



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 25, 2020 – 03:54 PM BST

PDB ID : 4EB6
Title : Tubulin-Vinblastine: Stathmin-like complex
Authors : Ranaivoson, F.M.; Gigant, B.; Knossow, M.
Deposited on : 2012-03-23
Resolution : 3.47 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 : 2.13
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) : 2.13

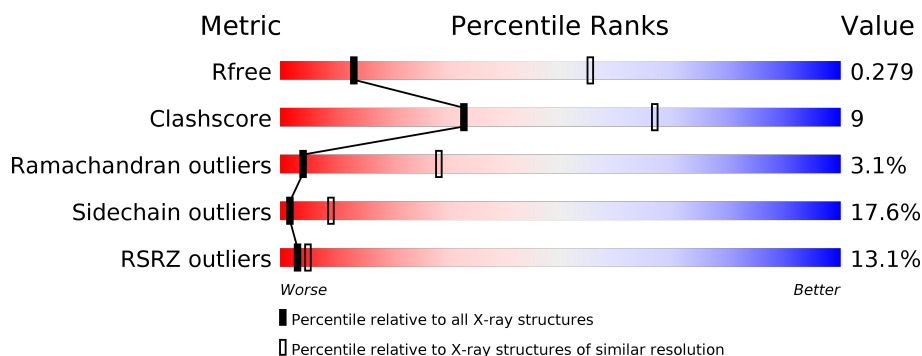
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.47 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	1379 (3.56-3.40)
Clashscore	141614	1461 (3.56-3.40)
Ramachandran outliers	138981	1424 (3.56-3.40)
Sidechain outliers	138945	1425 (3.56-3.40)
RSRZ outliers	127900	1289 (3.56-3.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria 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>16%</div> <div> <div></div> <div>63%</div> <div>28%</div> <div>• •</div> </div> </div>
1	C	451	<div> <div>10%</div> <div> <div></div> <div>65%</div> <div>26%</div> <div>5%</div> <div>•</div> </div> </div>
2	B	445	<div> <div>13%</div> <div> <div></div> <div>64%</div> <div>28%</div> <div>5%</div> <div>•</div> </div> </div>
2	D	445	<div> <div>9%</div> <div> <div></div> <div>64%</div> <div>29%</div> <div>• •</div> </div> </div>
3	E	142	<div> <div>18%</div> <div> <div></div> <div>68%</div> <div>21%</div> <div>• • 7%</div> </div> </div>

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	SO4	A	503	-	-	-	X
6	SO4	A	504	-	-	-	X

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 14918 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Tubulin alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	433	Total	C	N	O	S	0	1	0
			3399	2153	577	647	22			
1	C	432	Total	C	N	O	S	0	4	0
			3408	2161	576	648	23			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	232	SER	GLY	SEE REMARK 999	UNP D0VWZ0
A	340	SER	THR	SEE REMARK 999	UNP D0VWZ0
C	232	SER	GLY	SEE REMARK 999	UNP D0VWZ0
C	340	SER	THR	SEE REMARK 999	UNP D0VWZ0

- Molecule 2 is a protein called Tubulin beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	432	Total	C	N	O	S	0	2	0
			3400	2130	582	662	26			
2	D	432	Total	C	N	O	S	0	1	0
			3394	2127	580	661	26			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	317	THR	ALA	SEE REMARK 999	UNP D0VWY9
B	318	ILE	VAL	SEE REMARK 999	UNP D0VWY9
B	335	ILE	VAL	SEE REMARK 999	UNP D0VWY9
B	375	SER	ALA	SEE REMARK 999	UNP D0VWY9
D	317	THR	ALA	SEE REMARK 999	UNP D0VWY9
D	318	ILE	VAL	SEE REMARK 999	UNP D0VWY9
D	335	ILE	VAL	SEE REMARK 999	UNP D0VWY9
D	375	SER	ALA	SEE REMARK 999	UNP D0VWY9

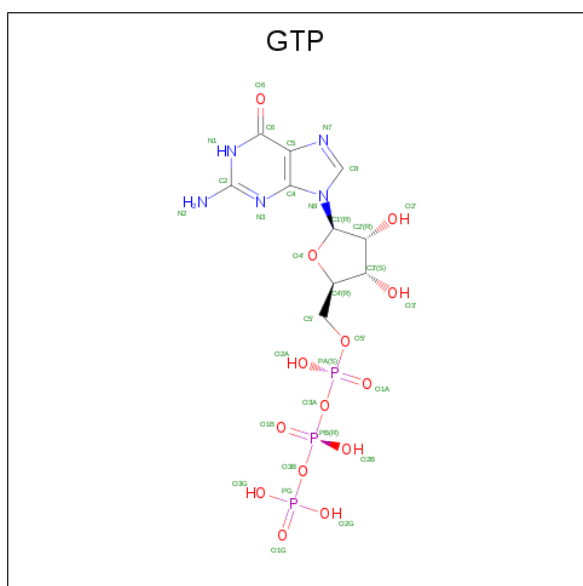
- Molecule 3 is a protein called Stathmin-4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	132	Total	C	N	O	S	0	1	0
			1080	669	195	212	4			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	4	ALA	-	EXPRESSION TAG	UNP P63043
E	14	ALA	CYS	ENGINEERED MUTATION	UNP P63043
E	20	TRP	PHE	ENGINEERED MUTATION	UNP P63043

- Molecule 4 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



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

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

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

Continued on next page...

Continued from previous page...

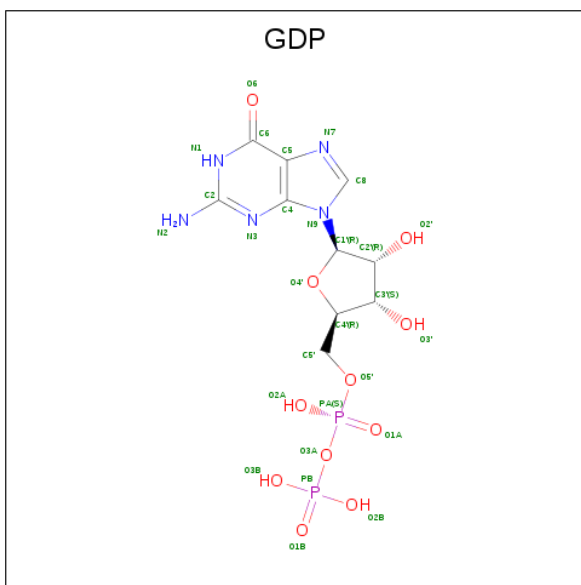
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	1	Total	Mg	0	0
			1	1		

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



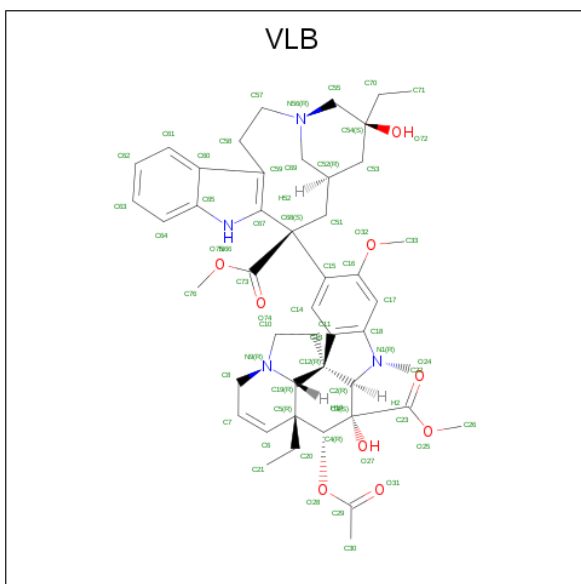
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	S	0	0
			5	4	1		
6	A	1	Total	O	S	0	0
			5	4	1		
6	B	1	Total	O	S	0	0
			5	4	1		
6	D	1	Total	O	S	0	0
			5	4	1		
6	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 7 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



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

- Molecule 8 is (2ALPHA,2'BETA,3BETA,4ALPHA,5BETA)-VINCALEUKOBLASTINE (three-letter code: VLB) (formula: $C_{46}H_{58}N_4O_9$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	C	1	Total	C	N	O	0	0
			59	46	4	9		

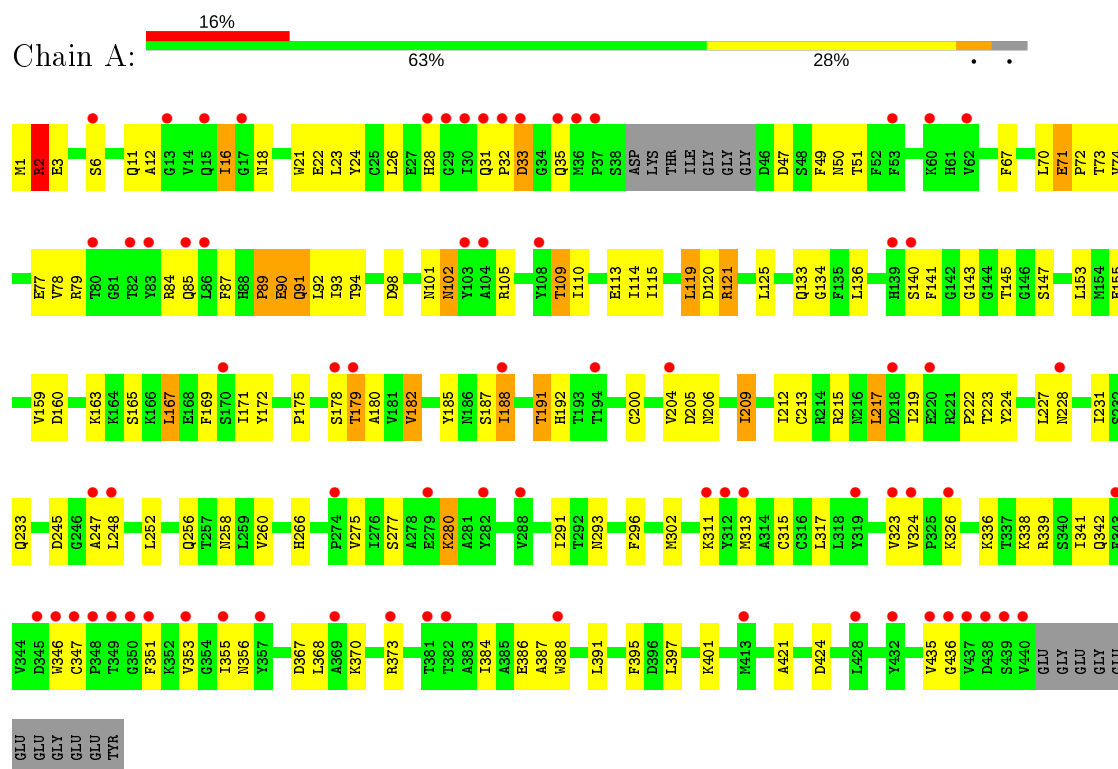
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	5	Total 5	O 5	0	0
9	B	3	Total 3	O 3	0	0
9	C	13	Total 13	O 13	0	0
9	D	9	Total 9	O 9	0	0
9	E	1	Total 1	O 1	0	0

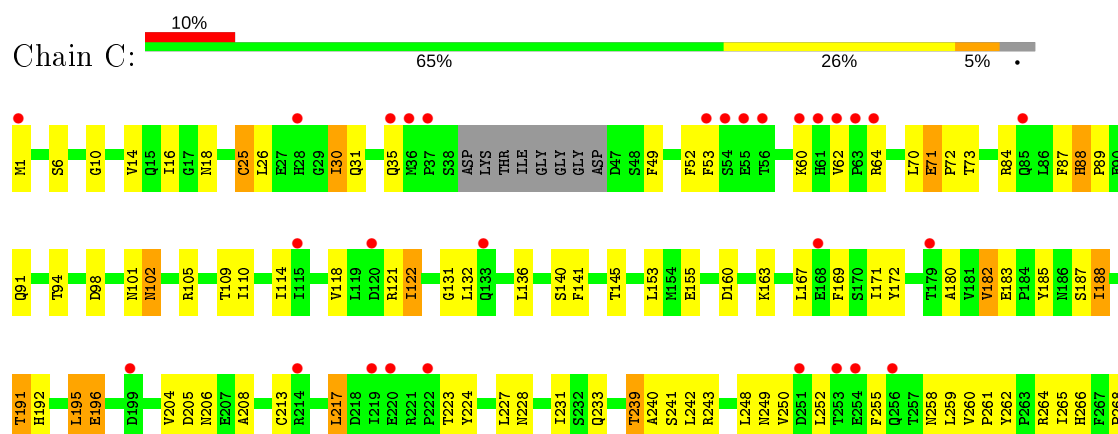
3 Residue-property plots [i](#)

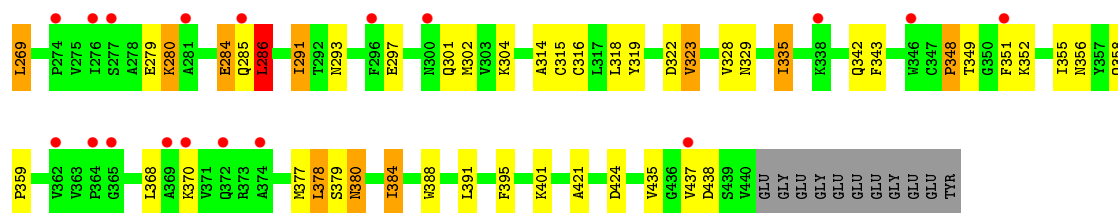
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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 chain

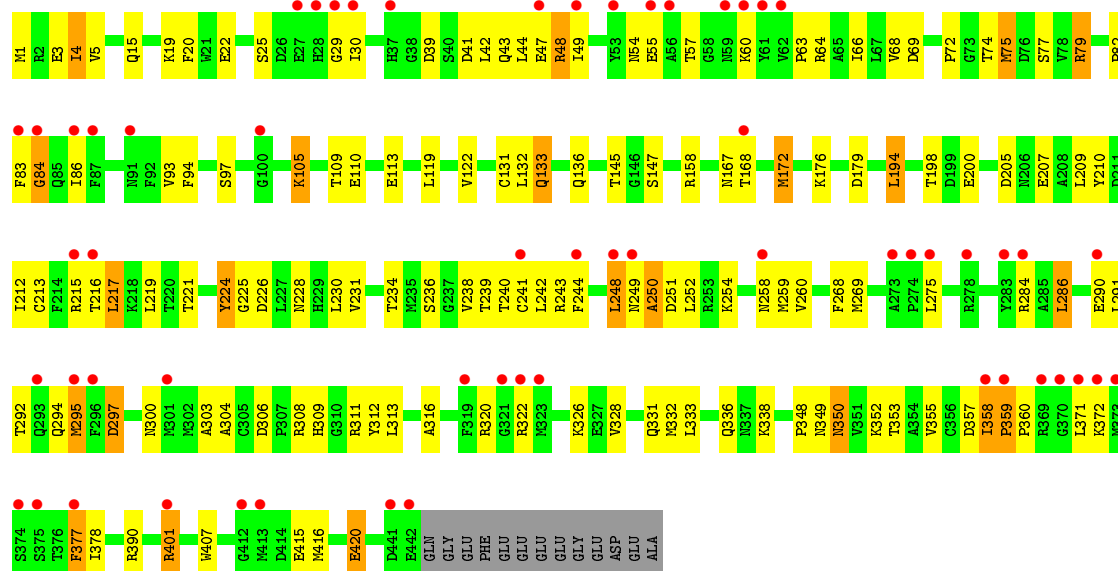


• Molecule 1: Tubulin alpha chain

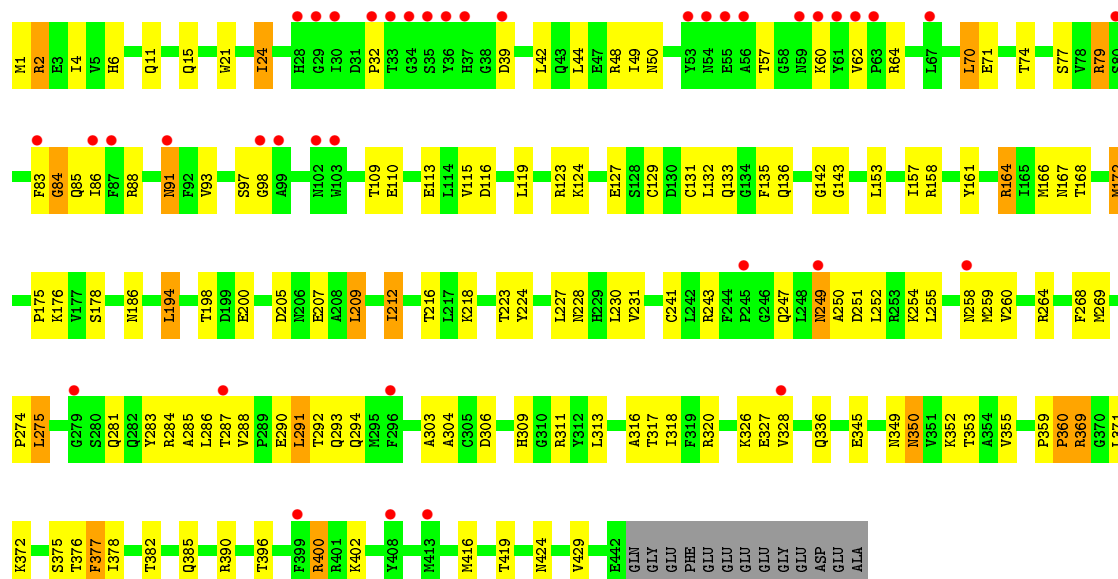




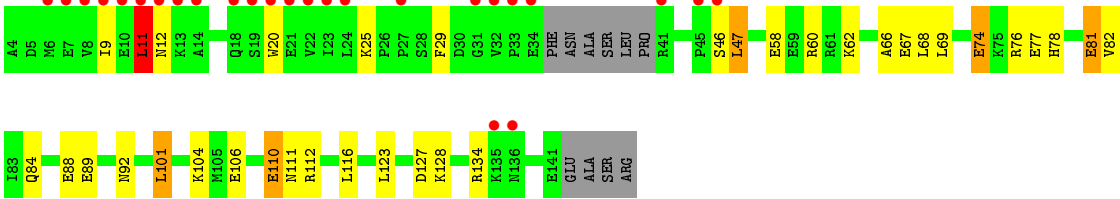
• Molecule 2: Tubulin beta chain



• Molecule 2: Tubulin beta chain



• Molecule 3: Stathmin-4



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	64.69Å 129.68Å 252.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.06 – 3.47 43.06 – 3.47	Depositor EDS
% Data completeness (in resolution range)	(Not available) (43.06-3.47) 99.2 (43.06-3.47)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.17 (at 3.48Å)	Xtriage
Refinement program	BUSTER 2.8.0	Depositor
R, R_{free}	0.213 , 0.253 0.231 , 0.279	Depositor DCC
R_{free} test set	1424 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	119.2	Xtriage
Anisotropy	0.677	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 140.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	14918	wwPDB-VP
Average B, all atoms (Å ²)	174.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.88% 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: GDP, GTP, MG, VLB, SO4

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	0.40	0/3479	0.72	1/4723 (0.0%)
1	C	0.40	0/3495	0.73	1/4745 (0.0%)
2	B	0.40	0/3485	0.73	0/4720
2	D	0.41	0/3471	0.73	0/4701
3	E	0.40	0/1095	0.68	0/1459
All	All	0.40	0/15025	0.73	2/20348 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	89	PRO	N-CA-C	5.41	126.17	112.10
1	C	348	PRO	C-N-CA	5.20	134.70	121.70

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	3399	0	3312	54	0
1	C	3408	0	3322	61	0
2	B	3400	0	3266	68	0
2	D	3394	0	3268	62	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	E	1080	0	1077	10	0
4	A	32	0	12	4	0
4	C	32	0	12	3	0
5	A	1	0	0	0	0
5	C	1	0	0	0	0
6	A	10	0	0	0	0
6	B	5	0	0	0	0
6	D	10	0	0	0	0
7	B	28	0	12	0	0
7	D	28	0	12	2	0
8	C	59	0	58	13	0
9	A	5	0	0	0	0
9	B	3	0	0	0	0
9	C	13	0	0	0	0
9	D	9	0	0	0	0
9	E	1	0	0	0	0
All	All	14918	0	14351	255	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 9.

All (255) 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)
8:C:503:VLB:H303	8:C:503:VLB:H213	1.50	0.93
2:B:212:ILE:HA	2:B:217:LEU:HG	1.55	0.86
2:B:221:THR:HA	8:C:503:VLB:H761	1.61	0.83
8:C:503:VLB:H582	8:C:503:VLB:H511	1.64	0.78
2:B:5:VAL:HG12	2:B:64:ARG:HG2	1.67	0.77
2:D:62:VAL:HG21	2:D:88:ARG:HG3	1.68	0.76
2:D:2:ARG:HB2	2:D:131:CYS:HB3	1.67	0.76
2:D:172:MET:HE1	2:D:390:ARG:HH22	1.53	0.74
2:D:317:THR:HG22	2:D:377:PHE:HD1	1.52	0.74
1:C:259:LEU:HD21	1:C:378:LEU:HB3	1.71	0.73
1:A:180:ALA:HA	2:B:258:ASN:HD21	1.53	0.73
2:B:359:PRO:HB2	2:B:360:PRO:CD	2.18	0.73
2:B:172:MET:HE1	2:B:390:ARG:HH22	1.53	0.73
2:D:212:ILE:HD11	2:D:230:LEU:HD22	1.72	0.71
1:C:206:ASN:HD21	4:C:501:GTP:HN22	1.38	0.70
1:A:206:ASN:HD21	4:A:501:GTP:HN22	1.38	0.69
2:B:359:PRO:HB2	2:B:360:PRO:HD2	1.74	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:167:LEU:HD21	1:A:252:LEU:HB2	1.75	0.68
2:D:21:TRP:HA	2:D:24:ILE:HG22	1.75	0.68
1:C:213:CYS:HA	1:C:217:LEU:HB2	1.77	0.66
2:D:320:ARG:HB3	2:D:359:PRO:HA	1.76	0.66
2:B:407:TRP:HZ2	1:C:260:VAL:HG13	1.62	0.65
2:B:297:ASP:HA	2:B:308:ARG:HH12	1.62	0.64
2:B:248:LEU:HG	2:B:249:ASN:H	1.63	0.64
2:D:11:GLN:HE21	2:D:15:GLN:HE22	1.47	0.63
2:B:228:ASN:HA	2:B:231:VAL:HG12	1.81	0.63
1:A:187:SER:HB3	1:A:391:LEU:HD21	1.79	0.63
2:B:1:MET:N	2:B:131:CYS:SG	2.72	0.63
1:C:187:SER:HB3	1:C:391:LEU:HD21	1.81	0.62
8:C:503:VLB:H512	8:C:503:VLB:H332	1.80	0.62
1:C:101:ASN:HD22	1:C:180:ALA:HB2	1.64	0.62
1:A:70:LEU:HD23	1:A:110:ILE:HG23	1.81	0.61
1:C:25:CYS:HB2	1:C:30:ILE:HB	1.83	0.61
2:B:216:THR:H	2:B:217:LEU:HD22	1.66	0.60
2:D:320:ARG:HE	2:D:360:PRO:HG3	1.65	0.60
1:C:191:THR:HG21	1:C:388:TRP:CH2	2.36	0.60
2:D:133:GLN:HG2	2:D:252:LEU:HB2	1.83	0.59
1:C:172:TYR:HB3	1:C:205:ASP:HA	1.82	0.59
1:A:87:PHE:HB3	1:A:91:GLN:HG3	1.83	0.59
1:A:101:ASN:HD22	1:A:180:ALA:HB2	1.66	0.59
3:E:11:LEU:H	3:E:20:TRP:HA	1.68	0.59
1:C:241:SER:HA	1:C:249:ASN:HD21	1.66	0.59
2:B:210:TYR:HE2	8:C:503:VLB:H333	1.67	0.59
1:C:250:VAL:HG11	1:C:352:LYS:HE3	1.84	0.58
2:D:209:LEU:HB3	2:D:230:LEU:HD11	1.86	0.58
1:C:239:THR:O	1:C:241:SER:N	2.36	0.58
1:A:2:ARG:HB2	1:A:133[A]:GLN:HE21	1.67	0.57
1:C:262:TYR:HB2	1:C:265:ILE:HD12	1.86	0.57
1:A:247:ALA:HB1	3:E:12:ASN:HB2	1.85	0.57
2:B:401:ARG:HH11	2:B:401:ARG:HB3	1.69	0.57
2:B:172:MET:CE	2:B:390:ARG:HH22	2.18	0.56
1:C:208:ALA:HB2	1:C:304:LYS:HG2	1.88	0.56
8:C:503:VLB:H691	8:C:503:VLB:C59	2.35	0.56
2:D:172:MET:CE	2:D:390:ARG:HH22	2.18	0.56
1:A:191:THR:HG21	1:A:388:TRP:CH2	2.41	0.56
2:D:142:GLY:HA3	7:D:501:GDP:H4'	1.88	0.56
2:D:133:GLN:HE21	2:D:252:LEU:H	1.53	0.56
1:A:172:TYR:HB3	1:A:205:ASP:HA	1.88	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:ASP:HA	1:A:85:GLN:HG3	1.88	0.55
2:B:306:ASP:HB3	2:B:309:HIS:HB2	1.88	0.55
2:D:21:TRP:HA	2:D:24:ILE:CG2	2.37	0.55
1:A:28:HIS:CD2	1:A:49:PHE:HB2	2.42	0.55
2:B:79:ARG:HA	2:B:84:GLY:HA3	1.89	0.55
1:A:16:ILE:HD11	1:A:231:ILE:HG13	1.89	0.54
1:A:11:GLN:HG3	1:A:74:VAL:HG11	1.90	0.54
1:A:213:CYS:SG	1:A:222:PRO:HG3	2.48	0.53
1:A:217:LEU:HA	1:A:277:SER:HB3	1.89	0.53
1:C:87:PHE:HB2	1:C:91:GLN:NE2	2.23	0.53
2:D:318:ILE:HB	2:D:376:THR:HG23	1.91	0.53
2:D:249:ASN:HB2	2:D:255:LEU:HA	1.91	0.52
1:A:67:PHE:HB2	1:A:92:LEU:HD22	1.91	0.52
2:B:86:ILE:HD12	2:B:86:ILE:H	1.74	0.52
2:B:407:TRP:CZ2	1:C:260:VAL:HG13	2.43	0.52
2:B:241:CYS:SG	2:B:248:LEU:HD11	2.49	0.52
2:D:116:ASP:HA	2:D:119:LEU:HG	1.92	0.52
2:D:385:GLN:HB2	2:D:429:VAL:HG13	1.90	0.52
2:D:24:ILE:HD11	2:D:243:ARG:HD3	1.91	0.51
1:A:93:ILE:HD11	1:A:121:ARG:HG2	1.92	0.51
1:C:206:ASN:ND2	4:C:501:GTP:HN22	2.07	0.51
1:A:206:ASN:ND2	4:A:501:GTP:HN22	2.08	0.51
2:B:5:VAL:HG22	2:B:132:LEU:HD11	1.93	0.51
2:D:205:ASP:HB3	2:D:303:ALA:HA	1.93	0.51
2:D:241:CYS:HB2	2:D:250:ALA:HA	1.93	0.51
1:C:204:VAL:HG11	1:C:231:ILE:HD12	1.92	0.51
1:A:397:LEU:HD23	2:B:348:PRO:HG3	1.93	0.50
1:C:318:LEU:HD13	1:C:378:LEU:HD23	1.94	0.50
1:A:159:VAL:HG11	3:E:47:LEU:HB2	1.94	0.50
1:A:204:VAL:HG11	1:A:231:ILE:HD12	1.93	0.50
2:D:161:TYR:HB3	2:D:164:ARG:HG3	1.92	0.50
2:D:251:ASP:HB3	2:D:254:LYS:HB2	1.93	0.50
2:B:269:MET:HG3	2:B:303:ALA:HB3	1.93	0.50
1:C:31:GLN:HB2	1:C:35:GLN:HB2	1.93	0.50
1:A:175:PRO:HA	1:A:179:THR:HG21	1.93	0.50
1:A:140:SER:HA	1:A:171:ILE:HB	1.94	0.50
2:B:234:THR:O	2:B:238:VAL:HG23	2.11	0.50
1:C:242:LEU:HD11	1:C:252:LEU:HB3	1.94	0.50
2:D:396:THR:O	2:D:400:ARG:HB2	2.11	0.50
2:B:205:ASP:HB3	2:B:303:ALA:HA	1.94	0.49
2:D:153:LEU:O	2:D:157:ILE:HG12	2.11	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:251:ASP:HB3	2:B:254:LYS:HB2	1.94	0.49
2:B:66:ILE:HD13	2:B:122:VAL:HG12	1.94	0.49
2:B:63:PRO:HD3	2:B:86:ILE:HG22	1.95	0.49
2:B:286:LEU:HD11	2:B:291:LEU:HD13	1.95	0.49
2:D:175:PRO:HA	2:D:178:SER:HB3	1.95	0.49
2:B:41:ASP:HA	2:B:44:LEU:HD12	1.95	0.49
1:C:259:LEU:HD11	1:C:316:CYS:HB2	1.95	0.49
1:A:105:ARG:HA	1:A:109:THR:HG23	1.95	0.48
2:B:236:SER:HA	2:B:239:THR:OG1	2.13	0.48
1:C:269:LEU:HD12	1:C:384:ILE:HD12	1.96	0.48
2:D:2:ARG:HB2	2:D:131:CYS:CB	2.41	0.48
2:D:79:ARG:HA	2:D:84:GLY:HA3	1.94	0.48
3:E:66:ALA:HA	3:E:69:LEU:HD12	1.94	0.48
1:C:70:LEU:HD22	1:C:145:THR:HG22	1.96	0.48
2:D:316:ALA:HB3	2:D:378:ILE:HB	1.94	0.48
8:C:503:VLB:C58	8:C:503:VLB:H511	2.40	0.48
1:C:136:LEU:HD22	1:C:169:PHE:HE1	1.79	0.47
2:D:269:MET:HG3	2:D:303:ALA:HB3	1.96	0.47
2:D:291:LEU:HG	2:D:375:SER:HB2	1.95	0.47
1:C:196:GLU:CD	1:C:196:GLU:H	2.18	0.47
1:C:140:SER:HA	1:C:171:ILE:HB	1.97	0.47
1:C:356:ASN:HD21	1:C:358:GLN:HB2	1.80	0.47
2:B:4:ILE:HD11	2:B:252:LEU:HD13	1.96	0.47
1:C:328:VAL:HG21	1:C:355:ILE:HD11	1.96	0.47
2:B:133:GLN:HE21	2:B:252:LEU:H	1.63	0.47
2:B:225:GLY:HA2	2:B:228:ASN:HB2	1.97	0.46
2:B:316:ALA:HB3	2:B:378:ILE:HB	1.96	0.46
2:B:77:SER:H	2:B:79:ARG:HH21	1.64	0.46
1:C:206:ASN:HD21	4:C:501:GTP:N2	2.10	0.46
1:A:2:ARG:HG3	1:A:51:THR:HG22	1.97	0.46
2:B:22:GLU:HB3	2:B:83:PHE:HB2	1.98	0.46
1:A:219:ILE:HD12	1:A:222:PRO:HB3	1.96	0.46
1:A:317:LEU:HB2	1:A:353:VAL:HG13	1.98	0.46
7:D:501:GDP:H8	7:D:501:GDP:H5'	1.80	0.45
1:A:21:TRP:HA	1:A:24:TYR:HB2	1.97	0.45
2:D:264:ARG:NH2	2:D:424:ASN:O	2.43	0.45
1:A:145:THR:O	4:A:501:GTP:O2B	2.35	0.45
2:B:48:ARG:HH22	2:B:250:ALA:HB1	1.82	0.45
2:B:44:LEU:O	2:B:49:ILE:HG13	2.17	0.45
1:C:314:ALA:HB3	1:C:380:ASN:H	1.82	0.45
2:D:77:SER:H	2:D:79:ARG:HH21	1.65	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:329:ASN:HD21	8:C:503:VLB:H66	1.62	0.45
1:A:90:GLU:C	1:A:121:ARG:HH12	2.20	0.45
1:A:167:LEU:HD12	1:A:200:CYS:HB3	1.98	0.45
2:B:243:ARG:HD2	2:B:243:ARG:N	2.32	0.45
1:C:71:GLU:HB2	1:C:98:ASP:HB3	1.99	0.45
2:D:157:ILE:HG13	2:D:166:MET:HE3	1.97	0.45
2:D:216:THR:HG21	2:D:275:LEU:HD13	1.99	0.45
1:C:88:HIS:HB2	1:C:89:PRO:HD2	1.98	0.45
1:A:209:ILE:HD11	1:A:227:LEU:HG	2.00	0.44
1:A:311:LYS:HD2	1:A:436:GLY:HA2	1.99	0.44
1:A:71:GLU:HB2	1:A:98:ASP:HB3	1.99	0.44
2:D:143:GLY:O	2:D:186:ASN:ND2	2.50	0.44
2:D:227:LEU:O	2:D:230:LEU:HG	2.17	0.44
2:B:350:ASN:HD22	2:B:350:ASN:H	1.65	0.44
2:D:205:ASP:CB	2:D:303:ALA:HA	2.48	0.44
1:C:286:LEU:HD21	1:C:291:ILE:HG23	1.99	0.44
1:C:319:TYR:HB2	1:C:355:ILE:HG12	1.99	0.44
2:D:176:LYS:HD2	2:D:207:GLU:HG3	1.98	0.44
2:D:274:PRO:HD2	2:D:371:LEU:HD23	1.99	0.44
2:B:176:LYS:HD2	2:B:207:GLU:HG3	1.98	0.44
2:D:350:ASN:H	2:D:350:ASN:HD22	1.66	0.44
2:B:238:VAL:HG22	2:B:378:ILE:HD11	1.99	0.44
3:E:106:GLU:O	3:E:110:GLU:HG3	2.18	0.44
2:B:68:VAL:HG22	2:B:93:VAL:HG13	2.00	0.44
2:B:350:ASN:HD22	2:B:350:ASN:N	2.16	0.44
1:A:31:GLN:O	1:A:33:ASP:N	2.51	0.43
2:B:312:TYR:CE2	2:B:377:PHE:HZ	2.36	0.43
1:C:239:THR:HB	1:C:243:ARG:HD3	2.01	0.43
2:D:228:ASN:HA	2:D:231:VAL:HB	2.00	0.43
2:B:205:ASP:CB	2:B:303:ALA:HA	2.48	0.43
1:C:10:GLY:O	1:C:14:VAL:HG22	2.18	0.43
2:D:32:PRO:HB3	2:D:83:PHE:HA	1.99	0.43
2:B:105:LYS:HG3	2:B:110:GLU:HG2	2.00	0.43
1:C:241:SER:HA	1:C:249:ASN:ND2	2.32	0.43
3:E:74:GLU:HA	3:E:77:GLU:HG2	2.00	0.43
1:A:136:LEU:HD22	1:A:169:PHE:HE1	1.84	0.43
2:B:248:LEU:CG	2:B:249:ASN:H	2.30	0.43
1:C:195:LEU:HD12	1:C:264:ARG:HG2	2.00	0.43
8:C:503:VLB:H692	8:C:503:VLB:H713	2.01	0.43
2:B:48:ARG:NH2	2:B:250:ALA:HB1	2.34	0.43
2:B:25:SER:HB3	2:B:30:ILE:HG13	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:115:VAL:HG22	2:D:119:LEU:HD23	2.01	0.43
1:C:180:ALA:O	1:C:183:GLU:HG3	2.19	0.43
1:C:319:TYR:HB3	1:C:323:VAL:HG21	2.01	0.43
1:C:180:ALA:HA	2:D:258:ASN:HD21	1.84	0.43
1:C:118:VAL:O	1:C:122:ILE:HB	2.18	0.43
1:C:88:HIS:HB2	1:C:89:PRO:CD	2.49	0.43
1:A:134:GLY:HA3	1:A:165:SER:O	2.19	0.43
1:C:228:ASN:HA	1:C:231:ILE:HG12	2.01	0.43
1:C:358:GLN:HA	1:C:359:PRO:HD3	1.95	0.43
1:C:378:LEU:HD13	1:C:378:LEU:HA	1.85	0.43
1:A:192:HIS:CG	1:A:421:ALA:HA	2.54	0.42
1:C:192:HIS:CG	1:C:421:ALA:HA	2.54	0.42
2:D:350:ASN:HD22	2:D:350:ASN:N	2.17	0.42
1:C:155:GLU:HB3	3:E:101:LEU:HD11	2.01	0.42
3:E:78:HIS:O	3:E:81:GLU:HG3	2.19	0.42
1:C:255:PHE:HA	1:C:258:ASN:HD22	1.83	0.42
2:D:259:MET:HB3	2:D:268:PHE:CE2	2.53	0.42
2:D:286:LEU:HD22	2:D:290:GLU:HB3	2.00	0.42
1:A:102:ASN:HD22	1:A:105:ARG:H	1.67	0.42
1:A:12:ALA:O	1:A:16:ILE:HB	2.20	0.42
2:D:200:GLU:HB2	2:D:268:PHE:HE1	1.84	0.42
2:B:176:LYS:O	8:C:503:VLB:H222	2.20	0.42
1:C:102:ASN:HD22	1:C:105:ARG:H	1.67	0.42
2:D:62:VAL:HG23	2:D:86:ILE:O	2.19	0.42
1:A:91:GLN:HA	1:A:121:ARG:NH1	2.35	0.42
1:A:206:ASN:HD21	4:A:501:GTP:N2	2.10	0.42
1:A:28:HIS:HD2	1:A:49:PHE:HB2	1.84	0.42
2:B:240:THR:HG21	2:B:320:ARG:HD2	2.01	0.42
2:B:292:THR:HG21	2:B:331:GLN:HB3	2.01	0.42
2:D:172:MET:SD	2:D:205:ASP:HA	2.60	0.42
1:A:143:GLY:O	1:A:147:SER:OG	2.32	0.42
1:A:228:ASN:HA	1:A:231:ILE:HG12	2.01	0.42
8:C:503:VLB:H582	8:C:503:VLB:C51	2.44	0.42
2:D:2:ARG:NH2	2:D:132:LEU:H	2.18	0.42
1:A:182:VAL:O	1:A:185:TYR:HB2	2.20	0.42
2:D:132:LEU:HD23	2:D:164:ARG:HD3	2.01	0.42
2:B:19:LYS:HA	2:B:22:GLU:HG2	2.00	0.41
2:B:200:GLU:HB2	2:B:268:PHE:HE2	1.84	0.41
1:C:182:VAL:O	1:C:185:TYR:HB2	2.20	0.41
2:B:240:THR:HA	2:B:244:PHE:HD1	1.85	0.41
2:B:401:ARG:HH21	1:C:435:VAL:HG12	1.84	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:70:LEU:HD23	1:C:110:ILE:HB	2.02	0.41
2:D:70:LEU:HB3	2:D:98:GLY:HA2	2.02	0.41
3:E:58:GLU:HG2	3:E:62:LYS:HD2	2.03	0.41
1:A:79:ARG:HG3	1:A:92:LEU:HD12	2.02	0.41
2:B:69:ASP:HB3	2:B:94:PHE:CD1	2.55	0.41
2:B:72:PRO:HA	2:B:75:MET:HG2	2.02	0.41
1:C:266:HIS:O	1:C:268:PRO:HD3	2.20	0.41
8:C:503:VLB:N1	8:C:503:VLB:H212	2.36	0.41
2:D:306:ASP:HB3	2:D:309:HIS:CG	2.55	0.41
1:A:313:MET:HE3	1:A:313:MET:HB3	1.91	0.41
2:D:136:GLN:HA	2:D:167:ASN:O	2.21	0.41
2:B:416:MET:O	2:B:420:GLU:HG3	2.21	0.41
2:D:129:CYS:HB3	2:D:131:CYS:O	2.21	0.41
2:B:136:GLN:HA	2:B:167:ASN:O	2.21	0.41
1:C:188:ILE:HD13	1:C:395:PHE:HB2	2.02	0.41
8:C:503:VLB:H52	8:C:503:VLB:C14	2.51	0.41
2:B:275:LEU:HD11	2:B:300:ASN:HA	2.03	0.41
1:C:335:ILE:HD11	1:C:351:PHE:CZ	2.56	0.41
2:B:259:MET:HB3	2:B:268:PHE:CE1	2.56	0.41
1:A:346:TRP:HB3	3:E:29:PHE:HD2	1.85	0.41
2:B:194:LEU:HD23	2:B:198:THR:HG21	2.02	0.41
1:C:224:TYR:HA	1:C:227:LEU:HB2	2.03	0.41
2:D:88:ARG:HB2	2:D:91:ASN:OD1	2.21	0.41
2:D:311:ARG:H	2:D:382:THR:HG1	1.69	0.41
2:D:6:HIS:CD2	2:D:21:TRP:HE1	2.39	0.41
1:A:188:ILE:HD13	1:A:395:PHE:HB2	2.02	0.40
1:C:259:LEU:O	1:C:261:PRO:HD3	2.21	0.40
2:D:194:LEU:HD23	2:D:198:THR:HG21	2.02	0.40
1:A:115:ILE:O	1:A:119:LEU:HD13	2.22	0.40
2:B:69:ASP:HA	2:B:145:THR:HG21	2.03	0.40
1:A:224:TYR:HA	1:A:227:LEU:HB2	2.03	0.40
2:B:172:MET:SD	2:B:205:ASP:HA	2.61	0.40
1:C:285:GLN:O	1:C:286:LEU:HB3	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	430/451 (95%)	374 (87%)	43 (10%)	13 (3%)	4	28
1	C	432/451 (96%)	382 (88%)	35 (8%)	15 (4%)	3	26
2	B	432/445 (97%)	380 (88%)	38 (9%)	14 (3%)	4	27
2	D	431/445 (97%)	385 (89%)	33 (8%)	13 (3%)	4	28
3	E	129/142 (91%)	114 (88%)	13 (10%)	2 (2%)	9	41
All	All	1854/1934 (96%)	1635 (88%)	162 (9%)	57 (3%)	4	28

All (57) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	32	PRO
1	A	89	PRO
1	A	179	THR
1	A	245	ASP
2	B	215	ARG
2	B	359	PRO
1	C	240	ALA
1	C	379	SER
1	C	437	VAL
2	D	369	ARG
3	E	11	LEU
1	A	2	ARG
1	A	3	GLU
1	A	178	SER
2	B	82	PRO
2	B	109	THR
2	B	224	TYR
2	B	372	LYS
1	C	109	THR
1	C	239	THR
1	C	284	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	286	LEU
1	C	322	ASP
1	C	348	PRO
2	D	84	GLY
2	D	97	SER
2	D	109	THR
1	A	280	LYS
2	B	84	GLY
2	B	295	MET
2	D	281	GLN
2	D	285	ALA
2	B	57	THR
2	B	286	LEU
2	B	304	ALA
2	B	358	ILE
1	C	280	LYS
2	D	50	ASN
2	D	249	ASN
2	D	283	TYR
2	D	294	GLN
2	D	304	ALA
2	D	360	PRO
3	E	46	SER
1	A	338	LYS
1	A	387	ALA
2	B	250	ALA
1	C	342	GLN
1	C	349	THR
2	D	57	THR
1	A	260	VAL
1	C	438	ASP
1	A	72	PRO
1	C	72	PRO
1	C	131	GLY
2	B	29	GLY
1	A	212	ILE

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	368/379 (97%)	295 (80%)	73 (20%)	1	5
1	C	370/379 (98%)	311 (84%)	59 (16%)	2	13
2	B	375/385 (97%)	313 (84%)	62 (16%)	2	12
2	D	374/385 (97%)	313 (84%)	61 (16%)	2	12
3	E	114/125 (91%)	89 (78%)	25 (22%)	1	4
All	All	1601/1653 (97%)	1321 (82%)	280 (18%)	2	9

All (280) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	2	ARG
1	A	6	SER
1	A	16	ILE
1	A	18	ASN
1	A	22	GLU
1	A	23	LEU
1	A	26	LEU
1	A	33	ASP
1	A	35	GLN
1	A	47	ASP
1	A	50	ASN
1	A	71	GLU
1	A	73	THR
1	A	77	GLU
1	A	78	VAL
1	A	84	ARG
1	A	90	GLU
1	A	91	GLN
1	A	94	THR
1	A	102	ASN
1	A	109	THR
1	A	113	GLU
1	A	114	ILE
1	A	119	LEU
1	A	120	ASP
1	A	121	ARG
1	A	125	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	141	PHE
1	A	153	LEU
1	A	155	GLU
1	A	160	ASP
1	A	163	LYS
1	A	167	LEU
1	A	182	VAL
1	A	188	ILE
1	A	191	THR
1	A	209	ILE
1	A	215	ARG
1	A	217	LEU
1	A	223	THR
1	A	233	GLN
1	A	248	LEU
1	A	256	GLN
1	A	258	ASN
1	A	266	HIS
1	A	275	VAL
1	A	280	LYS
1	A	291	ILE
1	A	293	ASN
1	A	296	PHE
1	A	302	MET
1	A	315	CYS
1	A	323	VAL
1	A	324	VAL
1	A	326	LYS
1	A	336	LYS
1	A	339	ARG
1	A	341	ILE
1	A	342	GLN
1	A	347	CYS
1	A	351	PHE
1	A	355	ILE
1	A	356	ASN
1	A	367	ASP
1	A	368	LEU
1	A	370	LYS
1	A	373	ARG
1	A	384	ILE
1	A	386	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	401	LYS
1	A	424	ASP
1	A	435	VAL
2	B	3	GLU
2	B	4	ILE
2	B	15	GLN
2	B	20	PHE
2	B	39	ASP
2	B	42	LEU
2	B	43	GLN
2	B	47	GLU
2	B	48	ARG
2	B	54	ASN
2	B	55	GLU
2	B	60	LYS
2	B	74	THR
2	B	75	MET
2	B	79	ARG
2	B	97	SER
2	B	105	LYS
2	B	113	GLU
2	B	119	LEU
2	B	133	GLN
2	B	147	SER
2	B	158	ARG
2	B	168	THR
2	B	172	MET
2	B	179	ASP
2	B	194	LEU
2	B	209	LEU
2	B	213	CYS
2	B	217	LEU
2	B	219	LEU
2	B	224	TYR
2	B	226	ASP
2	B	230	LEU
2	B	242	LEU
2	B	248	LEU
2	B	260	VAL
2	B	284	ARG
2	B	290	GLU
2	B	294	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	295	MET
2	B	297	ASP
2	B	311	ARG
2	B	313	LEU
2	B	322	ARG
2	B	326	LYS
2	B	328	VAL
2	B	332	MET
2	B	333	LEU
2	B	336	GLN
2	B	338	LYS
2	B	349	ASN
2	B	350	ASN
2	B	352	LYS
2	B	353	THR
2	B	355	VAL
2	B	357	ASP
2	B	358	ILE
2	B	371	LEU
2	B	377	PHE
2	B	401	ARG
2	B	415	GLU
2	B	420	GLU
1	C	1	MET
1	C	6	SER
1	C	16	ILE
1	C	18	ASN
1	C	25	CYS
1	C	26	LEU
1	C	30	ILE
1	C	49	PHE
1	C	52	PHE
1	C	53	PHE
1	C	60	LYS
1	C	62	VAL
1	C	64	ARG
1	C	71	GLU
1	C	73	THR
1	C	84	ARG
1	C	88	HIS
1	C	94	THR
1	C	102	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	114	ILE
1	C	121	ARG
1	C	122	ILE
1	C	132	LEU
1	C	141	PHE
1	C	153	LEU
1	C	160	ASP
1	C	163	LYS
1	C	167	LEU
1	C	182	VAL
1	C	188	ILE
1	C	191	THR
1	C	195	LEU
1	C	196	GLU
1	C	217	LEU
1	C	223	THR
1	C	233	GLN
1	C	248	LEU
1	C	269	LEU
1	C	279	GLU
1	C	280	LYS
1	C	284	GLU
1	C	286	LEU
1	C	291	ILE
1	C	293	ASN
1	C	297	GLU
1	C	301	GLN
1	C	302	MET
1	C	315	CYS
1	C	323	VAL
1	C	335	ILE
1	C	343	PHE
1	C	368	LEU
1	C	370	LYS
1	C	377	MET
1	C	378	LEU
1	C	380	ASN
1	C	384	ILE
1	C	401	LYS
1	C	424	ASP
2	D	1	MET
2	D	2	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	D	4	ILE
2	D	24	ILE
2	D	39	ASP
2	D	42	LEU
2	D	44	LEU
2	D	48	ARG
2	D	49	ILE
2	D	60	LYS
2	D	64	ARG
2	D	70	LEU
2	D	71	GLU
2	D	74	THR
2	D	79	ARG
2	D	85	GLN
2	D	91	ASN
2	D	93	VAL
2	D	110	GLU
2	D	113	GLU
2	D	123	ARG
2	D	124	LYS
2	D	127	GLU
2	D	135	PHE
2	D	158	ARG
2	D	164	ARG
2	D	168	THR
2	D	172	MET
2	D	194	LEU
2	D	209	LEU
2	D	212	ILE
2	D	218	LYS
2	D	223	THR
2	D	224	TYR
2	D	247	GLN
2	D	260	VAL
2	D	275	LEU
2	D	284	ARG
2	D	287	THR
2	D	288	VAL
2	D	291	LEU
2	D	292	THR
2	D	293	GLN
2	D	313	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	D	326	LYS
2	D	327	GLU
2	D	328	VAL
2	D	336	GLN
2	D	345	GLU
2	D	349	ASN
2	D	350	ASN
2	D	352	LYS
2	D	353	THR
2	D	355	VAL
2	D	369	ARG
2	D	372	LYS
2	D	377	PHE
2	D	400	ARG
2	D	402	LYS
2	D	416	MET
2	D	419	THR
3	E	9	ILE
3	E	11	LEU
3	E	25	LYS
3	E	47	LEU
3	E	60	ARG
3	E	67	GLU
3	E	68	LEU
3	E	74	GLU
3	E	76	ARG
3	E	81	GLU
3	E	82	VAL
3	E	84	GLN
3	E	88	GLU
3	E	89	GLU
3	E	92	ASN
3	E	101	LEU
3	E	104	LYS
3	E	110	GLU
3	E	111	ASN
3	E	112	ARG
3	E	116	LEU
3	E	123	LEU
3	E	127	ASP
3	E	128	LYS
3	E	134	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (46) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	HIS
1	A	35	GLN
1	A	101	ASN
1	A	102	ASN
1	A	206	ASN
1	A	285	GLN
1	A	356	ASN
1	A	358	GLN
1	A	380	ASN
2	B	14	ASN
2	B	50	ASN
2	B	133	GLN
2	B	136	GLN
2	B	139	HIS
2	B	249	ASN
2	B	258	ASN
2	B	331	GLN
2	B	350	ASN
2	B	380	ASN
2	B	385	GLN
2	B	436	GLN
1	C	8	HIS
1	C	11	GLN
1	C	101	ASN
1	C	102	ASN
1	C	139	HIS
1	C	206	ASN
1	C	249	ASN
1	C	293	ASN
1	C	356	ASN
2	D	14	ASN
2	D	15	GLN
2	D	85	GLN
2	D	133	GLN
2	D	136	GLN
2	D	139	HIS
2	D	186	ASN
2	D	258	ASN
2	D	334	ASN
2	D	350	ASN
2	D	380	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	D	385	GLN
2	D	436	GLN
3	E	90	ASN
3	E	91	ASN
3	E	115	HIS

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 12 ligands modelled in this entry, 2 are monoatomic - leaving 10 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	$\# Z > 2$
6	SO4	A	504	-	4,4,4	0.13	0	6,6,6	0.06	0
6	SO4	D	503	-	4,4,4	0.14	0	6,6,6	0.07	0
6	SO4	A	503	-	4,4,4	0.20	0	6,6,6	0.05	0
6	SO4	B	502	-	4,4,4	0.16	0	6,6,6	0.06	0
4	GTP	C	501	5	26,34,34	1.47	4 (15%)	33,54,54	2.21	10 (30%)
6	SO4	D	502	-	4,4,4	0.15	0	6,6,6	0.05	0
4	GTP	A	501	5	26,34,34	1.46	5 (19%)	33,54,54	2.27	10 (30%)
7	GDP	D	501	-	24,30,30	1.77	5 (20%)	31,47,47	2.20	9 (29%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	GDP	B	501	-	24,30,30	1.44	3 (12%)	31,47,47	2.04	8 (25%)
8	VLB	C	503	-	63,67,67	1.67	13 (20%)	79,108,108	2.48	24 (30%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GTP	C	501	5	-	6/18/38/38	0/3/3/3
4	GTP	A	501	5	-	6/18/38/38	0/3/3/3
7	GDP	B	501	-	-	3/12/32/32	0/3/3/3
8	VLB	C	503	-	-	20/38/131/131	0/7/9/9
7	GDP	D	501	-	-	2/12/32/32	0/3/3/3

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	C	503	VLB	C5-C6	-4.84	1.42	1.51
7	D	501	GDP	O4'-C1'	4.81	1.47	1.41
8	C	503	VLB	C6-C7	4.56	1.41	1.32
7	B	501	GDP	O4'-C1'	3.83	1.46	1.41
4	C	501	GTP	O4'-C1'	3.81	1.46	1.41
4	A	501	GTP	O4'-C1'	3.64	1.46	1.41
8	C	503	VLB	C8-C7	-3.51	1.39	1.49
8	C	503	VLB	C68-C67	3.50	1.57	1.53
7	D	501	GDP	C8-N7	-3.09	1.29	1.34
7	B	501	GDP	C6-N1	2.84	1.38	1.33
8	C	503	VLB	C18-N1	-2.84	1.34	1.39
8	C	503	VLB	C16-C15	2.77	1.44	1.39
7	D	501	GDP	C2-N2	2.67	1.39	1.33
8	C	503	VLB	C68-C73	2.67	1.55	1.53
8	C	503	VLB	O75-C73	2.57	1.38	1.33
7	D	501	GDP	PB-O2B	2.50	1.64	1.54
8	C	503	VLB	C30-C29	-2.43	1.41	1.49
4	A	501	GTP	C8-N7	-2.39	1.30	1.34
4	A	501	GTP	C6-N1	2.36	1.37	1.33
4	C	501	GTP	C8-N7	-2.24	1.30	1.34
8	C	503	VLB	C63-C64	2.16	1.41	1.36
8	C	503	VLB	C19-N9	2.14	1.50	1.47
4	C	501	GTP	C2-N2	2.14	1.38	1.33

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	501	GTP	C2-N2	2.14	1.38	1.33
8	C	503	VLB	C59-C67	2.12	1.42	1.39
4	C	501	GTP	C6-N1	2.11	1.36	1.33
8	C	503	VLB	O25-C23	2.11	1.37	1.33
4	A	501	GTP	C2-N1	2.08	1.39	1.35
7	B	501	GDP	C8-N7	-2.08	1.31	1.34
7	D	501	GDP	PB-O3B	2.00	1.62	1.54

All (61) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	C	503	VLB	O32-C16-C15	8.01	124.78	116.58
8	C	503	VLB	O75-C73-C68	7.16	122.08	111.32
8	C	503	VLB	O28-C29-C30	6.75	123.50	111.09
8	C	503	VLB	C33-O32-C16	-6.16	108.23	117.53
8	C	503	VLB	O32-C16-C17	-5.76	114.21	124.12
7	D	501	GDP	N3-C2-N1	-5.51	119.88	127.22
7	B	501	GDP	C2-N3-C4	5.29	121.40	115.36
4	C	501	GTP	C2-N3-C4	5.20	121.30	115.36
7	D	501	GDP	C2-N3-C4	5.13	121.22	115.36
4	A	501	GTP	PB-O3B-PG	-4.94	115.89	132.83
4	A	501	GTP	C2-N3-C4	4.90	120.95	115.36
4	A	501	GTP	N3-C2-N1	-4.80	120.81	127.22
8	C	503	VLB	C53-C54-C55	4.74	115.10	109.29
4	C	501	GTP	PB-O3B-PG	-4.73	116.60	132.83
7	B	501	GDP	PA-O3A-PB	-4.73	116.61	132.83
4	C	501	GTP	N3-C2-N1	-4.71	120.94	127.22
7	B	501	GDP	N3-C2-N1	-4.63	121.05	127.22
4	A	501	GTP	PA-O3A-PB	-4.44	117.58	132.83
7	D	501	GDP	PA-O3A-PB	-4.43	117.62	132.83
4	C	501	GTP	PA-O3A-PB	-4.40	117.74	132.83
8	C	503	VLB	C22-N1-C2	-4.35	108.60	119.21
7	D	501	GDP	C6-N1-C2	4.24	122.67	115.93
8	C	503	VLB	C69-N56-C55	4.21	116.05	111.01
8	C	503	VLB	C22-N1-C18	-4.07	107.82	120.84
7	B	501	GDP	C5-C6-N1	-4.06	117.88	123.43
4	A	501	GTP	C5-C6-N1	-3.97	118.00	123.43
4	C	501	GTP	C6-C5-C4	-3.82	117.15	120.80
7	D	501	GDP	C5-C6-N1	-3.73	118.33	123.43
8	C	503	VLB	C17-C18-C13	-3.64	117.67	122.00
8	C	503	VLB	O25-C23-C3	3.58	118.24	112.22
8	C	503	VLB	C20-C5-C6	-3.52	103.80	107.99

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	501	GTP	C6-N1-C2	3.52	121.52	115.93
7	B	501	GDP	C6-N1-C2	3.36	121.27	115.93
4	A	501	GTP	C6-C5-C4	-3.13	117.81	120.80
8	C	503	VLB	O74-C73-C68	-3.05	117.77	124.19
4	C	501	GTP	C6-N1-C2	3.02	120.72	115.93
4	C	501	GTP	C5-C6-N1	-3.01	119.31	123.43
4	A	501	GTP	C4-C5-N7	-2.90	106.38	109.40
8	C	503	VLB	C13-C12-C19	-2.89	105.62	115.16
4	A	501	GTP	O2G-PG-O3B	2.85	114.18	104.64
4	C	501	GTP	C4-C5-N7	-2.84	106.43	109.40
7	D	501	GDP	C6-C5-C4	-2.83	118.09	120.80
8	C	503	VLB	C2-C12-C19	2.72	118.66	114.07
7	B	501	GDP	C4-C5-N7	-2.65	106.64	109.40
7	B	501	GDP	C6-C5-C4	-2.61	118.30	120.80
7	D	501	GDP	N2-C2-N3	2.57	121.98	117.79
4	C	501	GTP	O2G-PG-O3B	2.47	112.92	104.64
8	C	503	VLB	C61-C60-C65	2.43	121.39	118.17
7	D	501	GDP	O2B-PB-O3A	2.42	112.76	104.64
8	C	503	VLB	O28-C29-O31	-2.42	118.16	122.96
8	C	503	VLB	C76-O75-C73	-2.36	111.95	115.94
8	C	503	VLB	C12-C19-C5	-2.31	116.49	118.20
4	C	501	GTP	C1'-N9-C4	-2.29	122.63	126.64
8	C	503	VLB	C5-C19-N9	2.25	116.47	111.72
8	C	503	VLB	O75-C73-O74	-2.16	120.14	123.93
8	C	503	VLB	C14-C13-C18	2.09	122.06	120.31
4	A	501	GTP	C1'-N9-C4	-2.07	123.00	126.64
8	C	503	VLB	C11-C12-C19	2.07	106.33	101.82
7	D	501	GDP	C4-C5-N7	-2.06	107.25	109.40
7	B	501	GDP	N2-C2-N1	2.01	120.38	117.25
8	C	503	VLB	C8-C7-C6	-2.01	119.74	123.02

There are no chirality outliers.

All (37) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	501	GTP	PB-O3B-PG-O2G
4	C	501	GTP	C5'-O5'-PA-O1A
4	C	501	GTP	C5'-O5'-PA-O2A
4	A	501	GTP	PB-O3B-PG-O2G
4	A	501	GTP	C5'-O5'-PA-O1A
4	A	501	GTP	C5'-O5'-PA-O2A
8	C	503	VLB	O72-C54-C70-C71

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
8	C	503	VLB	C55-C54-C70-C71
8	C	503	VLB	C53-C54-C70-C71
8	C	503	VLB	C51-C68-C73-O74
8	C	503	VLB	C51-C68-C73-O75
8	C	503	VLB	C67-C68-C73-O74
8	C	503	VLB	C67-C68-C73-O75
8	C	503	VLB	C15-C68-C73-O75
8	C	503	VLB	C21-C20-C5-C19
8	C	503	VLB	C21-C20-C5-C6
8	C	503	VLB	C21-C20-C5-C4
8	C	503	VLB	C30-C29-O28-C4
8	C	503	VLB	O31-C29-O28-C4
8	C	503	VLB	C3-C23-O25-C26
8	C	503	VLB	C68-C73-O75-C76
8	C	503	VLB	O24-C23-O25-C26
8	C	503	VLB	C15-C16-O32-C33
8	C	503	VLB	O74-C73-O75-C76
8	C	503	VLB	C17-C16-O32-C33
4	A	501	GTP	C5'-O5'-PA-O3A
7	D	501	GDP	PB-O3A-PA-O2A
7	B	501	GDP	PB-O3A-PA-O2A
7	B	501	GDP	C5'-O5'-PA-O2A
4	C	501	GTP	PB-O3A-PA-O1A
4	A	501	GTP	PB-O3A-PA-O1A
8	C	503	VLB	C15-C68-C73-O74
4	C	501	GTP	PB-O3B-PG-O3G
4	A	501	GTP	PB-O3B-PG-O3G
4	C	501	GTP	C5'-O5'-PA-O3A
7	B	501	GDP	C5'-O5'-PA-O3A
7	D	501	GDP	C5'-O5'-PA-O2A

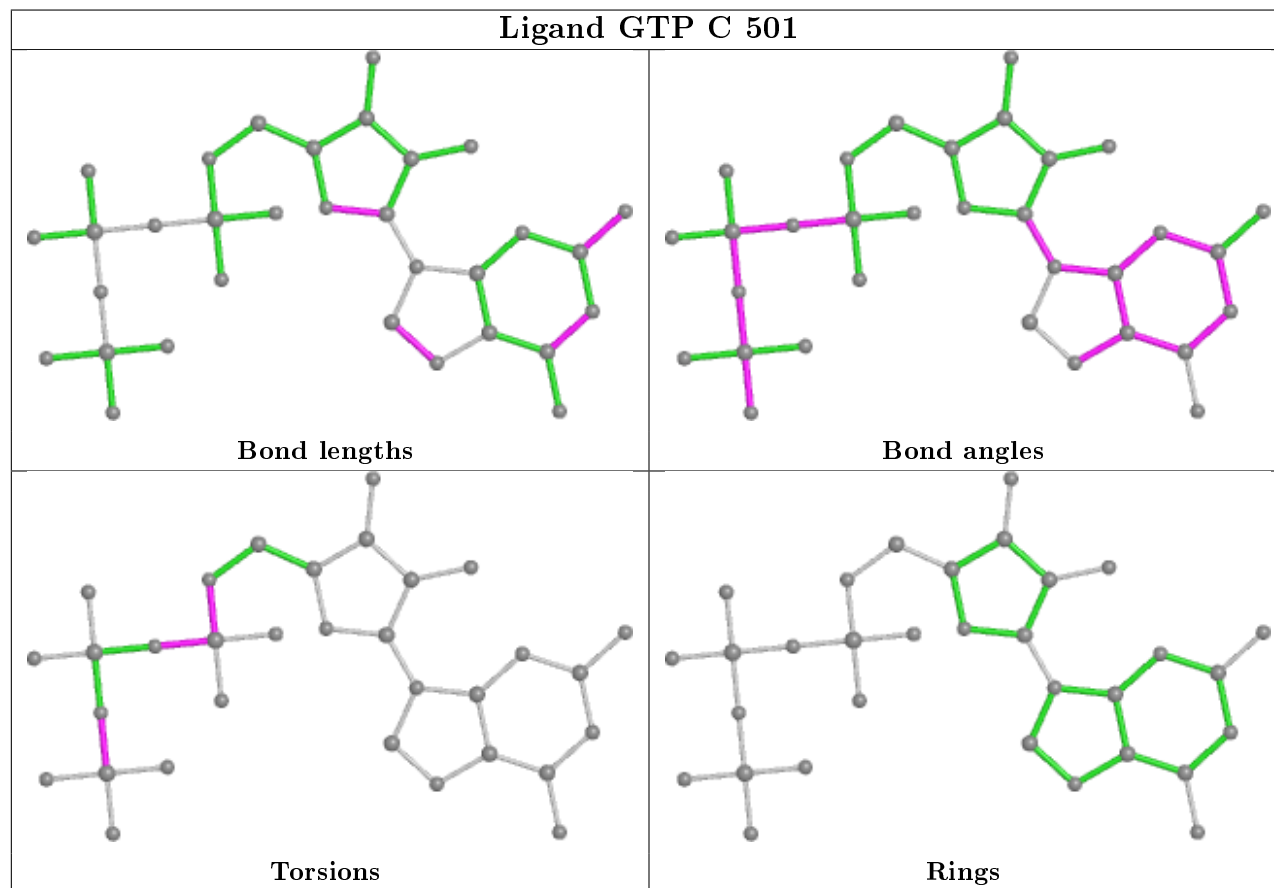
There are no ring outliers.

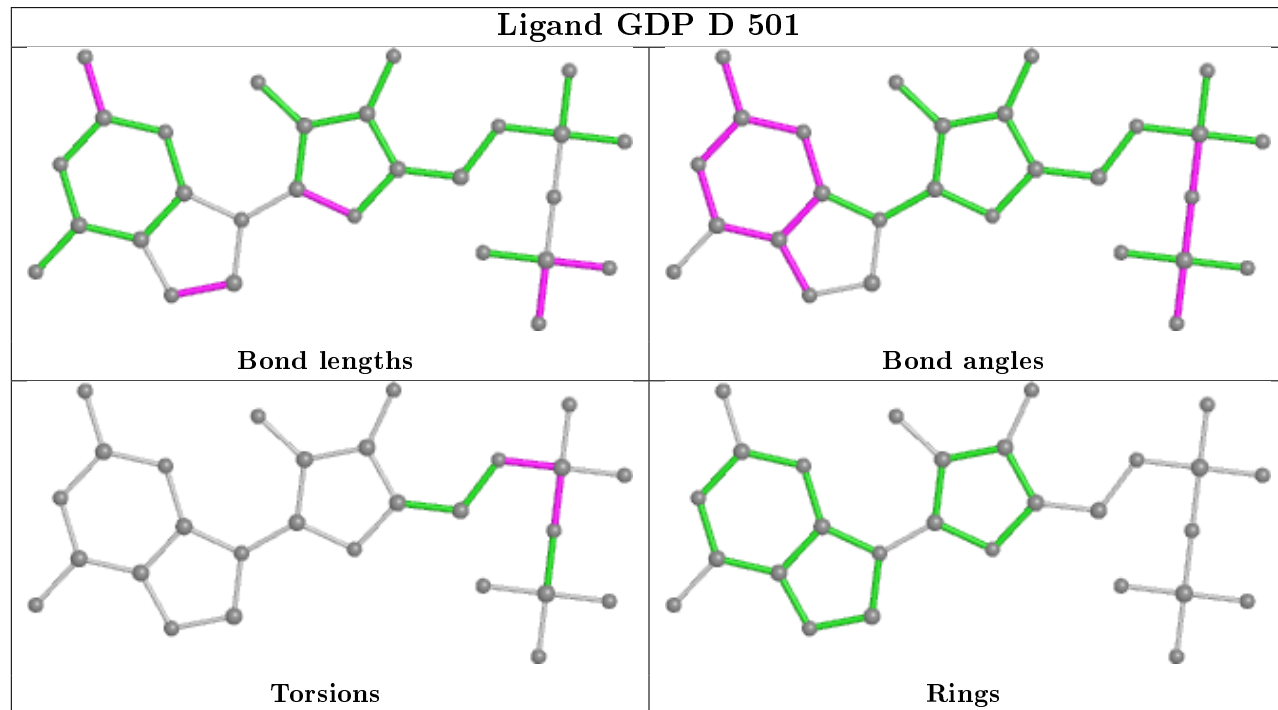
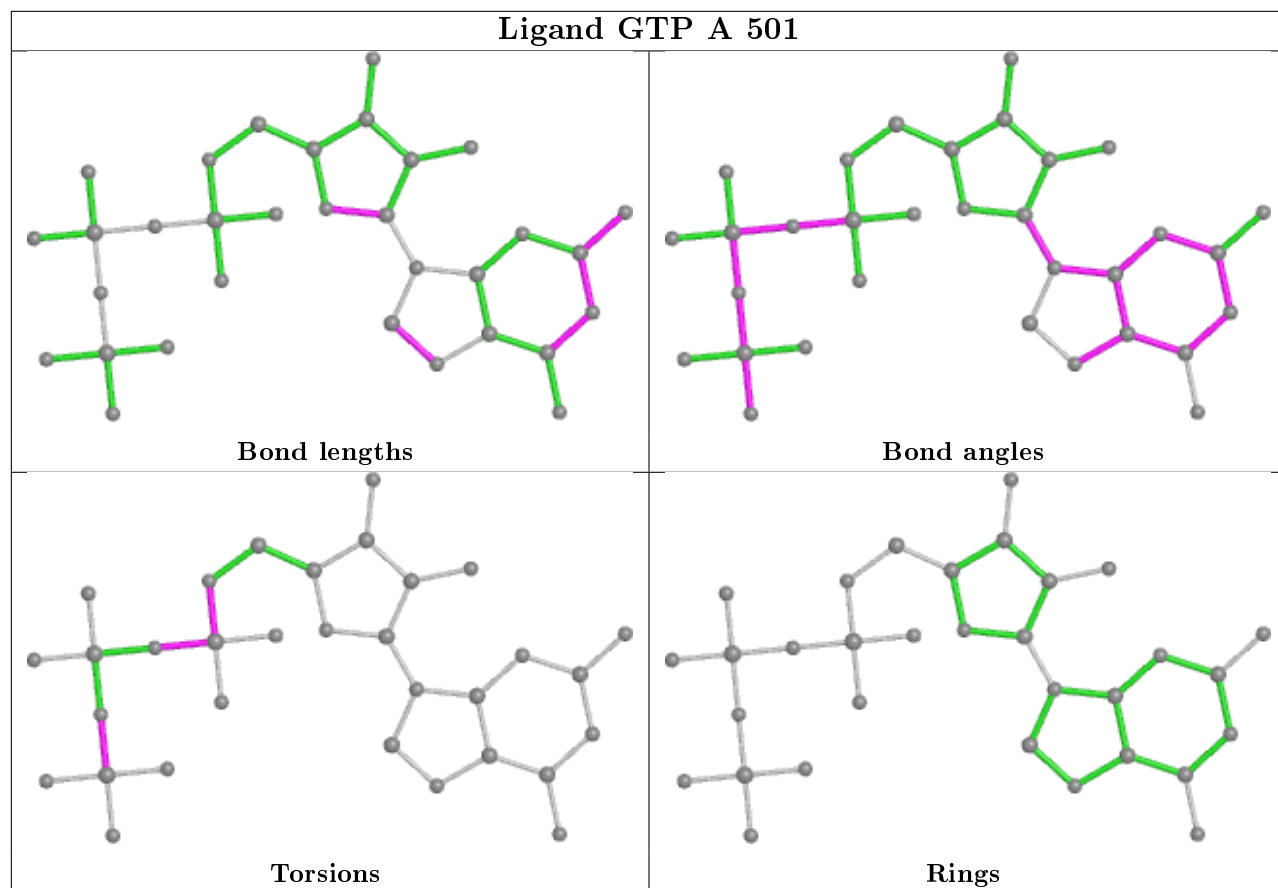
4 monomers are involved in 22 short contacts:

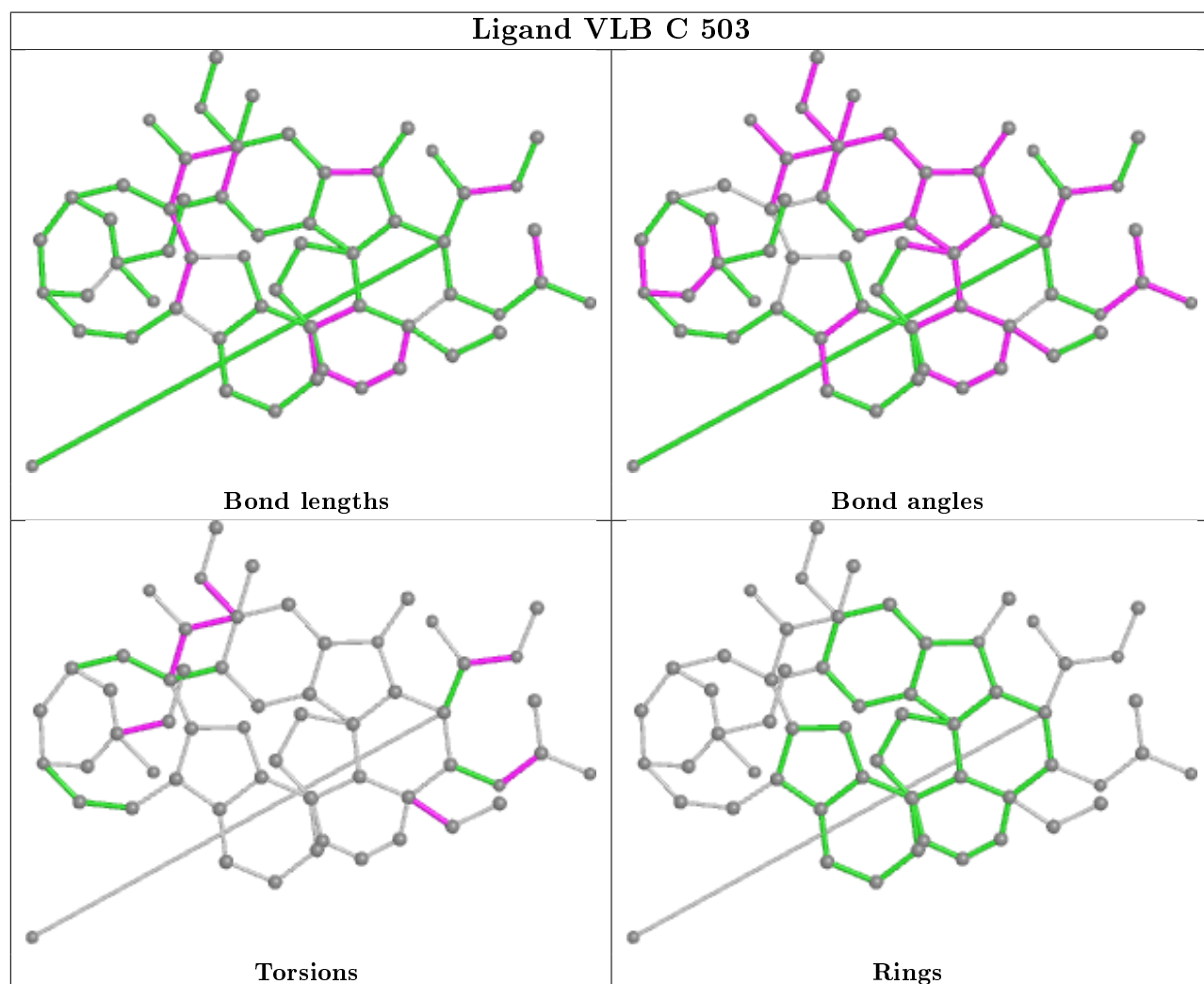
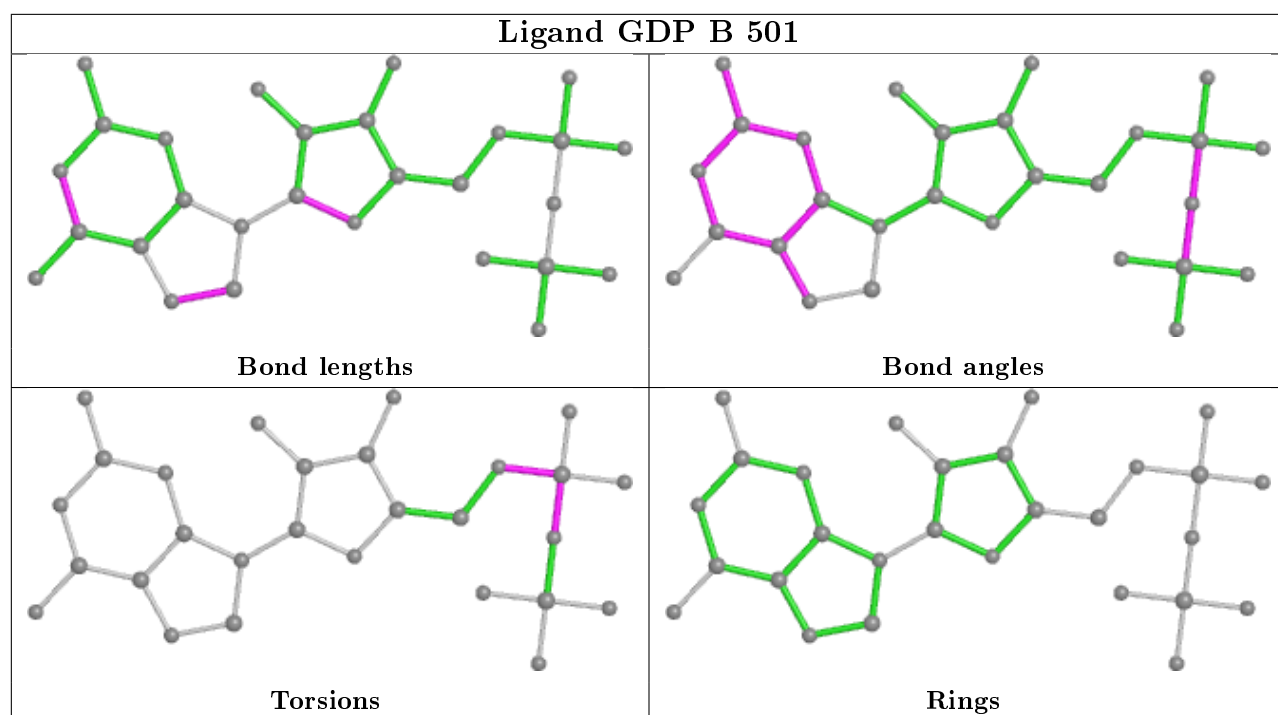
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	501	GTP	3	0
4	A	501	GTP	4	0
7	D	501	GDP	2	0
8	C	503	VLB	13	0

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

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	433/451 (96%)	0.90	73 (16%) 1 2	125, 187, 248, 265	0
1	C	432/451 (95%)	0.67	47 (10%) 5 7	105, 169, 233, 267	0
2	B	432/445 (97%)	0.70	58 (13%) 3 4	107, 165, 243, 269	2 (0%)
2	D	432/445 (97%)	0.50	39 (9%) 9 11	73, 142, 234, 251	2 (0%)
3	E	132/142 (92%)	0.98	26 (19%) 1 1	139, 209, 254, 266	0
All	All	1861/1934 (96%)	0.71	243 (13%) 3 5	73, 170, 244, 269	4 (0%)

All (243) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	61	HIS	11.3
1	A	313	MET	8.1
3	E	22	VAL	7.6
2	B	274	PRO	7.5
3	E	23	ILE	6.9
2	B	61	TYR	6.8
1	A	438	ASP	6.8
1	C	62	VAL	6.3
2	B	28	HIS	5.8
1	C	60	LYS	5.4
3	E	34	GLU	5.4
2	D	53	TYR	5.3
2	D	62	VAL	5.3
1	A	369	ALA	5.3
2	B	359	PRO	5.2
1	A	348	PRO	5.2
1	A	347	CYS	5.2
3	E	18	GLN	5.1
1	A	349	THR	5.1
2	B	375	SER	5.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
3	E	8	VAL	5.0
1	A	32	PRO	5.0
1	C	55	GLU	5.0
1	A	437	VAL	5.0
2	B	55	GLU	4.9
2	D	28	HIS	4.8
1	C	253	THR	4.7
2	B	295	MET	4.7
1	A	346	TRP	4.7
1	A	439	SER	4.6
3	E	33	PRO	4.6
3	E	6	MET	4.6
1	A	312	TYR	4.5
2	D	61	TYR	4.5
2	D	80	SER	4.5
2	D	99	ALA	4.5
2	B	86	ILE	4.3
2	B	249	ASN	4.1
2	D	413	MET	4.1
2	D	32	PRO	4.1
2	B	216	THR	4.1
3	E	13	LYS	4.1
3	E	24	LEU	4.0
2	B	49	ILE	4.0
2	B	273	ALA	4.0
2	B	84	GLY	3.9
3	E	19	SER	3.9
3	E	32	VAL	3.9
2	B	374	SER	3.8
2	D	63	PRO	3.8
2	D	34	GLY	3.8
1	A	170	SER	3.7
3	E	7	GLU	3.7
1	A	345	ASP	3.7
1	C	346	TRP	3.7
1	A	413	MET	3.7
2	D	59	ASN	3.7
1	C	296	PHE	3.7
2	D	36	TYR	3.7
2	B	372	LYS	3.6
1	A	220	GLU	3.6
1	A	381	THR	3.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	311	LYS	3.6
1	A	247	ALA	3.6
2	D	87	PHE	3.5
1	A	37	PRO	3.5
1	C	120[A]	ASP	3.5
1	A	35	GLN	3.5
1	C	364	PRO	3.5
1	A	28	HIS	3.5
1	A	139	HIS	3.5
2	B	284	ARG	3.4
2	B	293	GLN	3.4
2	D	91	ASN	3.4
2	B	62	VAL	3.4
2	B	358	ILE	3.4
2	B	371	LEU	3.4
2	B	373	MET	3.4
1	A	274	PRO	3.3
2	D	37	HIS	3.3
2	B	442	GLU	3.3
1	A	282	TYR	3.3
2	D	83	PHE	3.3
1	A	83	TYR	3.3
2	B	27	GLU	3.3
3	E	135	LYS	3.3
2	D	30	ILE	3.2
1	A	319	TYR	3.2
2	B	59	ASN	3.2
1	A	62	VAL	3.2
1	A	435	VAL	3.2
2	D	408	TYR	3.2
2	B	83	PHE	3.2
1	A	343	PHE	3.1
3	E	20	TRP	3.1
1	A	440	VAL	3.1
1	C	37	PRO	3.1
1	A	80	THR	3.1
1	A	103	TYR	3.1
1	C	36	MET	3.0
1	C	276	ILE	3.0
2	B	369	ARG	3.0
3	E	11	LEU	3.0
1	C	277	SER	3.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	13	GLY	3.0
2	B	283	TYR	3.0
2	B	275	LEU	3.0
2	D	296	PHE	3.0
1	A	248	LEU	3.0
1	A	323	VAL	3.0
1	A	428	LEU	2.9
1	A	86	LEU	2.9
1	C	370	LYS	2.9
1	C	437	VAL	2.9
1	C	115	ILE	2.9
2	B	100	GLY	2.9
1	A	178	SER	2.8
2	D	29	GLY	2.8
1	A	179	THR	2.8
3	E	41	ARG	2.8
2	B	319	PHE	2.8
2	D	33	THR	2.8
2	B	56	ALA	2.8
1	C	365	GLY	2.8
2	D	56	ALA	2.8
1	C	54	SER	2.8
1	C	199	ASP	2.8
3	E	10	GLU	2.7
2	B	241	CYS	2.7
2	B	244	PHE	2.7
2	D	86	ILE	2.7
1	A	357	TYR	2.7
3	E	21	GLU	2.7
2	B	53	TYR	2.7
2	B	37	HIS	2.7
3	E	27	PRO	2.7
1	A	355	ILE	2.7
2	D	258	ASN	2.7
2	B	401	ARG	2.6
1	C	219	ILE	2.6
1	C	351	PHE	2.6
2	B	412	GLY	2.6
1	C	256	GLN	2.6
3	E	12	ASN	2.6
2	B	296	PHE	2.6
1	C	274	PRO	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	29	GLY	2.6
2	B	321	GLY	2.6
1	C	220	GLU	2.6
2	D	98	GLY	2.6
1	C	222	PRO	2.6
2	B	248	LEU	2.6
1	A	432	TYR	2.6
1	C	63	PRO	2.5
2	B	301	MET	2.5
2	D	60	LYS	2.5
1	C	64	ARG	2.5
3	E	14	ALA	2.5
1	C	362	VAL	2.5
1	C	168	GLU	2.5
1	A	108	TYR	2.5
1	A	204	VAL	2.5
1	A	350	GLY	2.5
2	B	377	PHE	2.5
1	C	179	THR	2.5
2	B	323	MET	2.4
2	B	29	GLY	2.4
2	B	30	ILE	2.4
1	A	388	TRP	2.4
1	A	53	PHE	2.4
1	C	254	GLU	2.4
2	D	67	LEU	2.4
1	C	372	GLN	2.4
1	A	351	PHE	2.4
3	E	31	GLY	2.3
1	C	85	GLN	2.3
1	C	133	GLN	2.3
3	E	45	PRO	2.3
1	A	82	THR	2.3
2	D	39	ASP	2.3
2	B	370	GLY	2.3
2	B	322	ARG	2.3
2	B	87	PHE	2.3
1	A	382	THR	2.3
2	B	215	ARG	2.3
1	C	374	ALA	2.3
1	A	31	GLN	2.3
1	A	17	GLY	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	33	ASP	2.3
3	E	136	ASN	2.3
1	C	35	GLN	2.3
1	C	281	ALA	2.3
1	A	30	ILE	2.2
1	A	60	LYS	2.2
1	C	338	LYS	2.2
1	A	85	GLN	2.2
2	B	60	LYS	2.2
2	B	441	ASP	2.2
1	A	324	VAL	2.2
1	A	326	LYS	2.2
1	A	218	ASP	2.2
2	B	168	THR	2.2
2	D	54	ASN	2.2
1	C	285	GLN	2.2
2	B	413	MET	2.2
2	D	249	ASN	2.2
1	A	15	GLN	2.2
2	B	91	ASN	2.2
2	B	47	GLU	2.2
1	A	373	ARG	2.2
3	E	46	SER	2.2
2	B	258	ASN	2.2
2	D	328	VAL	2.2
1	A	279	GLU	2.2
2	D	279	GLY	2.2
2	D	399	PHE	2.2
2	D	103	TRP	2.2
1	A	140	SER	2.1
1	A	104	ALA	2.1
1	A	194	THR	2.1
1	A	228	ASN	2.1
1	C	53	PHE	2.1
1	A	288	VAL	2.1
2	D	287	THR	2.1
1	C	1	MET	2.1
1	C	251	ASP	2.1
1	C	369	ALA	2.1
1	A	6	SER	2.1
1	A	188	ILE	2.1
2	D	102	ASN	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	B	278	ARG	2.1
1	C	300	ASN	2.1
2	D	245	PRO	2.1
1	C	56	THR	2.1
2	B	290	GLU	2.1
3	E	9	ILE	2.1
1	C	28	HIS	2.1
2	D	55	GLU	2.1
1	A	353	VAL	2.0
1	A	36	MET	2.0
2	D	35	SER	2.0
1	A	436	GLY	2.0
1	C	214	ARG	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(\AA^2)	Q<0.9
6	SO4	A	503	5/5	0.65	0.46	232,237,238,238	0
6	SO4	A	504	5/5	0.66	0.48	246,250,251,251	0
6	SO4	D	502	5/5	0.80	0.47	219,223,224,224	0
6	SO4	B	502	5/5	0.85	0.18	243,248,249,249	0
6	SO4	D	503	5/5	0.85	0.24	159,164,165,165	0
8	VLB	C	503	59/59	0.90	0.26	154,159,166,170	0
4	GTP	C	501	32/32	0.95	0.27	134,138,144,149	0
7	GDP	D	501	28/28	0.97	0.16	113,117,125,130	0
4	GTP	A	501	32/32	0.97	0.31	140,148,158,159	0
5	MG	A	502	1/1	0.98	0.31	116,116,116,116	0

Continued on next page...

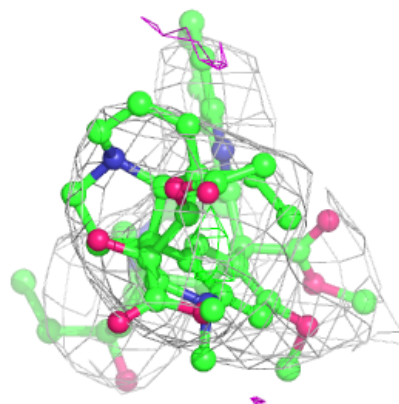
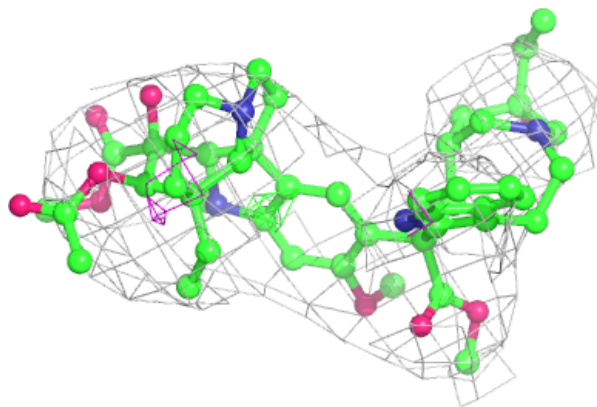
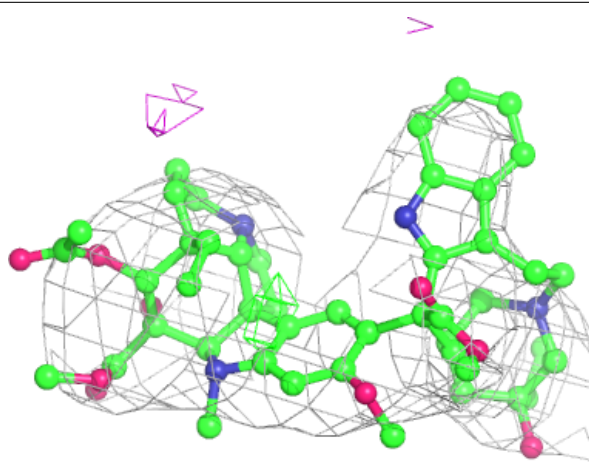
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
7	GDP	B	501	28/28	0.98	0.21	126,131,138,140	0
5	MG	C	502	1/1	0.98	0.21	121,121,121,121	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.

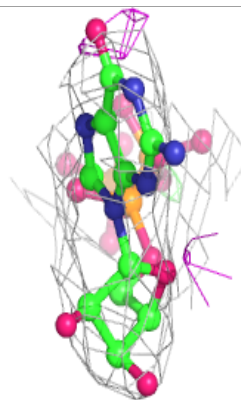
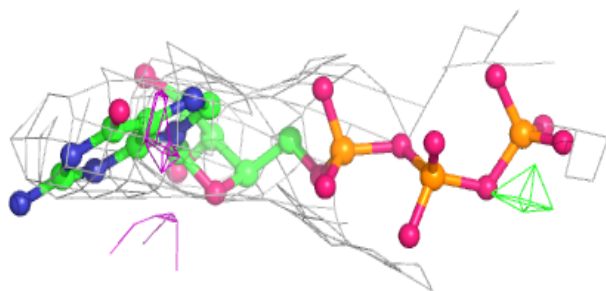
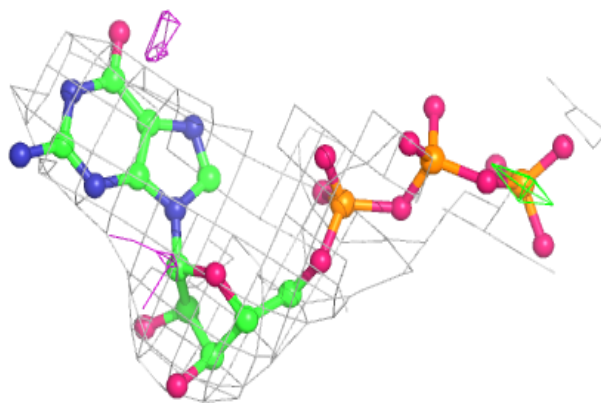
Electron density around VLB C 503:

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

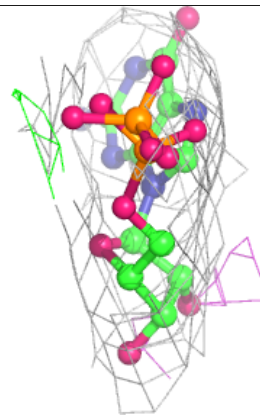
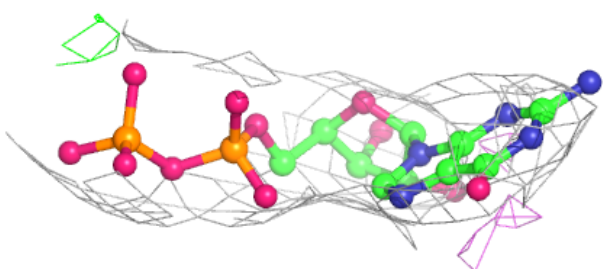
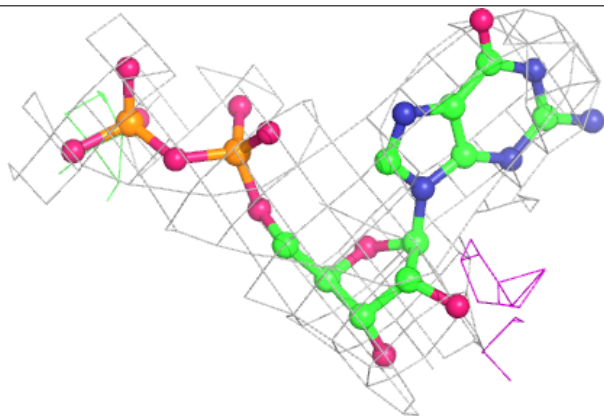


Electron density around GTP C 501:

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

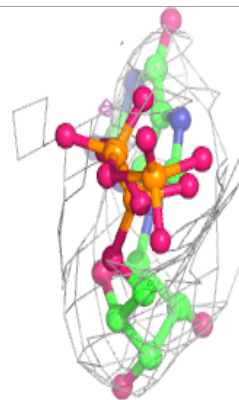
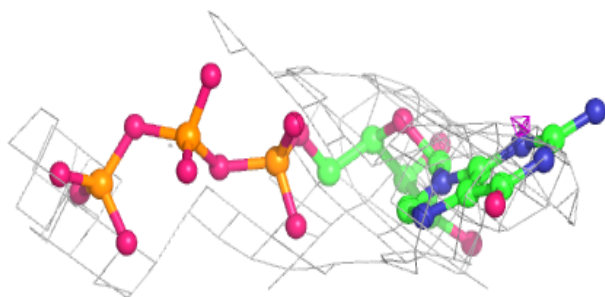
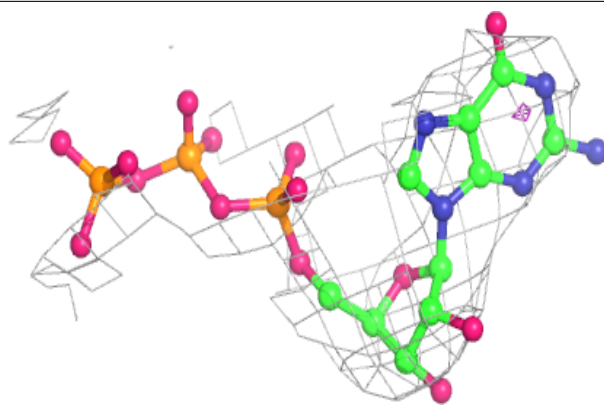
**Electron density around GDP D 501:**

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

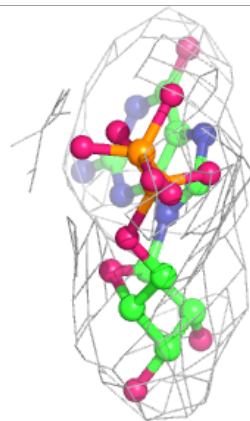
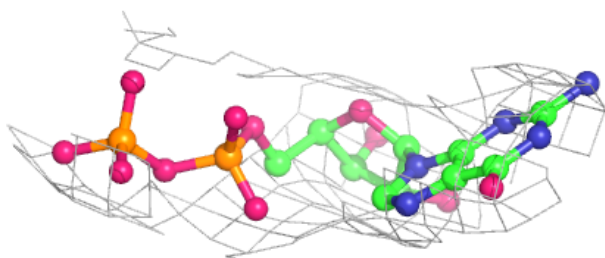
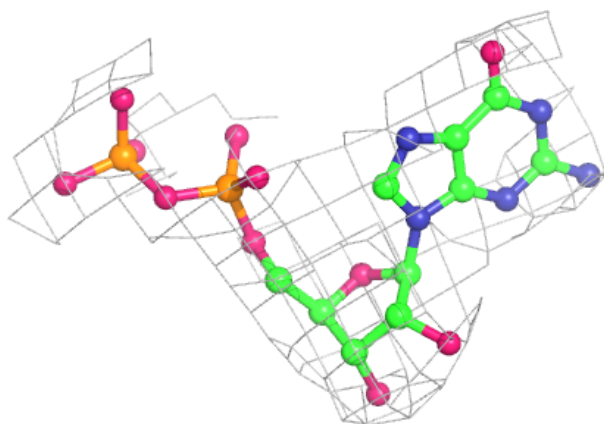


Electron density around GTP A 501:

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

**Electron density around 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.