



Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 01:44 am BST

PDB ID : 1TPZ
Title : Crystal Structure of IIGP1: a paradigm for interferon inducible p47 resistance GTPases
Authors : Ghosh, A.; Uthaiiah, R.; Howard, J.; Herrmann, C.; Wolf, E.
Deposited on : 2004-06-16
Resolution : 2.00 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 : 2.11
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) : 2.11

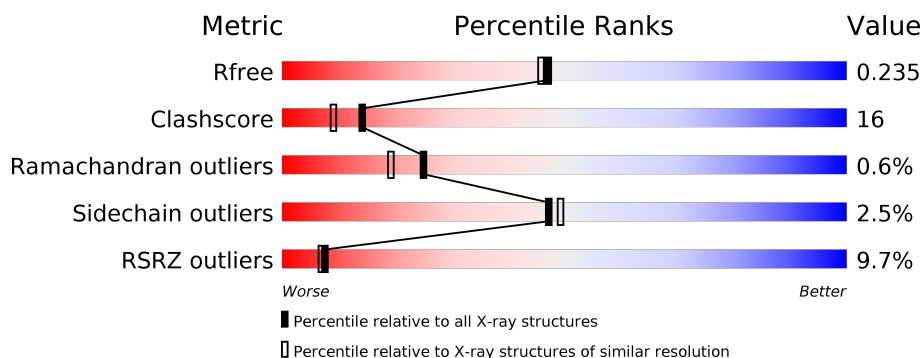
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	422	<div> <div>9%</div> <div> <div></div> <div>65%</div> <div>27%</div> <div>• 6%</div> </div> </div>
1	B	422	<div> <div>9%</div> <div> <div></div> <div>66%</div> <div>25%</div> <div>• 7%</div> </div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7034 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 interferon-inducible GTPase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	395	Total	C	N	O	S	0	0	0
			3200	2065	524	597	14			
1	B	392	Total	C	N	O	S	0	0	0
			3175	2047	520	594	14			

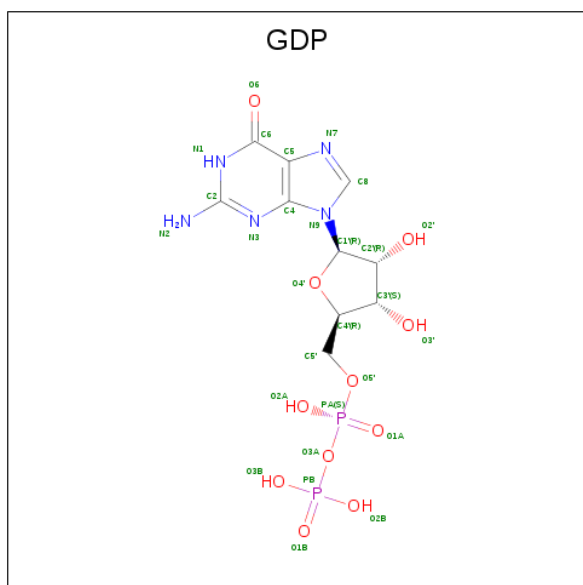
There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	412	LYS	-	CLONING ARTIFACT	UNP Q9QZ85
A	413	LEU	-	CLONING ARTIFACT	UNP Q9QZ85
A	414	GLY	-	CLONING ARTIFACT	UNP Q9QZ85
A	415	ARG	-	CLONING ARTIFACT	UNP Q9QZ85
A	416	LEU	-	CLONING ARTIFACT	UNP Q9QZ85
A	417	GLU	-	CLONING ARTIFACT	UNP Q9QZ85
A	418	ARG	-	CLONING ARTIFACT	UNP Q9QZ85
A	419	PRO	-	CLONING ARTIFACT	UNP Q9QZ85
A	420	HIS	-	CLONING ARTIFACT	UNP Q9QZ85
A	421	ARG	-	CLONING ARTIFACT	UNP Q9QZ85
A	422	ASP	-	CLONING ARTIFACT	UNP Q9QZ85
B	412	LYS	-	CLONING ARTIFACT	UNP Q9QZ85
B	413	LEU	-	CLONING ARTIFACT	UNP Q9QZ85
B	414	GLY	-	CLONING ARTIFACT	UNP Q9QZ85
B	415	ARG	-	CLONING ARTIFACT	UNP Q9QZ85
B	416	LEU	-	CLONING ARTIFACT	UNP Q9QZ85
B	417	GLU	-	CLONING ARTIFACT	UNP Q9QZ85
B	418	ARG	-	CLONING ARTIFACT	UNP Q9QZ85
B	419	PRO	-	CLONING ARTIFACT	UNP Q9QZ85
B	420	HIS	-	CLONING ARTIFACT	UNP Q9QZ85
B	421	ARG	-	CLONING ARTIFACT	UNP Q9QZ85
B	422	ASP	-	CLONING ARTIFACT	UNP Q9QZ85

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 3 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



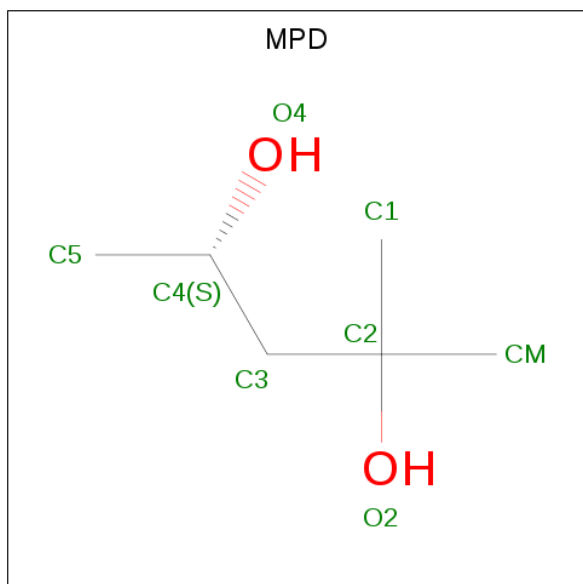
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O P 28 10 5 11 2	0	0
3	B	1	Total C N O P 28 10 5 11 2	0	0

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: $C_6H_{14}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			8	6	2		

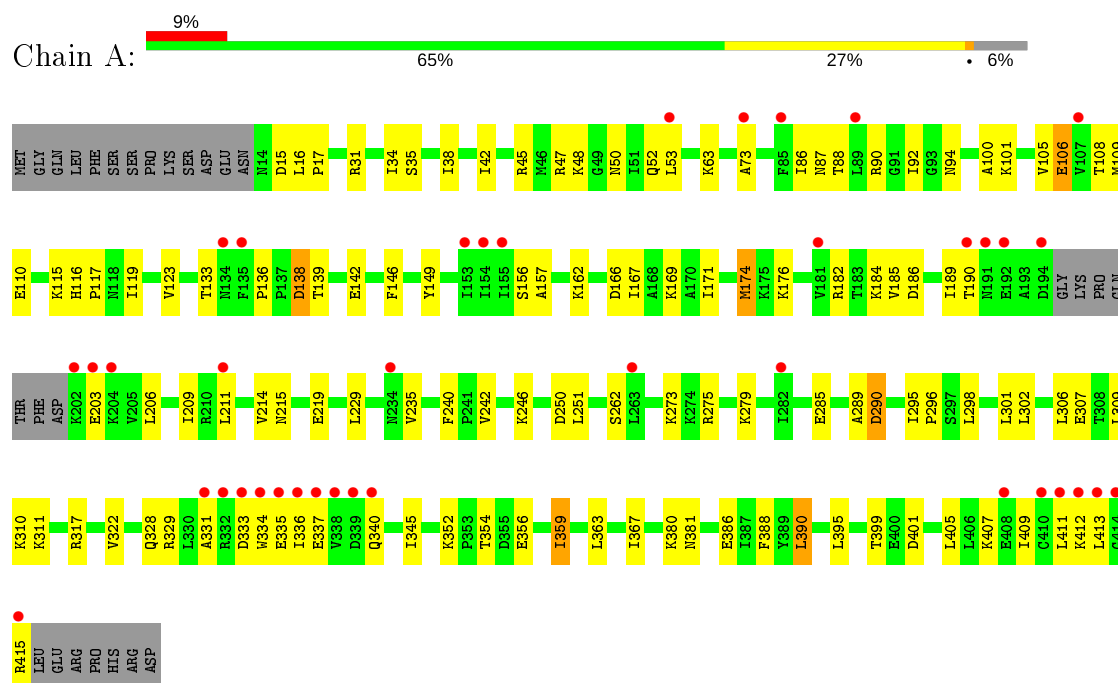
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	274	Total 274	O 274	0	0
6	B	315	Total 315	O 315	0	0

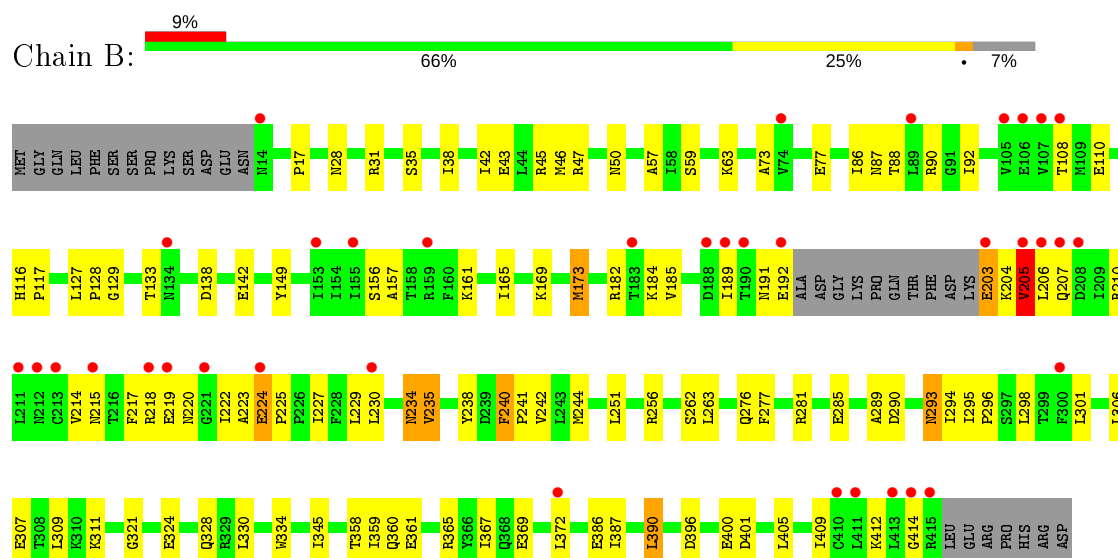
3 Residue-property plots

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

• Molecule 1: interferon-inducible GTPase



• Molecule 1: interferon-inducible GTPase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	80.54Å 91.89Å 143.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.00 29.95 – 2.00	Depositor EDS
% Data completeness (in resolution range)	96.9 (30.00-2.00) 96.9 (29.95-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.73 (at 2.00Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.208 , 0.241 0.201 , 0.235	Depositor DCC
R_{free} test set	5742 reflections (8.16%)	wwPDB-VP
Wilson B-factor (Å ²)	32.5	Xtriage
Anisotropy	0.517	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 47.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7034	wwPDB-VP
Average B, all atoms (Å ²)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.87% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

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	0.32	0/3264	0.56	0/4404
1	B	0.33	0/3239	0.55	0/4371
All	All	0.33	0/6503	0.56	0/8775

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

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	3200	0	3235	101	0
1	B	3175	0	3198	102	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	28	0	12	0	0
3	B	28	0	12	0	0
4	B	4	0	6	0	0
5	B	8	0	14	2	0
6	A	274	0	0	8	0
6	B	315	0	0	10	0
All	All	7034	0	6477	202	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 16.

All (202) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:87:ASN:HD21	1:A:100:ALA:H	0.99	0.97
1:A:189:ILE:HD11	1:A:206:LEU:HD11	1.61	0.83
1:B:214:VAL:HG13	1:B:224:GLU:HB2	1.61	0.82
1:B:17:PRO:HB2	1:B:47:ARG:NH1	1.95	0.81
1:A:174:MET:HB3	6:A:1654:HOH:O	1.80	0.80
1:B:28:ASN:HB3	6:B:2762:HOH:O	1.80	0.79
1:A:169:LYS:HD3	1:B:169:LYS:HD3	1.65	0.79
1:A:295:ILE:H	1:A:295:ILE:HD12	1.47	0.79
1:B:92:ILE:HD11	1:B:117:PRO:HG2	1.64	0.78
1:A:88:THR:HG23	1:A:235:VAL:HG12	1.67	0.77
1:A:87:ASN:ND2	1:A:100:ALA:H	1.81	0.76
1:A:182:ARG:NH1	1:A:209:ILE:HG23	2.02	0.75
1:A:174:MET:CE	1:A:176:LYS:HG3	2.17	0.75
1:A:306:LEU:HD11	1:A:310:LYS:HE3	1.70	0.74
1:A:354:THR:HG22	1:A:356:GLU:H	1.52	0.74
1:A:174:MET:HE2	1:A:176:LYS:HG3	1.70	0.73
1:A:211:LEU:O	1:A:214:VAL:HG12	1.89	0.72
1:A:52:GLN:H	1:A:52:GLN:CD	1.92	0.72
1:A:359:ILE:HD12	1:A:363:LEU:HG	1.69	0.72
1:A:88:THR:HG23	1:A:235:VAL:CG1	2.19	0.72
1:B:204:LYS:O	1:B:205:VAL:HG22	1.90	0.72
1:B:365:ARG:O	1:B:369:GLU:HG3	1.90	0.71
1:A:235:VAL:HG13	6:A:1764:HOH:O	1.91	0.70
1:B:298:LEU:HD11	1:B:301:LEU:HD13	1.71	0.70
1:B:293:ASN:HD22	1:B:293:ASN:C	1.94	0.70
1:A:185:VAL:HG11	1:A:229:LEU:HB3	1.75	0.68
1:A:246:LYS:HE2	1:A:250:ASP:OD1	1.94	0.68
1:A:45:ARG:HD3	1:A:53:LEU:HB3	1.75	0.67
1:A:87:ASN:HD21	1:A:100:ALA:N	1.82	0.66
1:A:88:THR:CG2	1:A:235:VAL:HG12	2.25	0.66
1:B:330:LEU:HD21	1:B:334:TRP:CZ3	2.30	0.65
1:B:330:LEU:HD21	1:B:334:TRP:CE3	2.33	0.64
1:B:295:ILE:HG13	6:B:2765:HOH:O	1.98	0.63
1:B:321:GLY:O	5:B:1000:MPD:H4	1.97	0.63
1:B:108:THR:HG22	1:B:110:GLU:H	1.62	0.63
1:B:386:GLU:HG3	6:B:2624:HOH:O	1.98	0.63
1:B:214:VAL:HG22	1:B:224:GLU:HG3	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:94:ASN:HD21	1:A:101:LYS:HA	1.63	0.63
1:B:210:ARG:O	1:B:214:VAL:HG23	1.99	0.63
1:B:157:ALA:HB1	1:B:184:LYS:HD2	1.80	0.62
1:B:173:MET:HG3	6:B:2709:HOH:O	1.99	0.62
1:B:204:LYS:HG2	1:B:205:VAL:HG13	1.81	0.62
1:A:48:LYS:HE3	1:A:50:ASN:HD21	1.64	0.61
1:A:92:ILE:HG21	1:A:117:PRO:HG2	1.81	0.61
1:B:281:ARG:HH11	1:B:281:ARG:HG2	1.65	0.61
1:B:296:PRO:HA	1:B:386:GLU:HG2	1.83	0.61
1:B:242:VAL:HG23	6:B:2778:HOH:O	1.99	0.60
1:A:162:LYS:HG2	1:A:166:ASP:OD2	2.02	0.60
1:B:217:PHE:HE2	1:B:227:ILE:HD11	1.67	0.60
1:B:87:ASN:HB3	1:B:92:ILE:O	2.02	0.60
1:B:396:ASP:O	1:B:400:GLU:HG3	2.02	0.59
1:B:217:PHE:CE2	1:B:227:ILE:HD11	2.37	0.59
1:B:324:GLU:O	1:B:328:GLN:HG3	2.02	0.59
1:B:59:SER:O	1:B:63:LYS:HG3	2.02	0.59
1:B:215:ASN:ND2	1:B:218:ARG:HH22	2.00	0.59
1:A:295:ILE:N	1:A:295:ILE:HD12	2.17	0.58
1:B:50:ASN:HB2	6:B:2712:HOH:O	2.04	0.58
1:A:411:LEU:HD12	1:A:412:LYS:N	2.18	0.58
1:B:185:VAL:HG21	1:B:229:LEU:HB3	1.84	0.58
1:B:367:ILE:HG13	1:B:390:LEU:HD13	1.85	0.58
1:A:242:VAL:HG13	6:A:1607:HOH:O	2.03	0.57
1:A:307:GLU:O	1:A:311:LYS:HG3	2.04	0.57
1:A:295:ILE:H	1:A:295:ILE:CD1	2.17	0.57
1:A:157:ALA:HB1	1:A:184:LYS:HD2	1.84	0.57
1:A:352:LYS:HB2	1:A:352:LYS:NZ	2.20	0.57
1:A:289:ALA:O	1:A:290:ASP:HB2	2.04	0.56
1:A:395:LEU:O	1:A:399:THR:HG23	2.05	0.56
1:A:317:ARG:HD2	1:A:322:VAL:O	2.04	0.56
1:A:108:THR:HG22	1:A:110:GLU:H	1.70	0.56
1:A:15:ASP:OD2	1:A:17:PRO:HD2	2.06	0.56
1:B:43:GLU:OE2	1:B:47:ARG:NH1	2.39	0.56
1:B:289:ALA:O	1:B:290:ASP:HB2	2.05	0.56
1:B:165:ILE:HG22	1:B:169:LYS:HE3	1.88	0.55
1:B:214:VAL:HG12	1:B:218:ARG:NH1	2.21	0.55
1:B:185:VAL:O	1:B:189:ILE:HG12	2.06	0.55
1:B:222:ILE:O	1:B:223:ALA:HB3	2.07	0.55
1:A:167:ILE:O	1:A:171:ILE:HG13	2.08	0.54
1:B:367:ILE:CG1	1:B:390:LEU:HD13	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:192:GLU:HG3	1:B:205:VAL:HG11	1.90	0.54
1:B:358:THR:OG1	1:B:361:GLU:HG3	2.08	0.53
1:B:31:ARG:HD3	1:B:276:GLN:OE1	2.09	0.53
1:B:330:LEU:C	1:B:330:LEU:HD23	2.29	0.53
1:A:336:ILE:HG13	1:A:337:GLU:N	2.23	0.53
1:B:293:ASN:ND2	1:B:293:ASN:C	2.62	0.53
1:B:281:ARG:NH1	1:B:285:GLU:OE2	2.42	0.53
1:A:73:ALA:HB2	1:A:149:TYR:CG	2.43	0.53
1:A:171:ILE:HG23	1:A:176:LYS:HB2	1.91	0.53
1:B:218:ARG:C	1:B:220:ASN:H	2.12	0.52
1:B:345:ILE:HB	1:B:401:ASP:CG	2.30	0.52
1:B:35:SER:OG	1:B:38:ILE:HG12	2.09	0.52
1:A:86:ILE:O	1:A:90:ARG:HD3	2.09	0.52
1:A:329:ARG:HH11	1:A:329:ARG:HG3	1.75	0.51
1:B:203:GLU:O	1:B:207:GLN:HG2	2.11	0.51
1:A:367:ILE:CG1	1:A:390:LEU:HD13	2.39	0.51
1:B:372:LEU:HD12	6:B:2553:HOH:O	2.10	0.51
1:A:115:LYS:HG2	1:A:123:VAL:HG22	1.93	0.51
1:B:244:MET:HE3	1:B:263:LEU:HD13	1.93	0.51
1:A:336:ILE:HD11	1:A:340:GLN:HG3	1.92	0.51
1:B:309:LEU:HD21	1:B:387:ILE:HG13	1.92	0.51
1:B:129:GLY:O	1:B:133:THR:HG23	2.11	0.50
1:B:86:ILE:O	1:B:90:ARG:HD3	2.11	0.50
1:A:306:LEU:HD11	1:A:310:LYS:CE	2.39	0.50
1:A:306:LEU:C	1:A:306:LEU:HD13	2.32	0.50
1:A:386:GLU:HG3	6:A:1661:HOH:O	2.11	0.50
1:B:161:LYS:O	1:B:165:ILE:HG12	2.12	0.50
1:B:182:ARG:HB3	1:B:229:LEU:HD23	1.94	0.50
1:B:405:LEU:O	1:B:409:ILE:HG13	2.12	0.50
1:B:138:ASP:O	1:B:142:GLU:HG3	2.13	0.49
1:A:285:GLU:HG2	1:A:388:PHE:CE2	2.47	0.49
1:A:407:LYS:O	1:A:411:LEU:HG	2.12	0.49
1:A:105:VAL:HG23	6:A:1724:HOH:O	2.12	0.49
1:B:73:ALA:HB2	1:B:149:TYR:CG	2.48	0.48
1:A:186:ASP:O	1:A:190:THR:HG23	2.14	0.48
1:A:215:ASN:O	1:A:219:GLU:HB2	2.13	0.48
1:B:281:ARG:HG2	1:B:281:ARG:NH1	2.29	0.48
1:A:182:ARG:HB3	1:A:229:LEU:HD22	1.96	0.48
1:B:189:ILE:HD13	1:B:205:VAL:CG2	2.43	0.48
1:A:31:ARG:HD2	1:A:273:LYS:HG3	1.95	0.48
1:B:256:ARG:HB3	1:B:277:PHE:HE2	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:42:ILE:O	1:B:46:MET:HG3	2.13	0.47
1:A:302:LEU:HD12	1:A:302:LEU:N	2.29	0.47
1:A:38:ILE:O	1:A:42:ILE:HG13	2.13	0.47
1:B:234:ASN:HD22	1:B:234:ASN:C	2.16	0.47
1:A:109:MET:SD	1:A:133:THR:HG22	2.55	0.47
1:A:35:SER:OG	1:A:38:ILE:HG12	2.14	0.47
1:A:34:ILE:HD11	1:A:38:ILE:CG2	2.44	0.47
1:A:146:PHE:HB2	1:A:174:MET:HE1	1.97	0.47
1:B:306:LEU:HD11	1:B:359:ILE:CD1	2.45	0.46
1:A:47:ARG:HG2	1:A:47:ARG:HH11	1.80	0.46
1:A:405:LEU:O	1:A:409:ILE:HG13	2.15	0.46
1:B:110:GLU:HG3	6:B:2663:HOH:O	2.14	0.46
1:B:116:HIS:CD2	1:B:262:SER:HB2	2.50	0.46
1:B:43:GLU:HG2	1:B:47:ARG:HH11	1.80	0.46
1:A:174:MET:HE3	1:A:176:LYS:HG3	1.95	0.46
1:B:17:PRO:CB	1:B:47:ARG:NH1	2.73	0.46
1:A:345:ILE:HB	1:A:401:ASP:CG	2.35	0.46
1:B:45:ARG:NH1	1:B:57:ALA:HB2	2.30	0.46
1:A:116:HIS:CD2	1:A:262:SER:HB2	2.51	0.46
1:A:119:ILE:HG23	6:A:1715:HOH:O	2.15	0.46
1:A:285:GLU:HG2	1:A:388:PHE:HE2	1.80	0.46
1:A:90:ARG:NH1	1:A:92:ILE:HD11	2.31	0.45
1:B:359:ILE:HG23	1:B:360:GLN:N	2.31	0.45
1:A:334:TRP:O	1:A:336:ILE:N	2.44	0.45
1:B:238:TYR:N	1:B:238:TYR:CD2	2.83	0.45
1:A:411:LEU:HD12	1:A:411:LEU:C	2.37	0.45
1:B:225:PRO:O	1:B:227:ILE:HG13	2.17	0.45
1:A:367:ILE:HG12	1:A:390:LEU:HD13	1.98	0.45
1:A:309:LEU:HD11	1:A:390:LEU:HD23	1.98	0.45
1:B:17:PRO:HB2	1:B:47:ARG:HH12	1.76	0.45
1:A:298:LEU:HB2	1:A:367:ILE:HD12	1.98	0.45
1:B:110:GLU:N	1:B:110:GLU:OE2	2.49	0.45
1:B:189:ILE:HD11	1:B:206:LEU:CD2	2.47	0.45
1:B:281:ARG:O	1:B:285:GLU:HG3	2.17	0.45
1:B:295:ILE:HB	6:B:2766:HOH:O	2.15	0.45
1:B:306:LEU:HD11	1:B:359:ILE:HD11	1.98	0.45
1:A:182:ARG:HH11	1:A:209:ILE:HG23	1.79	0.44
1:A:106:GLU:N	1:A:106:GLU:OE1	2.50	0.44
1:A:92:ILE:CG2	1:A:117:PRO:HG2	2.47	0.44
1:B:108:THR:HG23	6:B:2769:HOH:O	2.16	0.44
1:B:215:ASN:HD22	1:B:218:ARG:HH12	1.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:412:LYS:C	1:B:414:GLY:H	2.21	0.44
1:A:136:PRO:HD2	1:A:139:THR:HB	1.99	0.44
1:A:302:LEU:HD12	1:A:302:LEU:H	1.83	0.44
1:B:230:LEU:C	1:B:230:LEU:HD12	2.38	0.44
1:B:215:ASN:O	1:B:219:GLU:HG2	2.19	0.43
1:B:240:PHE:N	1:B:241:PRO:CD	2.82	0.43
1:A:73:ALA:HB2	1:A:149:TYR:CD1	2.53	0.43
1:B:45:ARG:HB3	1:B:50:ASN:OD1	2.19	0.43
1:B:204:LYS:C	1:B:206:LEU:H	2.22	0.43
1:A:171:ILE:CG2	1:A:176:LYS:HB2	2.48	0.43
1:B:334:TRP:CD2	1:B:412:LYS:HE3	2.54	0.43
1:B:372:LEU:O	1:B:372:LEU:HD13	2.19	0.43
1:A:119:ILE:CG2	6:A:1715:HOH:O	2.66	0.43
1:B:127:LEU:HA	1:B:128:PRO:HD3	1.91	0.42
1:A:413:LEU:C	1:A:415:ARG:H	2.23	0.42
1:A:328:GLN:O	1:A:331:ALA:HB3	2.18	0.42
1:A:90:ARG:HB3	1:A:117:PRO:HD3	2.01	0.42
1:A:367:ILE:HG13	1:A:390:LEU:HD13	2.01	0.42
1:A:47:ARG:HG2	1:A:47:ARG:NH1	2.34	0.42
1:B:88:THR:HG23	1:B:235:VAL:HG22	2.01	0.42
1:A:295:ILE:HA	1:A:296:PRO:HD3	1.94	0.42
1:B:156:SER:O	1:B:182:ARG:HA	2.19	0.42
1:B:293:ASN:HD22	1:B:294:ILE:N	2.17	0.41
1:B:330:LEU:HD12	5:B:1000:MPD:C5	2.50	0.41
1:A:156:SER:O	1:A:182:ARG:HD2	2.20	0.41
1:B:203:GLU:N	1:B:203:GLU:OE1	2.54	0.41
1:A:301:LEU:CD2	1:A:359:ILE:HG23	2.49	0.41
1:A:275:ARG:O	1:A:279:LYS:HG3	2.20	0.41
1:B:157:ALA:CB	1:B:184:LYS:HD2	2.49	0.41
1:A:301:LEU:HD21	1:A:306:LEU:HD23	2.02	0.41
1:A:380:LYS:O	1:A:381:ASN:HB2	2.20	0.41
1:B:295:ILE:HA	1:B:296:PRO:HD3	1.92	0.41
1:B:372:LEU:C	1:B:372:LEU:HD13	2.42	0.41
1:A:94:ASN:ND2	1:A:101:LYS:HA	2.32	0.41
1:A:138:ASP:O	1:A:142:GLU:HG3	2.21	0.41
1:A:45:ARG:HD3	1:A:53:LEU:CB	2.47	0.40
1:B:191:ASN:N	1:B:191:ASN:HD22	2.20	0.40
1:A:63:LYS:HG3	6:A:1772:HOH:O	2.22	0.40
1:A:16:LEU:HB2	1:A:17:PRO:HD3	2.04	0.40
1:A:329:ARG:HG3	1:A:329:ARG:NH1	2.35	0.40
1:B:307:GLU:O	1:B:311:LYS:HG3	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:223:ALA:O	1:B:224:GLU:C	2.60	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	391/422 (93%)	372 (95%)	16 (4%)	3 (1%)	19	13
1	B	388/422 (92%)	369 (95%)	17 (4%)	2 (0%)	29	23
All	All	779/844 (92%)	741 (95%)	33 (4%)	5 (1%)	25	19

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	205	VAL
1	A	203	GLU
1	B	224	GLU
1	A	290	ASP
1	A	335	GLU

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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	359/386 (93%)	351 (98%)	8 (2%)	52	55
1	B	356/386 (92%)	346 (97%)	10 (3%)	43	44
All	All	715/772 (93%)	697 (98%)	18 (2%)	47	49

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	106	GLU
1	A	138	ASP
1	A	174	MET
1	A	240	PHE
1	A	251	LEU
1	A	333	ASP
1	A	359	ILE
1	A	390	LEU
1	B	77	GLU
1	B	173	MET
1	B	203	GLU
1	B	205	VAL
1	B	234	ASN
1	B	235	VAL
1	B	240	PHE
1	B	251	LEU
1	B	293	ASN
1	B	390	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	50	ASN
1	A	87	ASN
1	A	94	ASN
1	A	191	ASN
1	A	215	ASN
1	A	293	ASN
1	A	328	GLN
1	B	134	ASN
1	B	163	ASN

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Mol	Chain	Res	Type
1	B	191	ASN
1	B	215	ASN
1	B	234	ASN
1	B	237	HIS
1	B	258	ASN
1	B	293	ASN
1	B	368	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	MPD	B	1000	-	7,7,7	0.75	0	9,10,10	0.67	0
3	GDP	B	2500	2	24,30,30	1.97	5 (20%)	31,47,47	2.50	12 (38%)
3	GDP	A	1500	2	24,30,30	2.00	6 (25%)	31,47,47	2.53	13 (41%)
4	EDO	B	2000	-	3,3,3	0.81	0	2,2,2	0.41	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	MPD	B	1000	-	-	1/5/5/5	-
3	GDP	B	2500	2	-	1/12/32/32	0/3/3/3
3	GDP	A	1500	2	-	1/12/32/32	0/3/3/3
4	EDO	B	2000	-	-	1/1/1/1	-

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1500	GDP	C6-N1	7.03	1.45	1.33
3	B	2500	GDP	C6-N1	6.82	1.44	1.33
3	B	2500	GDP	C2-N1	2.92	1.40	1.35
3	A	1500	GDP	C2-N1	2.80	1.40	1.35
3	A	1500	GDP	C6-C5	2.74	1.46	1.41
3	B	2500	GDP	C4-N3	2.58	1.39	1.35
3	A	1500	GDP	C4-N3	2.58	1.39	1.35
3	B	2500	GDP	C6-C5	2.53	1.45	1.41
3	B	2500	GDP	C8-N7	-2.36	1.30	1.34
3	A	1500	GDP	C8-N7	-2.27	1.30	1.34
3	A	1500	GDP	C2'-C1'	-2.16	1.50	1.53

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1500	GDP	C5-C6-N1	-7.54	113.12	123.43
3	B	2500	GDP	C5-C6-N1	-7.49	113.18	123.43
3	A	1500	GDP	C6-N1-C2	5.73	125.04	115.93
3	B	2500	GDP	C6-N1-C2	5.71	125.00	115.93
3	A	1500	GDP	C6-C5-C4	-4.25	116.74	120.80
3	B	2500	GDP	C6-C5-C4	-3.93	117.04	120.80
3	A	1500	GDP	C1'-N9-C4	-3.86	119.86	126.64
3	A	1500	GDP	N3-C2-N1	-3.62	122.40	127.22
3	B	2500	GDP	N3-C2-N1	-3.57	122.46	127.22
3	B	2500	GDP	PA-O3A-PB	-3.32	121.43	132.83
3	B	2500	GDP	C1'-N9-C4	-3.15	121.11	126.64
3	A	1500	GDP	PA-O3A-PB	-3.02	122.45	132.83
3	A	1500	GDP	O2A-PA-O5'	2.73	120.44	107.75
3	B	2500	GDP	O2A-PA-O5'	2.68	120.21	107.75
3	B	2500	GDP	C2-N3-C4	-2.63	112.35	115.36
3	A	1500	GDP	C2-N3-C4	-2.52	112.48	115.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	2500	GDP	O3B-PB-O3A	2.51	113.04	104.64
3	A	1500	GDP	O3'-C3'-C4'	-2.43	104.03	111.05
3	A	1500	GDP	O4'-C4'-C3'	-2.36	100.45	105.11
3	B	2500	GDP	O3'-C3'-C4'	-2.21	104.66	111.05
3	B	2500	GDP	O4'-C4'-C3'	-2.10	100.97	105.11
3	B	2500	GDP	N2-C2-N3	2.09	121.20	117.79
3	A	1500	GDP	O3B-PB-O3A	2.06	111.56	104.64
3	A	1500	GDP	N2-C2-N3	2.02	121.08	117.79
3	A	1500	GDP	O4'-C4'-C5'	2.00	115.97	109.37

There are no chirality outliers.

All (4) torsion outliers are listed below:

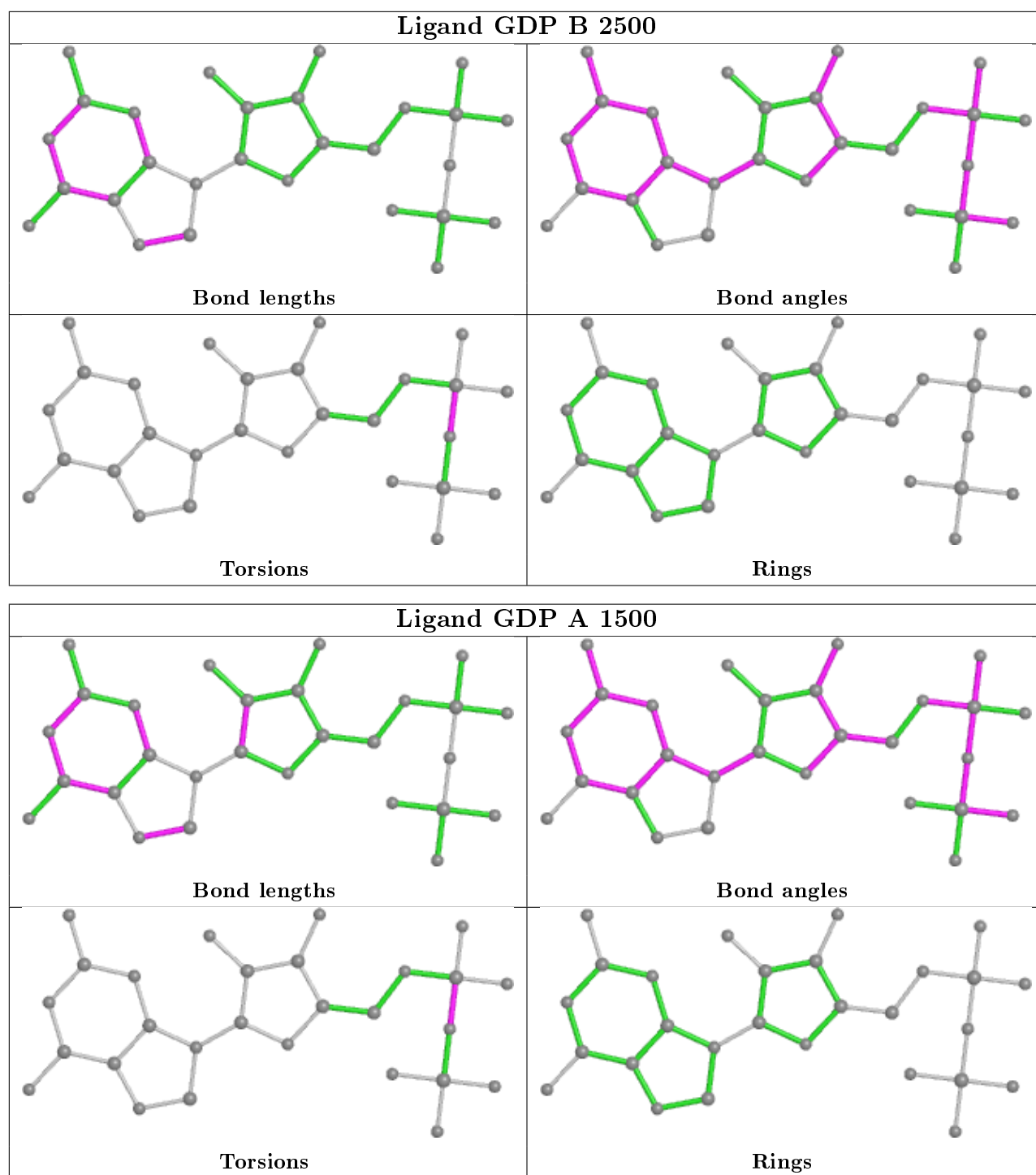
Mol	Chain	Res	Type	Atoms
4	B	2000	EDO	O1-C1-C2-O2
3	A	1500	GDP	PB-O3A-PA-O2A
3	B	2500	GDP	PB-O3A-PA-O2A
5	B	1000	MPD	CM-C2-C3-C4

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	1000	MPD	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 [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	395/422 (93%)	0.48	39 (9%) 7 6	24, 40, 76, 81	0
1	B	392/422 (92%)	0.44	37 (9%) 8 8	22, 38, 79, 81	0
All	All	787/844 (93%)	0.46	76 (9%) 7 7	22, 39, 79, 81	0

All (76) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	202	LYS	9.6
1	A	414	GLY	7.9
1	A	411	LEU	7.4
1	A	194	ASP	7.4
1	A	413	LEU	5.4
1	B	189	ILE	5.1
1	A	415	ARG	5.0
1	B	192	GLU	4.8
1	A	332	ARG	4.6
1	B	414	GLY	4.4
1	A	334	TRP	4.1
1	B	415	ARG	4.1
1	B	215	ASN	4.0
1	B	205	VAL	3.9
1	A	335	GLU	3.7
1	B	190	THR	3.7
1	A	192	GLU	3.6
1	B	153	ILE	3.4
1	A	134	ASN	3.4
1	A	412	LYS	3.3
1	B	207	GLN	3.3
1	A	410	CYS	3.2
1	B	221	GLY	3.1
1	A	336	ILE	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	337	GLU	3.1
1	A	107	VAL	3.1
1	B	203	GLU	3.0
1	B	219	GLU	3.0
1	B	206	LEU	3.0
1	B	208	ASP	2.9
1	A	89	LEU	2.9
1	A	333	ASP	2.9
1	B	413	LEU	2.9
1	A	338	VAL	2.8
1	B	188	ASP	2.8
1	A	203	GLU	2.8
1	B	218	ARG	2.8
1	A	181	VAL	2.7
1	B	155	ILE	2.7
1	A	339	ASP	2.7
1	B	14	ASN	2.7
1	A	204	LYS	2.7
1	B	89	LEU	2.6
1	B	105	VAL	2.6
1	A	190	THR	2.6
1	A	331	ALA	2.6
1	A	155	ILE	2.5
1	B	106	GLU	2.5
1	A	135	PHE	2.5
1	B	410	CYS	2.5
1	B	211	LEU	2.4
1	B	300	PHE	2.4
1	B	372	LEU	2.4
1	A	154	ILE	2.4
1	A	282	ILE	2.4
1	A	153	ILE	2.3
1	A	85	PHE	2.3
1	B	230	LEU	2.3
1	B	183	THR	2.3
1	B	212	ASN	2.3
1	A	211	LEU	2.3
1	A	73	ALA	2.3
1	B	134	ASN	2.2
1	A	53	LEU	2.2
1	A	408	GLU	2.2
1	B	213	CYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	340	GLN	2.2
1	B	224	GLU	2.2
1	A	234	ASN	2.2
1	B	159	ARG	2.2
1	B	411	LEU	2.1
1	B	108	THR	2.1
1	B	107	VAL	2.1
1	A	191	ASN	2.1
1	A	263	LEU	2.1
1	B	74	VAL	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 carbohydrates in this entry.

6.4 Ligands [i](#)

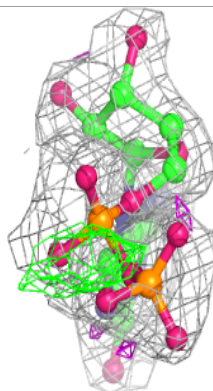
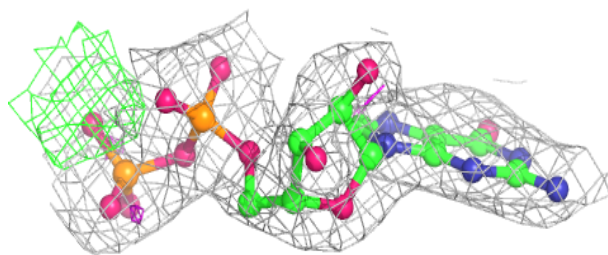
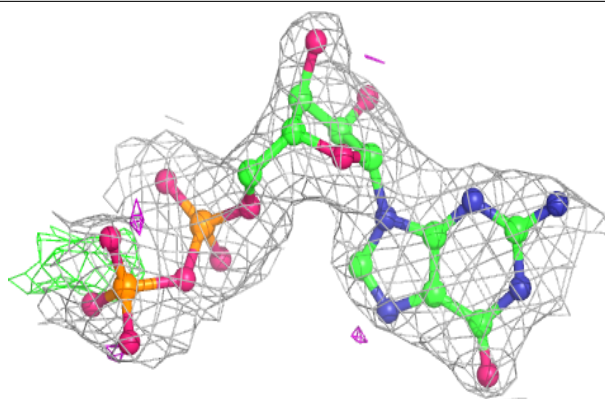
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	MPD	B	1000	8/8	0.88	0.21	41,47,54,56	0
4	EDO	B	2000	4/4	0.90	0.31	66,67,67,67	0
3	GDP	B	2500	28/28	0.95	0.13	39,55,61,62	0
2	MG	A	1501	1/1	0.96	0.39	29,29,29,29	0
3	GDP	A	1500	28/28	0.96	0.12	34,41,45,46	0
2	MG	B	2501	1/1	0.99	0.18	26,26,26,26	0

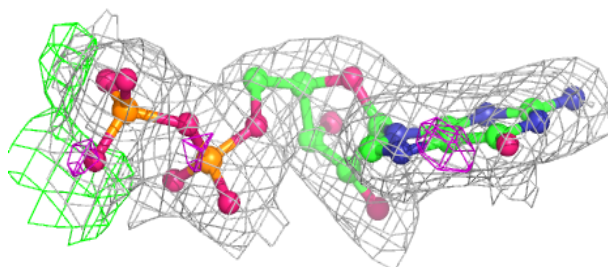
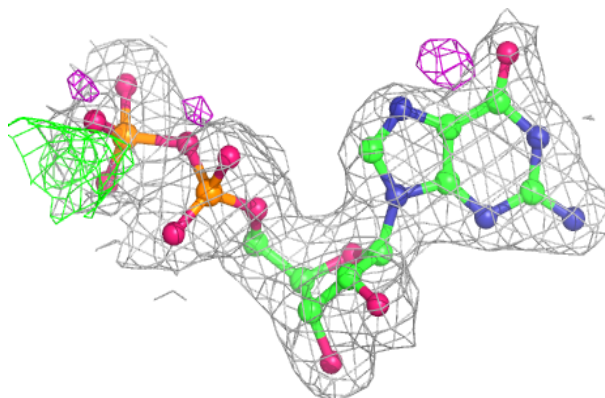
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around GDP B 2500:

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

**Electron density around GDP A 1500:**

$2mF_o-DF_c$ (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.