	1:C:335:ILE:HD13	2.40	0.56
2:D:19:LYS:O	2:D:23:VAL:HG23	2.06	0.56
1:A:79:ARG:HG2	1:A:92:LEU:HD12	1.88	0.56
2:B:297:ASP:OD2	2:B:299:LYS:NZ	2.35	0.56
4:F:10:ASN:CB	4:F:44:ARG:HH22	2.16	0.56
1:A:172:TYR:HB3	1:A:205:ASP:HA	1.88	0.56
1:A:178:SER:OG	1:A:183:GLU:OE1	2.18	0.56
1:A:265:ILE:HG23	1:A:432:TYR:CZ	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:351:PHE:HE1	3:E:24:LEU:HD11	1.71	0.55
2:B:286:LEU:HD12	2:B:290:GLU:OE1	2.06	0.55
2:B:402:LYS:CB	2:B:405:LEU:HD12	2.37	0.55
2:B:370:GLY:O	2:B:371:LEU:HD23	2.07	0.55
2:D:11:GLN:HA	2:D:74:THR:HG21	1.88	0.55
4:F:82:LYS:NZ	4:F:97:SER:O	2.35	0.55
2:D:397:ALA:O	2:D:401:ARG:NH1	2.40	0.55
1:A:227:LEU:O	1:A:231:ILE:HG13	2.07	0.55
1:A:141:PHE:HB3	1:A:187:SER:OG	2.08	0.54
2:D:172:MET:HG3	2:D:387:LEU:HD11	1.90	0.54
4:F:214:TYR:HB3	4:F:375:PHE:HB3	1.89	0.54
2:B:420:GLU:OE1	12:B:601:HOH:O	2.18	0.54
4:F:2:TYR:CE1	4:F:359:PHE:HB3	2.43	0.54
1:C:75:ILE:HD12	1:C:94:THR:HG22	1.89	0.54
1:C:93:ILE:HG22	1:C:114:ILE:HD11	1.90	0.54
2:D:152:LEU:O	2:D:156:LYS:HG2	2.07	0.54
4:F:19:ARG:HD2	4:F:19:ARG:O	2.08	0.54
4:F:159:GLY:C	4:F:160:ILE:HD12	2.28	0.54
2:B:88:ARG:NH1	2:B:90:ASP:HB2	2.23	0.53
2:B:191:VAL:O	2:B:195:VAL:HG23	2.08	0.53
1:C:286:LEU:HA	1:C:290:GLU:OE1	2.08	0.53
2:B:172:MET:HG3	2:B:387:LEU:HD11	1.90	0.53
1:C:270:ALA:O	1:C:302:MET:HG2	2.09	0.53
4:F:147:TRP:HB2	4:F:169:LEU:HD11	1.90	0.53
4:F:286:GLN:O	4:F:290:ILE:HG13	2.08	0.53
2:D:173:PRO:HG3	2:D:187:ALA:HB2	1.90	0.53
1:A:209:ILE:HG22	1:A:227:LEU:HD22	1.90	0.53
2:B:396:THR:HG23	12:B:667:HOH:O	2.09	0.53
2:B:141:LEU:HD12	2:B:172:MET:SD	2.49	0.53
2:B:188:THR:HG23	2:B:425:MET:HE2	1.90	0.52
4:F:259:GLY:O	4:F:261:GLU:HG3	2.09	0.52
1:A:188:ILE:HD12	1:A:395:PHE:HB2	1.91	0.52
4:F:246:GLN:O	4:F:250:SER:HB3	2.09	0.52
1:A:179:THR:HA	2:B:352:LYS:HD2	1.90	0.52
2:B:284:ARG:NH2	2:B:290:GLU:OE2	2.43	0.52
2:D:22:GLU:HG2	2:D:83:PHE:CD1	2.44	0.52
1:A:265:ILE:HG23	1:A:432:TYR:CE1	2.45	0.52
2:D:124:LYS:C	2:D:124:LYS:HD3	2.29	0.52
4:F:371:PRO:HA	4:F:372:THR:C	2.29	0.52
1:C:292:THR:HG22	1:C:335:ILE:HD12	1.92	0.52
1:A:274:PRO:HB3	1:A:286:LEU:HD12	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:HIS:CD2	1:A:91:GLN:HG3	2.45	0.51
1:C:419:SER:O	1:C:423:GLU:HG3	2.10	0.51
2:B:251:ASP:OD2	2:B:254:LYS:HB2	2.11	0.51
2:D:12:CYS:HB2	8:D:501:GDP:C8	2.45	0.51
4:F:205:VAL:HG21	4:F:291:ILE:HD13	1.93	0.51
2:D:115:VAL:HG23	2:D:153:LEU:HD23	1.93	0.51
2:B:163:ASP:OD1	12:B:602:HOH:O	2.19	0.50
2:B:223:THR:O	2:B:227:LEU:HD13	2.12	0.50
4:F:132:LEU:HD21	4:F:170:LEU:HD11	1.92	0.50
1:A:300:ASN:HB3	12:A:601:HOH:O	2.10	0.50
1:C:244:PHE:CD1	1:C:358:GLN:HG2	2.45	0.50
1:C:214:ARG:HG2	1:C:219:ILE:O	2.11	0.50
2:D:69:ASP:O	2:D:94:PHE:HA	2.11	0.50
1:A:136:LEU:HD21	1:A:252:LEU:CD2	2.42	0.50
2:D:11:GLN:O	2:D:15:GLN:HG2	2.12	0.50
1:A:289:ALA:HA	1:A:331:ALA:CB	2.42	0.50
1:A:188:ILE:HD12	1:A:395:PHE:CD2	2.47	0.50
1:A:211:ASP:OD2	1:A:304:LYS:NZ	2.37	0.49
2:D:1:MET:HE3	2:D:50:ASN:HB2	1.92	0.49
2:D:165:ILE:HG21	2:D:252:LEU:HB3	1.94	0.49
2:B:82:PRO:O	12:B:603:HOH:O	2.20	0.49
1:C:196:GLU:HG2	12:C:677:HOH:O	2.12	0.49
4:F:151:SER:HB3	4:F:180:HIS:CD2	2.47	0.49
4:F:220:VAL:HG12	4:F:263:PHE:CE1	2.47	0.49
2:D:318:ILE:N	2:D:318:ILE:HD12	2.27	0.49
2:B:38:GLY:HA3	2:B:45:GLN:OE1	2.11	0.49
1:C:165:SER:HA	1:C:199:ASP:OD2	2.12	0.49
2:B:292:THR:HG22	2:B:335:VAL:HG21	1.94	0.49
2:D:106:GLY:O	2:D:111:GLY:HA3	2.12	0.49
1:A:226:ASN:ND2	1:A:367:ASP:OD2	2.46	0.49
2:D:143:GLY:HA3	8:D:501:GDP:O3A	2.12	0.49
2:B:290:GLU:O	2:B:294:GLN:HG3	2.13	0.49
2:D:107:HIS:O	2:D:152:LEU:HD22	2.12	0.49
2:B:124:LYS:HD3	2:B:124:LYS:C	2.33	0.48
1:A:271:THR:HG23	1:A:300:ASN:HD22	1.77	0.48
2:D:46:LEU:HA	2:D:49:ILE:HB	1.95	0.48
2:D:75:MET:HE3	2:D:92:PHE:CD2	2.48	0.48
4:F:146:VAL:HG22	4:F:164:SER:HB3	1.95	0.48
2:B:318:ILE:N	2:B:318:ILE:HD12	2.28	0.48
1:C:166:LYS:HE2	1:C:197:HIS:O	2.14	0.48
2:B:345:GLU:OE1	2:B:345:GLU:N	2.36	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:88:HIS:HE1	1:C:90:GLU:HG3	1.77	0.48
3:E:48:GLU:HG2	3:E:52:LYS:HE3	1.95	0.48
4:F:3:THR:HA	4:F:28:LYS:O	2.12	0.48
2:D:36:TYR:CD2	2:D:46:LEU:HD11	2.49	0.48
4:F:348:GLN:NE2	4:F:352:ASP:OD1	2.47	0.48
2:D:123:ARG:O	2:D:127:GLU:HG3	2.13	0.48
4:F:350:ILE:O	4:F:354:ALA:HB3	2.14	0.47
4:F:296:MET:SD	4:F:380:HIS:HB2	2.54	0.47
1:C:108:TYR:O	1:C:112:LYS:HG2	2.15	0.47
4:F:80:LEU:HD12	4:F:84:SER:OG	2.15	0.47
4:F:201:ILE:HG12	4:F:221:LEU:HG	1.95	0.47
2:B:70:LEU:HD12	2:B:99:ALA:HB2	1.97	0.47
2:B:309:HIS:ND1	2:B:386:GLU:OE2	2.44	0.47
1:C:100:ALA:HA	2:D:254:LYS:HG3	1.97	0.47
2:B:295:MET:CG	2:B:377:PHE:HB2	2.44	0.47
1:C:172:TYR:HB3	1:C:205:ASP:HA	1.97	0.47
3:E:44:ASP:HB3	3:E:45:PRO:HD2	1.97	0.47
4:F:299:GLU:HB3	4:F:300:PRO:HD3	1.96	0.47
2:B:46:LEU:HA	2:B:49:ILE:HB	1.97	0.47
2:D:2:ARG:HB3	2:D:133:GLN:CG	2.45	0.47
2:D:75:MET:HE3	2:D:92:PHE:HD2	1.80	0.47
2:D:1:MET:HG3	2:D:50:ASN:HB2	1.97	0.46
2:D:318:ILE:HG12	12:D:610:HOH:O	2.14	0.46
2:B:42:LEU:H	2:B:42:LEU:HD12	1.80	0.46
2:B:67:LEU:N	2:B:67:LEU:HD12	2.30	0.46
1:A:103:TYR:CD2	1:A:148:GLY:HA2	2.51	0.46
2:B:104:ALA:HB2	2:B:413:MET:SD	2.55	0.46
2:B:253[A]:ARG:NH1	9:B:504:MES:S	2.75	0.46
2:D:88:ARG:NH1	2:D:90:ASP:HB2	2.31	0.46
2:D:23:VAL:HG21	2:D:232:SER:HB2	1.97	0.46
1:A:103:TYR:CE2	1:A:148:GLY:HA2	2.51	0.46
1:C:296:PHE:CE1	1:C:335:ILE:HD13	2.50	0.46
2:D:6:HIS:CD2	2:D:21:TRP:HE1	2.33	0.46
1:C:187:SER:HB3	1:C:391:LEU:HD21	1.98	0.46
1:C:7:ILE:HG21	1:C:153:LEU:HD21	1.97	0.46
1:A:335:ILE:HG23	1:A:339:ARG:CG	2.39	0.46
2:B:323:MET:CE	2:B:373:MET:HB2	2.46	0.46
2:B:164:ARG:HD2	12:B:653:HOH:O	2.15	0.46
1:C:344:VAL:HG21	1:C:346:TRP:CE2	2.51	0.46
1:C:88:HIS:CE1	1:C:90:GLU:HG3	2.50	0.46
1:C:93:ILE:CD1	1:C:121:ARG:HG3	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:15:GLN:O	2:D:19:LYS:HG2	2.16	0.45
3:E:7:GLU:O	3:E:22:VAL:HA	2.17	0.45
4:F:147:TRP:HB2	4:F:169:LEU:CD1	2.46	0.45
1:A:71:GLU:HG2	1:A:72:PRO:N	2.32	0.45
1:A:289:ALA:HA	1:A:331:ALA:HB1	1.97	0.45
3:E:72:LEU:O	3:E:76:ARG:HG2	2.16	0.45
4:F:200:ASP:OD1	4:F:222:ARG:HB2	2.16	0.45
1:A:275:VAL:HG13	1:A:368:LEU:CD2	2.46	0.45
1:C:26:LEU:HD12	1:C:363:VAL:HG22	1.98	0.45
2:D:213:CYS:HA	2:D:217:LEU:HB2	1.97	0.45
4:F:69:ASP:OD1	4:F:69:ASP:N	2.49	0.45
1:A:70:LEU:HB2	1:A:98:ASP:HA	1.99	0.45
2:B:244:PHE:CE1	2:B:358:ILE:HD12	2.52	0.45
3:E:106:GLU:O	3:E:110:GLU:HG3	2.17	0.45
1:A:55:GLU:HA	1:A:60:LYS:O	2.17	0.45
1:A:187:SER:CB	1:A:391:LEU:HD21	2.46	0.45
2:B:40:SER:OG	2:B:42:LEU:HD13	2.17	0.45
2:B:334:ASN:OD1	2:B:338:LYS:HD3	2.16	0.45
4:F:197:ARG:HB2	4:F:224:SER:O	2.16	0.45
1:A:3:GLU:OE1	1:A:3:GLU:N	2.49	0.45
2:D:1:MET:CE	2:D:50:ASN:HB2	2.46	0.45
2:B:75:MET:HE3	2:B:92:PHE:HD2	1.82	0.45
1:C:274:PRO:HG2	1:C:371:VAL:HG11	1.99	0.45
4:F:219:GLY:HA3	4:F:264:PHE:CZ	2.52	0.45
1:A:254:GLU:HG2	1:A:258:ASN:ND2	2.32	0.44
2:B:295:MET:HG2	2:B:377:PHE:HB2	2.00	0.44
2:D:295:MET:HB2	2:D:295:MET:HE3	1.83	0.44
2:B:187:ALA:O	2:B:191:VAL:HG23	2.17	0.44
2:B:305:CYS:O	2:B:307:PRO:HD3	2.17	0.44
1:C:163:LYS:HG3	3:E:90:ASN:OD1	2.17	0.44
4:F:17:VAL:O	4:F:21:LEU:HG	2.18	0.44
4:F:198:LYS:HG2	4:F:199:PHE:H	1.83	0.44
1:A:211:ASP:HB3	1:A:215:ARG:NH2	2.33	0.44
1:C:6:SER:O	1:C:65:ALA:HA	2.18	0.44
1:C:186:ASN:O	1:C:190:THR:HG22	2.18	0.44
2:D:180:THR:HB	2:D:183:GLU:HG3	1.99	0.44
1:A:209:ILE:HG22	1:A:227:LEU:CD2	2.47	0.43
2:B:334:ASN:O	2:B:338:LYS:HG3	2.18	0.43
2:D:347:ILE:HG22	2:D:350:ASN:HB3	2.00	0.43
1:A:54:SER:O	1:A:61:HIS:HA	2.17	0.43
4:F:80:LEU:HD12	4:F:84:SER:HG	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:23:VAL:HG21	2:B:232:SER:HB3	2.01	0.43
2:D:67:LEU:N	2:D:67:LEU:HD12	2.33	0.43
1:A:209:ILE:HG23	1:A:230:LEU:HD23	2.00	0.43
2:B:114:LEU:O	2:B:114:LEU:HG	2.19	0.43
4:F:160:ILE:HD12	4:F:160:ILE:N	2.34	0.43
4:F:191:LEU:HD12	4:F:196:HIS:CE1	2.54	0.43
2:B:21:TRP:CZ3	2:B:63:PRO:HB3	2.54	0.43
1:C:234:ILE:HD12	1:C:234:ILE:H	1.84	0.43
2:B:237:GLY:HA3	2:B:376:THR:OG1	2.19	0.43
1:C:341:ILE:HD12	1:C:341:ILE:N	2.34	0.43
2:D:327:GLU:O	2:D:331:GLN:HG2	2.17	0.43
2:B:31:ASP:HB2	2:B:32:PRO:CD	2.48	0.43
2:B:255:LEU:HD11	2:B:259:MET:HG3	2.01	0.43
1:C:63:PRO:HG2	1:C:87:PHE:CE1	2.54	0.43
4:F:101:TYR:CD2	4:F:179:VAL:HG22	2.54	0.43
1:A:188:ILE:HD12	1:A:395:PHE:CB	2.49	0.42
1:A:180:ALA:HA	2:B:258:ASN:OD1	2.18	0.42
2:B:324:SER:O	2:B:328:VAL:HG23	2.18	0.42
1:C:71:GLU:HB3	1:C:98:ASP:HB3	2.01	0.42
1:A:75:ILE:HD12	1:A:94:THR:HG22	2.02	0.42
2:B:396:THR:O	2:B:400:ARG:HG2	2.20	0.42
2:D:141:LEU:HD22	2:D:190:SER:HB3	2.00	0.42
2:D:177:VAL:HG21	2:D:206:ASN:HB3	2.02	0.42
3:E:45:PRO:HA	3:E:49:GLU:OE1	2.20	0.42
1:A:272:TYR:O	1:A:300:ASN:HB2	2.20	0.42
2:B:163:ASP:O	2:B:253[A]:ARG:NH2	2.50	0.42
2:B:9:ALA:HA	2:B:68:VAL:O	2.20	0.42
2:B:291:LEU:HD23	2:B:291:LEU:HA	1.94	0.42
1:C:174:ALA:O	1:C:178:SER:HB3	2.19	0.42
1:C:234:ILE:HG12	1:C:302:MET:CE	2.48	0.42
2:D:150:GLY:O	2:D:154:ILE:HG13	2.20	0.42
4:F:198:LYS:HZ1	11:F:401:ACP:C2	2.33	0.42
2:B:16:ILE:HG21	2:B:231:VAL:HG11	2.02	0.42
2:B:255:LEU:CD1	2:B:259:MET:HG3	2.50	0.42
2:D:115:VAL:HG23	2:D:153:LEU:CD2	2.50	0.42
1:A:25:CYS:SG	1:A:86:LEU:HD11	2.60	0.41
2:B:188:THR:HA	2:B:425:MET:HE2	2.02	0.41
2:B:241:CYS:SG	2:B:318:ILE:HG12	2.60	0.41
2:B:323:MET:HE2	2:B:373:MET:HB2	2.02	0.41
1:C:151:SER:HB2	1:C:193:THR:CG2	2.50	0.41
2:D:284:ARG:O	2:D:285:ALA:HB3	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:316:ALA:HB3	2:D:378:ILE:HB	2.02	0.41
4:F:86:GLU:HB3	12:F:511:HOH:O	2.19	0.41
1:A:141:PHE:O	1:A:147:SER:HB3	2.20	0.41
1:A:234:ILE:HD12	1:A:234:ILE:N	2.35	0.41
11:F:401:ACP:O3G	11:F:401:ACP:O1B	2.38	0.41
1:A:167:LEU:HD13	1:A:252:LEU:HD22	2.02	0.41
1:A:233:GLN:HG3	1:A:368:LEU:CD1	2.51	0.41
1:C:188:ILE:HG13	1:C:425:MET:HG3	2.02	0.41
1:A:167:LEU:HD12	1:A:167:LEU:N	2.36	0.41
1:A:284:GLU:CD	1:A:284:GLU:H	2.24	0.41
2:B:88:ARG:NH1	2:B:90:ASP:OD2	2.54	0.41
1:C:14:VAL:HG13	1:C:67:PHE:HD2	1.85	0.41
2:D:387:LEU:HD23	2:D:387:LEU:C	2.40	0.41
2:B:289:PRO:O	2:B:293:GLN:HG3	2.20	0.41
1:C:2:ARG:O	1:C:51:THR:HG22	2.21	0.41
1:C:179:THR:HG21	12:C:631:HOH:O	2.20	0.41
1:C:286:LEU:HD23	1:C:290:GLU:OE1	2.21	0.41
2:D:26:ASP:OD2	2:D:369:ARG:HD2	2.20	0.41
2:D:345:GLU:H	2:D:345:GLU:HG2	1.71	0.41
4:F:96:GLU:O	4:F:183:GLN:HA	2.20	0.41
4:F:141:GLY:O	4:F:142:ARG:HB2	2.20	0.41
1:A:260:VAL:HG11	1:A:266:HIS:HB3	2.01	0.41
2:B:431:GLU:O	2:B:434:GLN:HG2	2.20	0.41
1:C:21:TRP:CZ3	1:C:63:PRO:HB3	2.56	0.41
1:A:12:ALA:HB3	1:A:140:SER:HB3	2.03	0.41
1:A:176:GLN:HG3	4:F:56:PRO:HB3	2.02	0.41
1:C:46:ASP:OD1	1:C:46:ASP:N	2.49	0.41
1:C:174:ALA:CB	1:C:207:GLU:HB2	2.51	0.41
4:F:205:VAL:CG2	4:F:291:ILE:HD13	2.51	0.41
4:F:216:TYR:CZ	4:F:218:GLU:HB2	2.56	0.41
4:F:240:LEU:HD12	4:F:240:LEU:N	2.36	0.41
1:A:414:GLU:HB3	12:A:657:HOH:O	2.20	0.41
2:D:208:ALA:O	2:D:212:ILE:HG13	2.21	0.41
3:E:101:LEU:O	3:E:105:MET:HG2	2.20	0.41
2:B:105:LYS:HA	2:B:109:THR:OG1	2.21	0.40
2:D:217:LEU:CA	2:D:277:SER:HB3	2.36	0.40
1:A:69:ASP:O	1:A:94:THR:HA	2.21	0.40
1:A:335:ILE:CG2	1:A:339:ARG:HG3	2.44	0.40
2:B:200:GLU:OE2	2:B:255:LEU:HG	2.21	0.40
4:F:87:LEU:O	4:F:91:CYS:HB2	2.21	0.40
1:C:174:ALA:HB1	1:C:207:GLU:HB2	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:209:ILE:HG22	1:C:227:LEU:HD22	2.02	0.40
3:E:128:LYS:HD3	3:E:128:LYS:O	2.21	0.40
1:A:70:LEU:HD13	1:A:110:ILE:HG21	2.03	0.40
2:B:42:LEU:HD12	2:B:42:LEU:N	2.36	0.40
1:C:167:LEU:HG	1:C:200:CYS:HB3	2.03	0.40
1:A:362:VAL:HG22	12:A:611:HOH:O	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	436/451 (97%)	426 (98%)	9 (2%)	1 (0%)	47	58
1	C	438/451 (97%)	428 (98%)	10 (2%)	0	100	100
2	B	422/445 (95%)	409 (97%)	12 (3%)	1 (0%)	47	58
2	D	424/445 (95%)	412 (97%)	10 (2%)	2 (0%)	29	35
3	E	119/143 (83%)	118 (99%)	1 (1%)	0	100	100
4	F	344/384 (90%)	334 (97%)	10 (3%)	0	100	100
All	All	2183/2319 (94%)	2127 (97%)	52 (2%)	4 (0%)	47	58

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	282	TYR
2	D	285	ALA
2	D	82	PRO
2	B	82	PRO

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	369/379 (97%)	364 (99%)	5 (1%)	67	80
1	C	371/379 (98%)	368 (99%)	3 (1%)	81	90
2	B	368/383 (96%)	365 (99%)	3 (1%)	81	90
2	D	368/383 (96%)	364 (99%)	4 (1%)	73	85
3	E	110/127 (87%)	110 (100%)	0	100	100
4	F	315/342 (92%)	314 (100%)	1 (0%)	92	96
All	All	1901/1993 (95%)	1885 (99%)	16 (1%)	81	90

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	71	GLU
1	A	221	ARG
1	A	282	TYR
1	A	300	ASN
1	A	381	THR
2	B	139	HIS
2	B	214	PHE
2	B	430	SER
1	C	71	GLU
1	C	221	ARG
1	C	381	THR
2	D	39	ASP
2	D	139	HIS
2	D	229	HIS
2	D	247	GLN
4	F	257	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	88	HIS

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Mol	Chain	Res	Type
1	A	300	ASN
2	B	15	GLN
2	B	294	GLN
2	B	337	ASN
1	C	11	GLN
2	D	167	ASN
2	D	294	GLN
4	F	196	HIS
4	F	229	ASN
4	F	333	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	1.46	4 (12%)
10	S9S	B	505	-	14,14,14	0.32	0	18,19,19	0.40	0
5	GTP	A	501	6	26,34,34	1.15	2 (7%)	32,54,54	1.38	6 (18%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	GDP	B	501	6	24,30,30	0.95	1 (4%)	30,47,47	1.09	3 (10%)
9	MES	B	504	-	12,12,12	2.22	1 (8%)	14,16,16	2.04	5 (35%)
5	GTP	C	501	6	26,34,34	1.15	2 (7%)	32,54,54	1.36	6 (18%)
8	GDP	D	501	6	24,30,30	0.94	1 (4%)	30,47,47	1.12	3 (10%)

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	-	8/15/38/38	0/3/3/3
10	S9S	B	505	-	-	4/7/7/7	0/1/1/1
5	GTP	A	501	6	-	9/18/38/38	0/3/3/3
8	GDP	B	501	6	-	3/12/32/32	0/3/3/3
9	MES	B	504	-	-	4/6/14/14	0/1/1/1
5	GTP	C	501	6	-	8/18/38/38	0/3/3/3
8	GDP	D	501	6	-	6/12/32/32	0/3/3/3

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	B	504	MES	C8-S	-7.43	1.67	1.77
5	C	501	GTP	C5-C6	-4.10	1.39	1.47
5	A	501	GTP	C5-C6	-4.00	1.39	1.47
11	F	401	ACP	PG-O3G	2.95	1.61	1.54
11	F	401	ACP	PG-O2G	2.92	1.61	1.54
11	F	401	ACP	PB-O3A	2.78	1.61	1.58
11	F	401	ACP	C5-C4	2.51	1.47	1.40
8	B	501	GDP	C6-N1	-2.41	1.34	1.37
8	D	501	GDP	C6-N1	-2.25	1.34	1.37
11	F	401	ACP	PB-O2B	2.25	1.61	1.56
5	C	501	GTP	C2-N3	2.09	1.38	1.33
5	A	501	GTP	C2-N3	2.01	1.38	1.33

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	F	401	ACP	PB-O3A-PA	-3.97	119.97	132.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	B	504	MES	C5-N4-C3	3.56	116.84	108.83
11	F	401	ACP	C3'-C2'-C1'	3.39	106.08	100.98
9	B	504	MES	C6-C5-N4	-3.17	105.29	110.10
9	B	504	MES	O1S-S-C8	3.17	110.73	106.92
11	F	401	ACP	N3-C2-N1	-3.11	123.83	128.68
5	A	501	GTP	C8-N7-C5	3.06	108.83	102.99
5	A	501	GTP	C5-C6-N1	3.05	119.34	113.95
5	C	501	GTP	C5-C6-N1	3.00	119.25	113.95
5	C	501	GTP	C8-N7-C5	2.96	108.63	102.99
5	A	501	GTP	PA-O3A-PB	-2.96	122.68	132.83
5	C	501	GTP	C2-N1-C6	-2.77	119.99	125.10
11	F	401	ACP	C4-C5-N7	-2.74	106.55	109.40
8	D	501	GDP	PA-O3A-PB	-2.72	123.50	132.83
5	A	501	GTP	C2-N1-C6	-2.70	120.12	125.10
5	C	501	GTP	PA-O3A-PB	-2.70	123.57	132.83
9	B	504	MES	O3S-S-C8	2.60	109.98	105.77
5	C	501	GTP	PB-O3B-PG	-2.53	124.15	132.83
8	B	501	GDP	C5-C6-N1	2.50	118.36	113.95
8	B	501	GDP	PA-O3A-PB	-2.49	124.28	132.83
9	B	504	MES	C7-N4-C5	2.41	117.41	111.23
8	D	501	GDP	C8-N7-C5	2.33	107.43	102.99
8	B	501	GDP	C8-N7-C5	2.32	107.42	102.99
5	A	501	GTP	PB-O3B-PG	-2.31	124.90	132.83
8	D	501	GDP	C5-C6-N1	2.30	118.02	113.95
5	C	501	GTP	O6-C6-C5	-2.23	120.02	124.37
5	A	501	GTP	O6-C6-C5	-2.20	120.07	124.37

There are no chirality outliers.

All (42) 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

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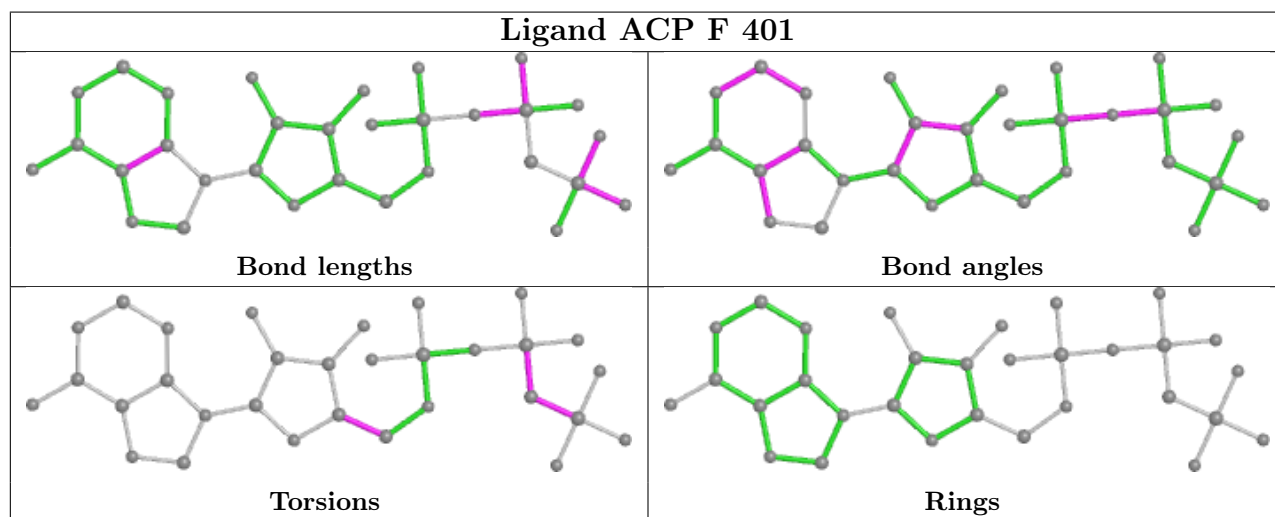
Mol	Chain	Res	Type	Atoms
10	B	505	S9S	C1-N-S-C
11	F	401	ACP	PB-C3B-PG-O1G
11	F	401	ACP	PG-C3B-PB-O1B
11	F	401	ACP	PG-C3B-PB-O2B
11	F	401	ACP	PG-C3B-PB-O3A
11	F	401	ACP	O4'-C4'-C5'-O5'
11	F	401	ACP	C3'-C4'-C5'-O5'
10	B	505	S9S	C1-N-S-O
5	A	501	GTP	PB-O3B-PG-O1G
5	C	501	GTP	PB-O3B-PG-O1G
8	D	501	GDP	PA-O3A-PB-O1B
10	B	505	S9S	C1-C2-C3-C4
10	B	505	S9S	C1-C2-C3-C8
8	D	501	GDP	C5'-O5'-PA-O3A
9	B	504	MES	C7-C8-S-O1S
11	F	401	ACP	PB-C3B-PG-O2G
11	F	401	ACP	PB-C3B-PG-O3G
5	C	501	GTP	PB-O3A-PA-O2A
5	C	501	GTP	C4'-C5'-O5'-PA
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
8	D	501	GDP	PA-O3A-PB-O2B
8	D	501	GDP	PA-O3A-PB-O3B
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	A	501	GTP	C4'-C5'-O5'-PA

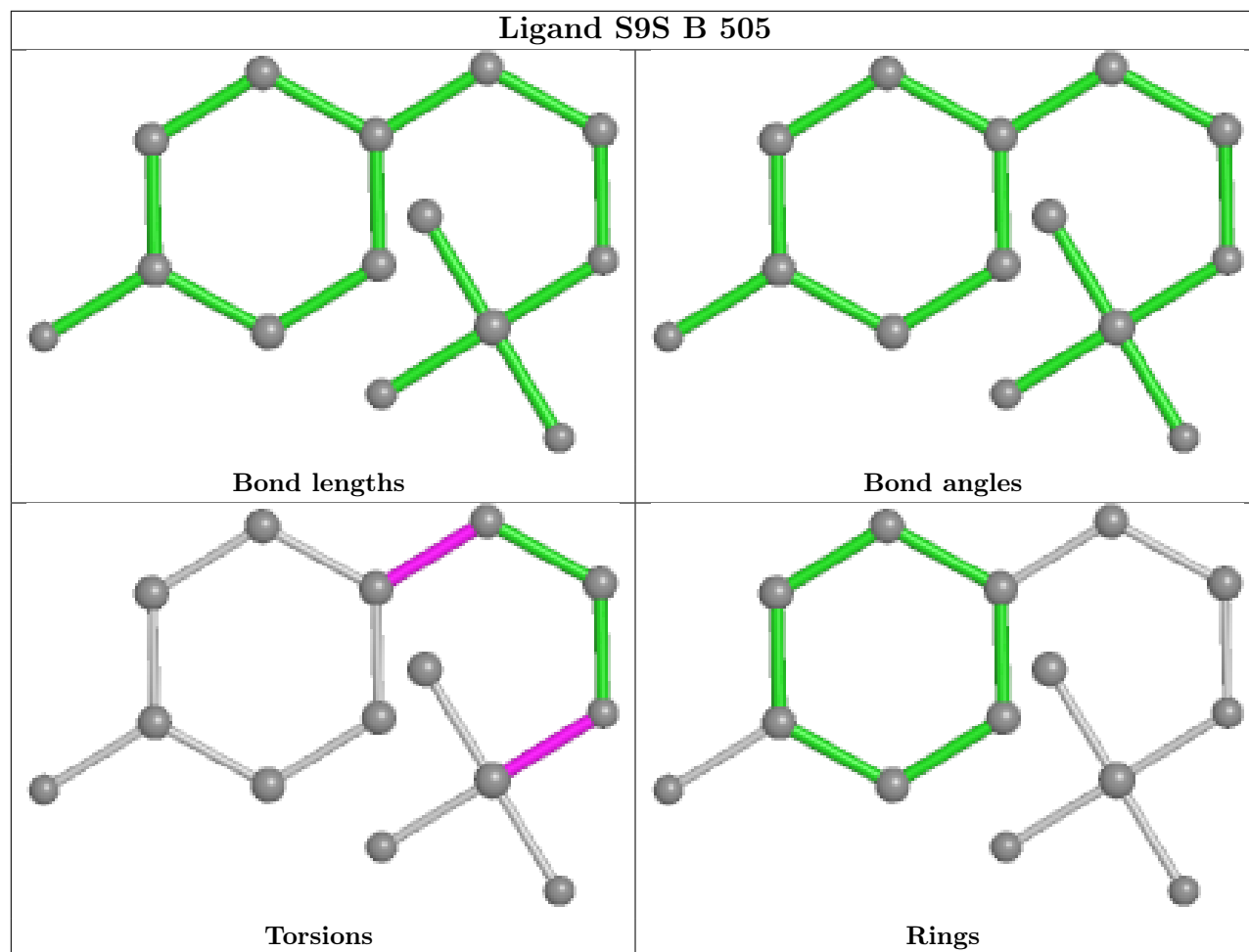
There are no ring outliers.

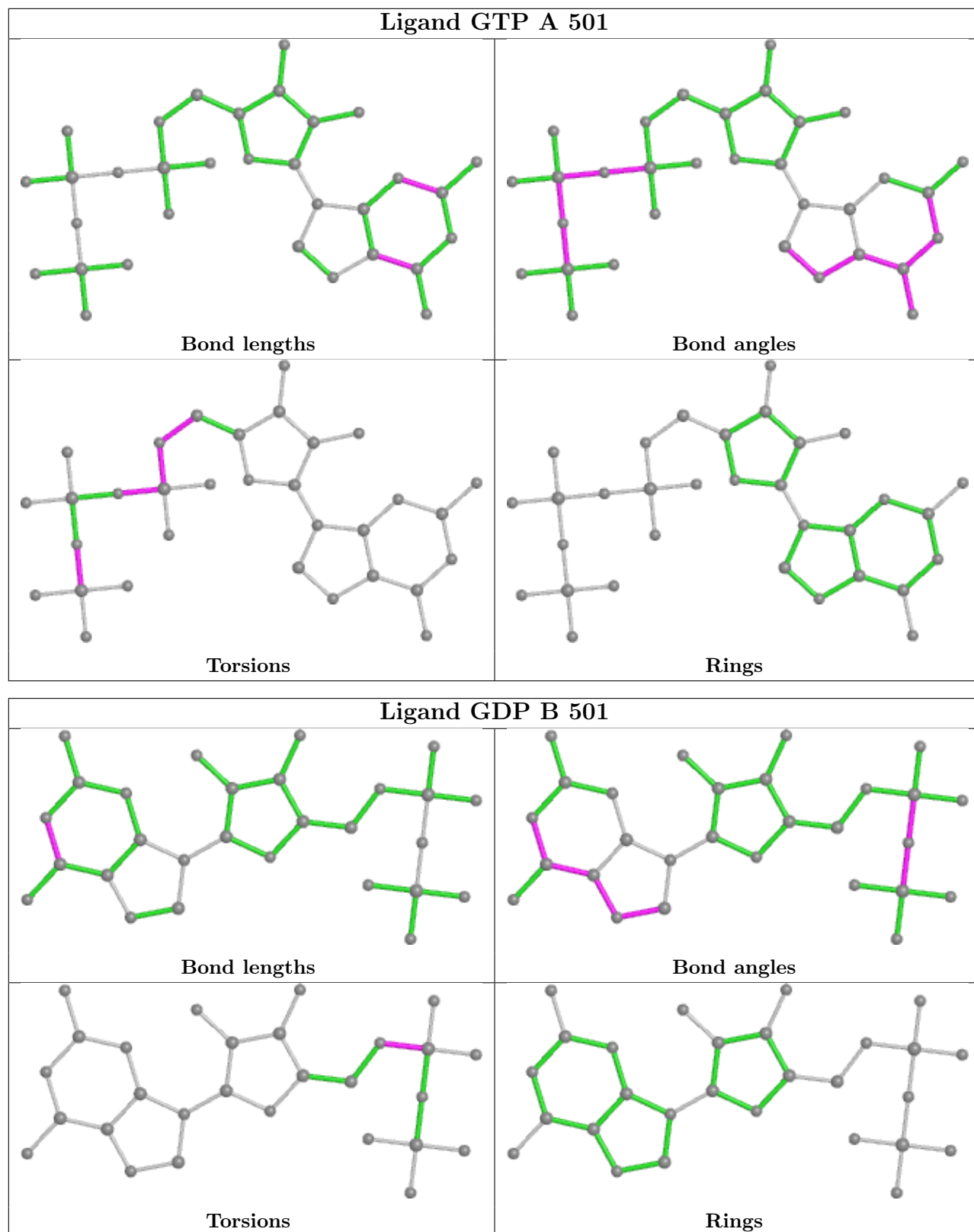
5 monomers are involved in 13 short contacts:

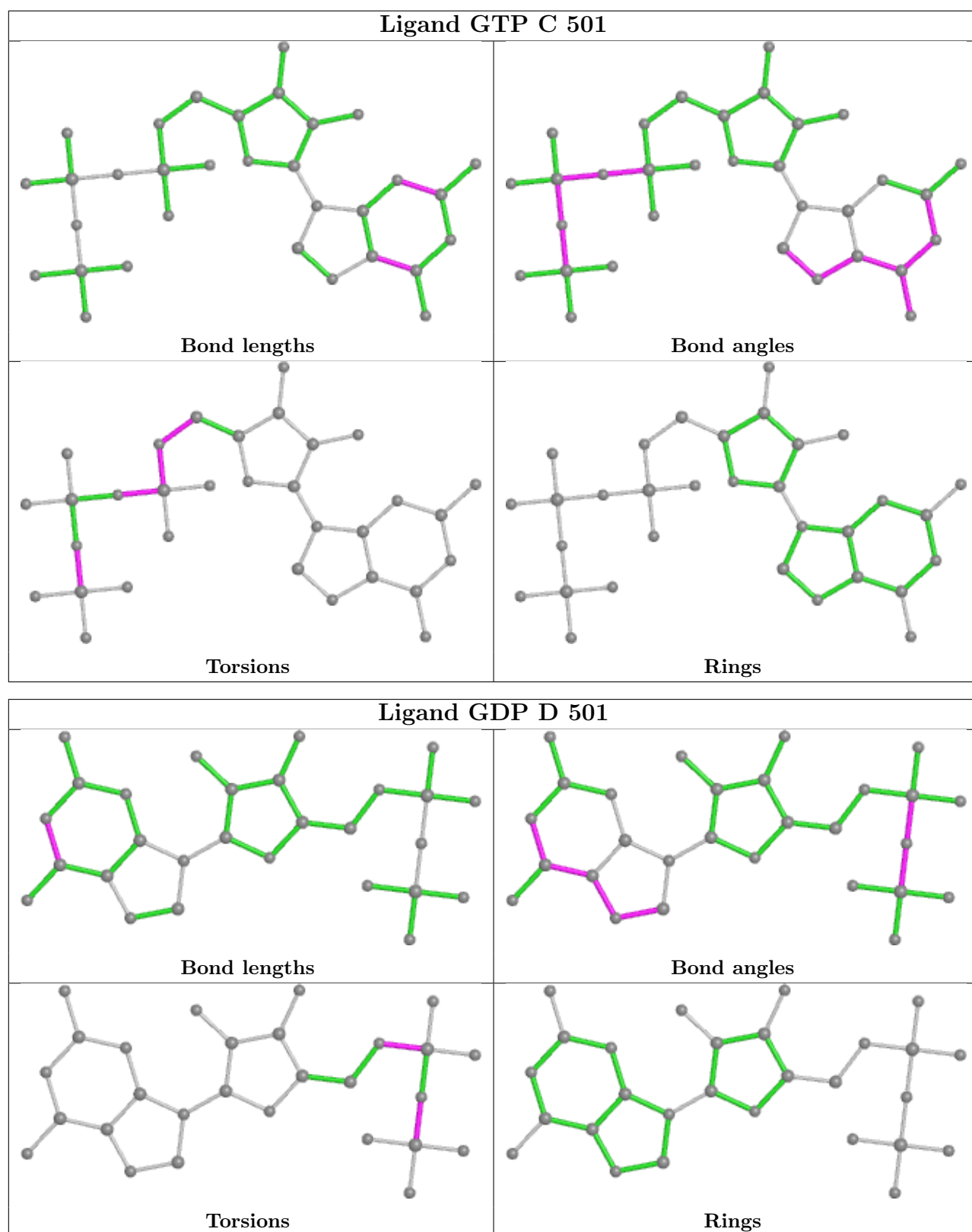
Mol	Chain	Res	Type	Clashes	Symm-Clashes
11	F	401	ACP	6	0
10	B	505	S9S	1	0
5	A	501	GTP	1	0
9	B	504	MES	3	0
8	D	501	GDP	2	0

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.









5.7 Other polymers [i](#)

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%)	0.43	14 (3%) 47 55	48, 66, 104, 171	0
1	C	440/451 (97%)	0.39	8 (1%) 68 75	41, 54, 78, 110	0
2	B	425/445 (95%)	0.67	27 (6%) 19 25	42, 66, 118, 163	2 (0%)
2	D	428/445 (96%)	0.46	19 (4%) 34 41	48, 71, 106, 170	4 (0%)
3	E	123/143 (86%)	0.77	11 (8%) 9 13	52, 76, 121, 144	0
4	F	352/384 (91%)	0.78	40 (11%) 5 7	59, 94, 161, 201	0
All	All	2206/2319 (95%)	0.55	119 (5%) 25 32	41, 68, 127, 201	6 (0%)

All (119) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	278	ARG	8.4
2	D	277	SER	8.0
2	B	281	GLN	7.5
4	F	173	ILE	7.1
2	D	276	THR	6.4
2	B	284	ARG	6.1
4	F	240	LEU	5.7
4	F	243	HIS	5.6
4	F	249	TYR	5.6
3	E	26	PRO	5.6
2	B	276	THR	5.5
2	B	333	LEU	5.1
3	E	24	LEU	5.0
3	E	6	MET	5.0
2	B	1	MET	4.2
2	D	285	ALA	4.2
2	B	283	TYR	4.0
2	B	337	ASN	4.0
4	F	142	ARG	3.9

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Mol	Chain	Res	Type	RSRZ
4	F	233	PHE	3.9
2	B	325	MET	3.9
3	E	27	PRO	3.8
2	D	215	ARG	3.7
4	F	131	PHE	3.7
2	B	249	ASN	3.6
4	F	236	LYS	3.6
2	D	1	MET	3.5
4	F	379	HIS	3.5
4	F	161	LEU	3.4
4	F	330	ILE	3.4
4	F	125	THR	3.4
4	F	169	LEU	3.3
2	B	340	SER	3.3
2	B	57	THR	3.3
1	A	282	TYR	3.3
1	C	286	LEU	3.3
4	F	99	VAL	3.3
4	F	152	SER	3.2
4	F	90	SER	3.2
1	A	340	SER	3.2
1	A	339	ARG	3.1
3	E	50	ILE	3.1
1	A	262	TYR	3.1
3	E	25	LYS	3.1
4	F	105	LEU	3.1
4	F	241	THR	3.0
1	A	351	PHE	3.0
1	A	438	ASP	2.9
2	B	286	LEU	2.9
2	D	217	LEU	2.9
4	F	89	GLU	2.9
2	B	277	SER	2.8
2	B	58	GLY	2.8
2	D	83	PHE	2.8
4	F	253	TYR	2.8
2	B	275	LEU	2.7
2	D	82	PRO	2.7
2	D	279	GLY	2.7
2	B	437	ASP	2.7
2	B	255	LEU	2.7
4	F	334	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
2	D	293	GLN	2.7
1	A	346	TRP	2.6
4	F	130	VAL	2.6
2	B	358	ILE	2.6
4	F	181	VAL	2.6
4	F	221	LEU	2.6
2	D	299	LYS	2.6
4	F	234	GLN	2.6
4	F	248	GLU	2.5
3	E	116	LEU	2.5
1	A	348	PRO	2.5
4	F	245	ILE	2.5
2	D	219	LEU	2.4
1	C	283	HIS	2.4
4	F	31	ARG	2.4
2	D	404	PHE	2.4
2	B	248	LEU	2.4
4	F	244	CYS	2.4
4	F	162	ILE	2.4
2	D	216	THR	2.4
4	F	143	GLU	2.4
2	D	284	ARG	2.3
2	B	336	GLN	2.3
2	B	369	ARG	2.3
4	F	250	SER	2.3
2	B	59	ASN	2.3
2	D	57	THR	2.3
1	A	341	ILE	2.3
2	B	360	PRO	2.3
2	B	285	ALA	2.3
1	C	368	LEU	2.3
3	E	124	GLN	2.3
1	A	281	ALA	2.3
4	F	20	LEU	2.3
1	C	308	ARG	2.3
3	E	22	VAL	2.2
1	A	68	VAL	2.2
1	C	335	ILE	2.2
2	D	229	HIS	2.2
1	A	284	GLU	2.2
3	E	121	GLU	2.1
4	F	213	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	162	GLY	2.1
1	A	335	ILE	2.1
4	F	100	ILE	2.1
1	A	349	THR	2.1
4	F	335	ALA	2.1
1	C	357	TYR	2.1
2	B	328	VAL	2.1
2	D	154	ILE	2.1
2	B	332	MET	2.1
2	B	318	ILE	2.0
4	F	206	LEU	2.0
4	F	371	PRO	2.0
4	F	251	LYS	2.0
1	C	281	ALA	2.0
4	F	147	TRP	2.0
3	E	47	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no monosaccharides 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.

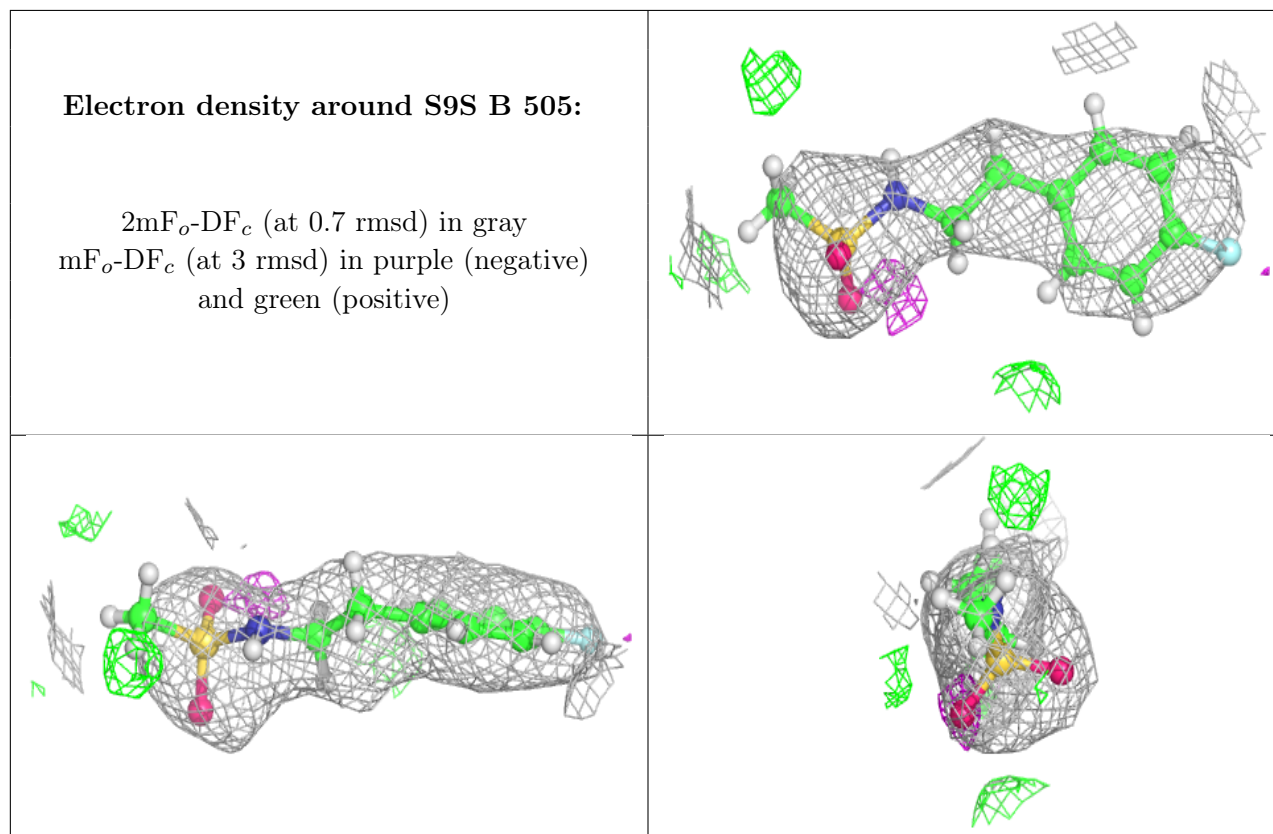
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
7	CA	B	503	1/1	0.69	0.10	104,104,104,104	0
6	MG	D	502	1/1	0.85	0.14	63,63,63,63	0
7	CA	A	504	1/1	0.86	0.13	97,97,97,97	0
10	S9S	B	505	14/14	0.89	0.21	87,106,116,125	0
11	ACP	F	401	31/31	0.89	0.14	96,102,112,117	0
9	MES	B	504	12/12	0.92	0.15	76,82,91,96	0
6	MG	A	502	1/1	0.94	0.13	49,49,49,49	0

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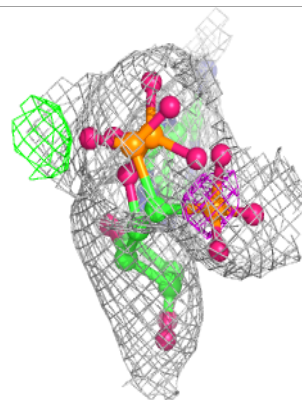
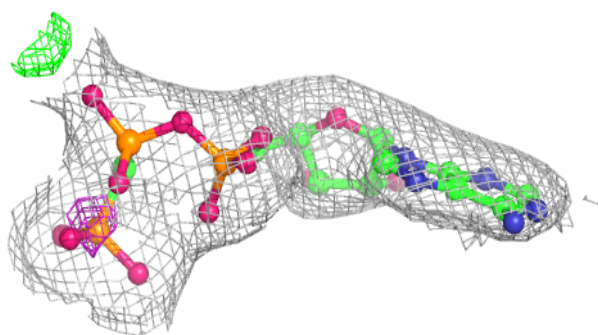
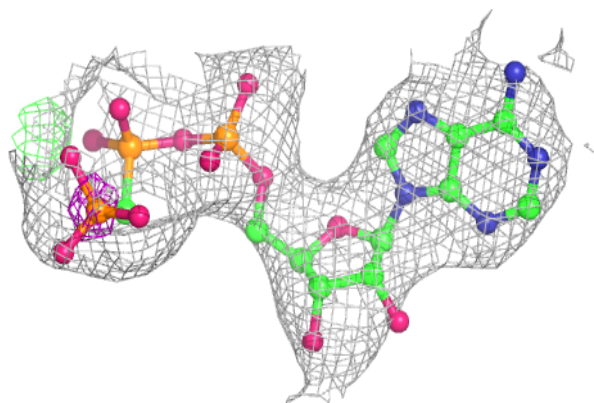
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
7	CA	A	503	1/1	0.95	0.09	86,86,86,86	0
6	MG	B	502	1/1	0.95	0.15	46,46,46,46	0
8	GDP	D	501	28/28	0.96	0.14	60,65,76,81	0
6	MG	F	402	1/1	0.96	0.06	95,95,95,95	0
6	MG	C	502	1/1	0.97	0.11	49,49,49,49	0
7	CA	C	503	1/1	0.97	0.11	71,71,71,71	0
5	GTP	A	501	32/32	0.98	0.16	45,51,54,56	0
8	GDP	B	501	28/28	0.98	0.16	43,50,53,57	0
5	GTP	C	501	32/32	0.99	0.17	38,45,48,51	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.

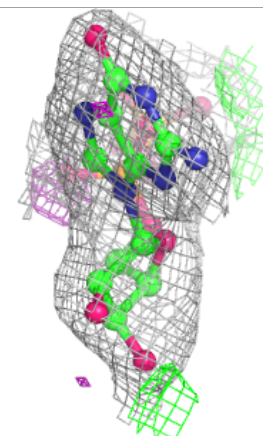
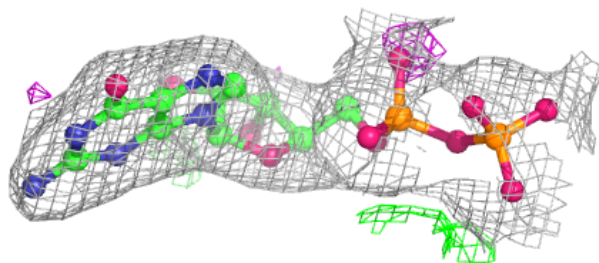
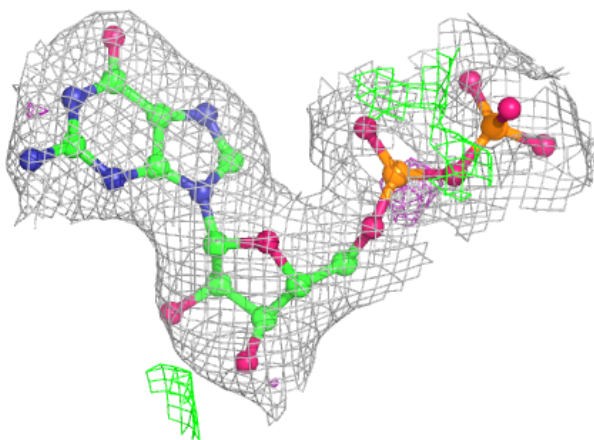


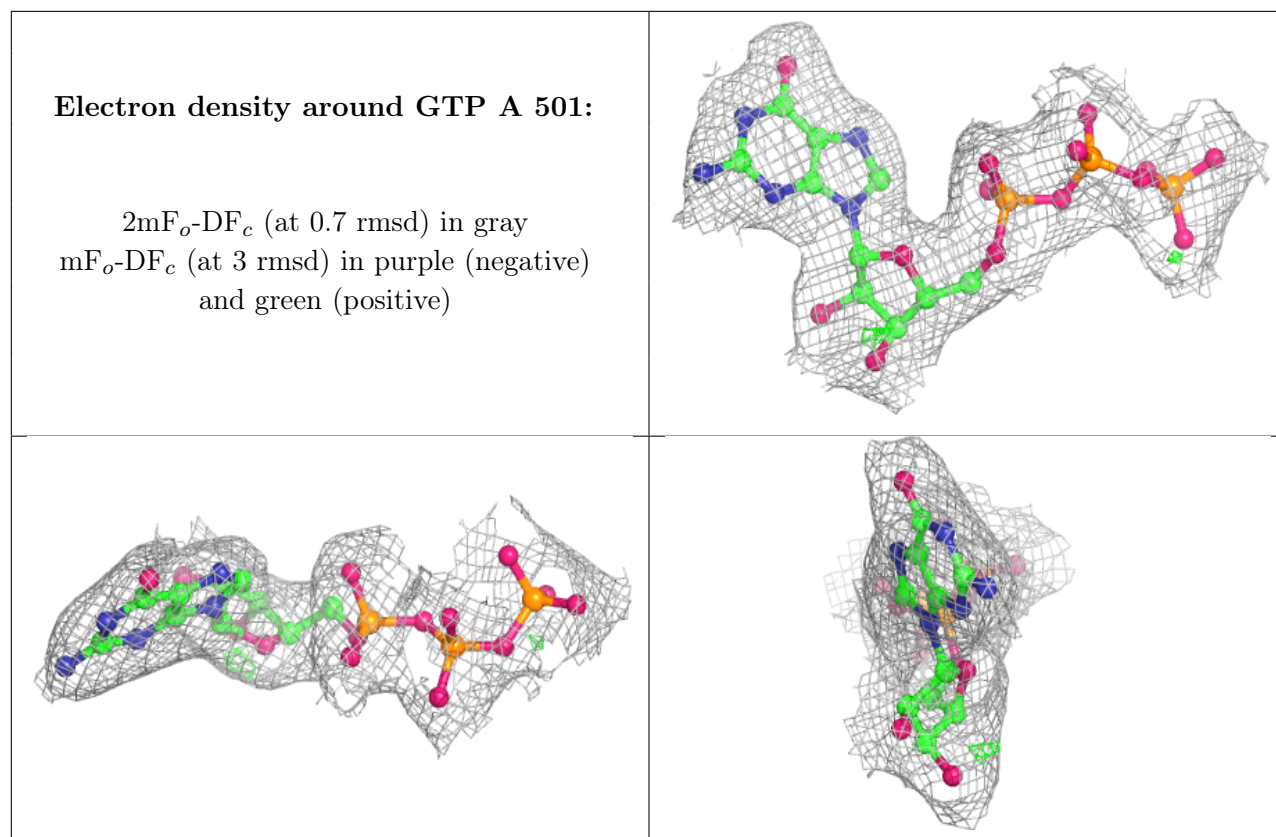
Electron density around ACP F 401:

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

**Electron density around GDP D 501:**

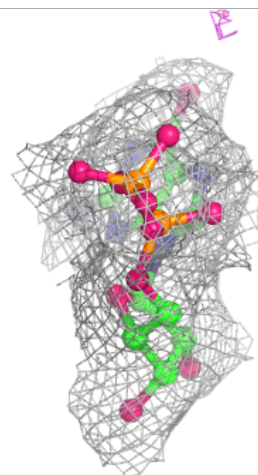
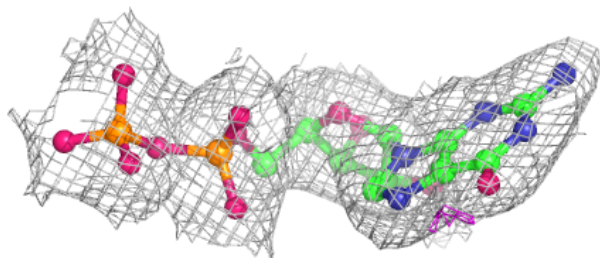
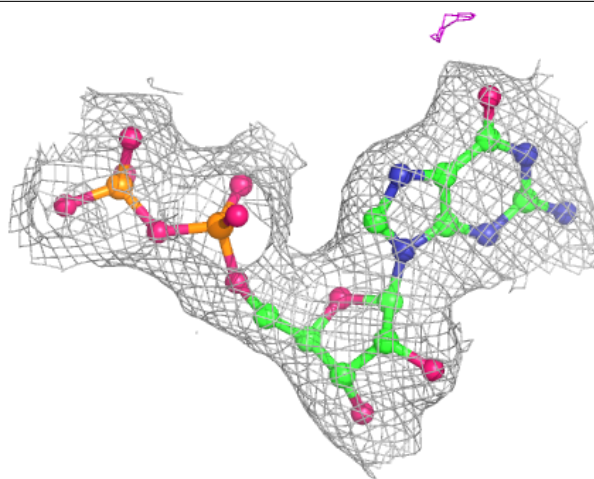
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

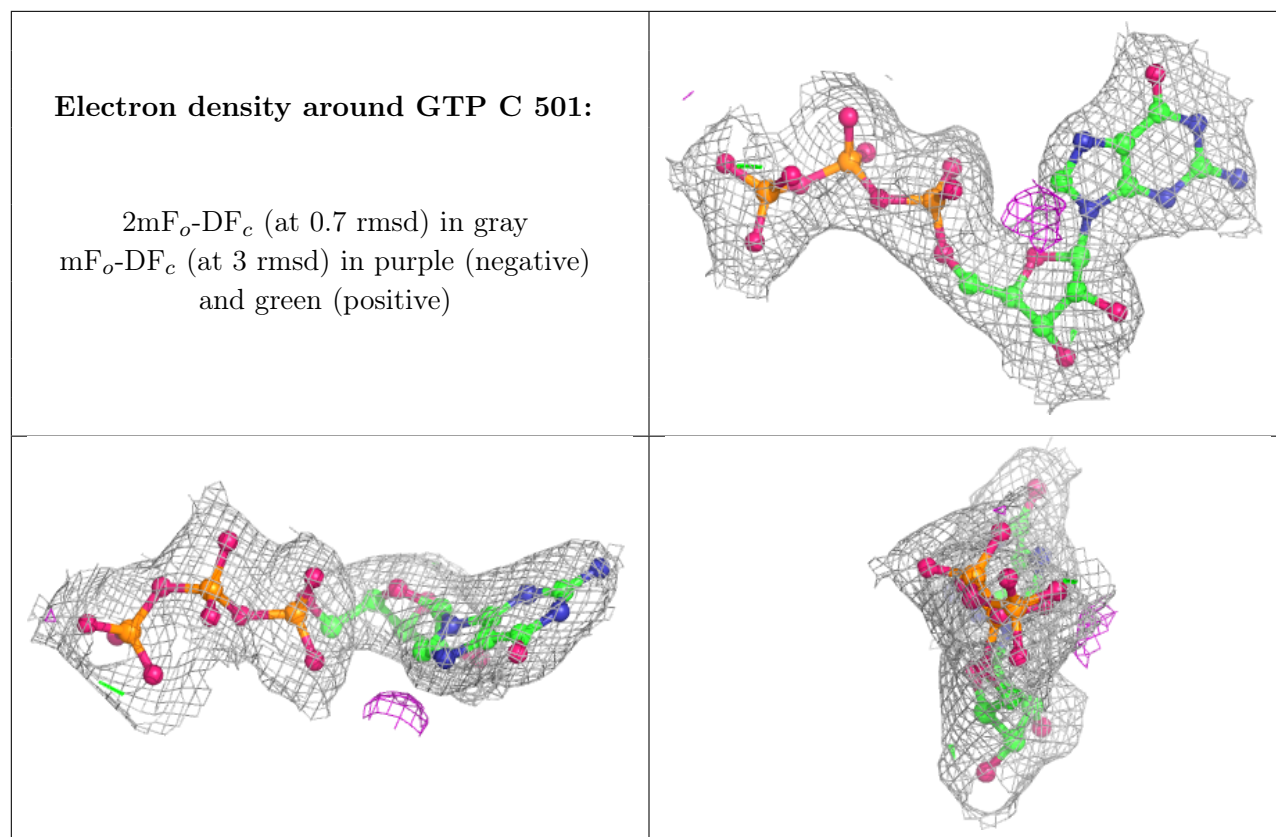




Electron density around GDP B 501:

$2mF_o-DF_c$ (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.