



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 01:12 AM UTC

PDB ID : 7B51 / pdb_00007b51
Title : Crystal structure of human CRM1 covalently modified by 2-mercaptoethanol at Cys528
Authors : Shaikhqasem, A.; Ficner, R.
Deposited on : 2020-12-03
Resolution : 2.58 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

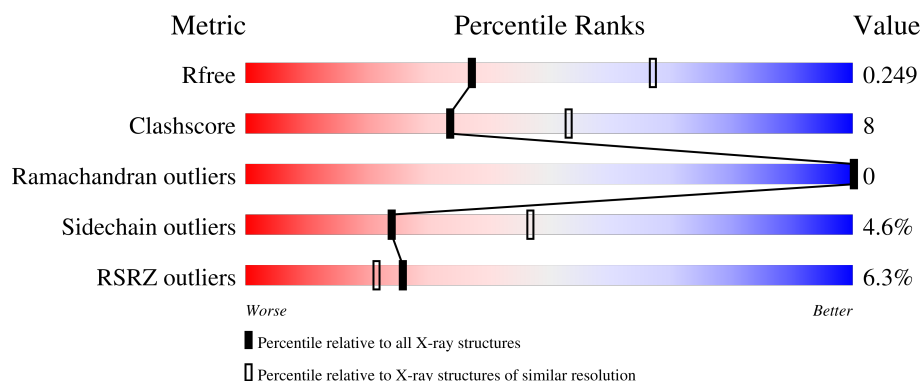
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.58 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}	180053	4770 (2.60-2.56)
Clashscore	190562	5124 (2.60-2.56)
Ramachandran outliers	187476	5046 (2.60-2.56)
Sidechain outliers	187428	5046 (2.60-2.56)
RSRZ outliers	180081	4770 (2.60-2.56)

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	B	182	5% 78% 16% • •
2	A	1060	6% 76% 19% • •

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9786 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 GTP-binding nuclear protein Ran.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	174	Total	C	N	O	S	0	0	0
			1414	919	247	243	5			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	MET	-	initiating methionine	UNP P62826
B	0	GLY	-	expression tag	UNP P62826
B	69	LEU	GLN	engineered mutation	UNP P62826

- Molecule 2 is a protein called Exportin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	1013	Total	C	N	O	S	0	0	0
			8199	5266	1374	1506	53			

There are 27 discrepancies between the modelled and reference sequences:

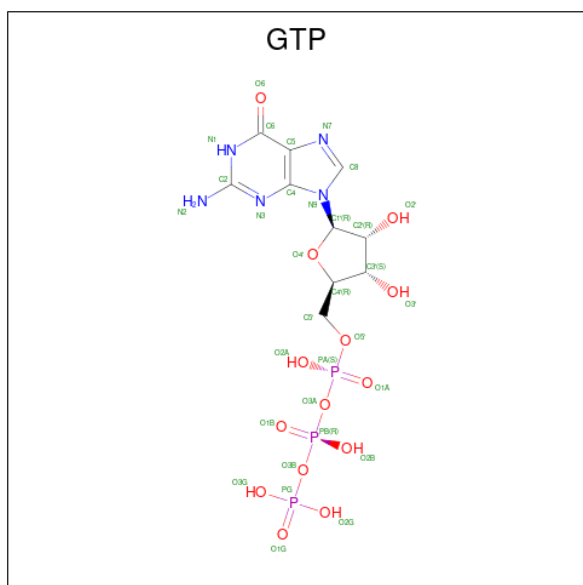
Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	initiating methionine	UNP O14980
A	-12	ALA	-	expression tag	UNP O14980
A	-11	SER	-	expression tag	UNP O14980
A	-10	MET	-	expression tag	UNP O14980
A	-9	THR	-	expression tag	UNP O14980
A	-8	GLY	-	expression tag	UNP O14980
A	-7	GLY	-	expression tag	UNP O14980
A	-6	GLN	-	expression tag	UNP O14980
A	-5	GLN	-	expression tag	UNP O14980
A	-4	MET	-	expression tag	UNP O14980
A	-3	GLY	-	expression tag	UNP O14980
A	-2	ARG	-	expression tag	UNP O14980
A	-1	GLY	-	expression tag	UNP O14980

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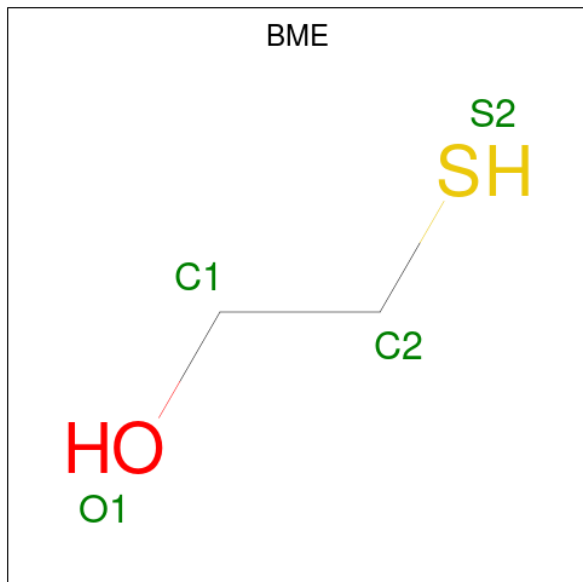
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Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP O14980
A	430	ALA	VAL	engineered mutation	UNP O14980
A	431	ALA	LEU	engineered mutation	UNP O14980
A	432	ALA	VAL	engineered mutation	UNP O14980
A	1037	ARG	-	expression tag	UNP O14980
A	1038	SER	-	expression tag	UNP O14980
A	1039	ARG	-	expression tag	UNP O14980
A	1040	SER	-	expression tag	UNP O14980
A	1041	HIS	-	expression tag	UNP O14980
A	1042	HIS	-	expression tag	UNP O14980
A	1043	HIS	-	expression tag	UNP O14980
A	1044	HIS	-	expression tag	UNP O14980
A	1045	HIS	-	expression tag	UNP O14980
A	1046	HIS	-	expression tag	UNP O14980

- Molecule 3 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



- Molecule 5 is BETA-MERCAPTOETHANOL (CCD ID: BME) (formula: C_2H_6OS) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	O	S	0	0
			4	2	1	1		

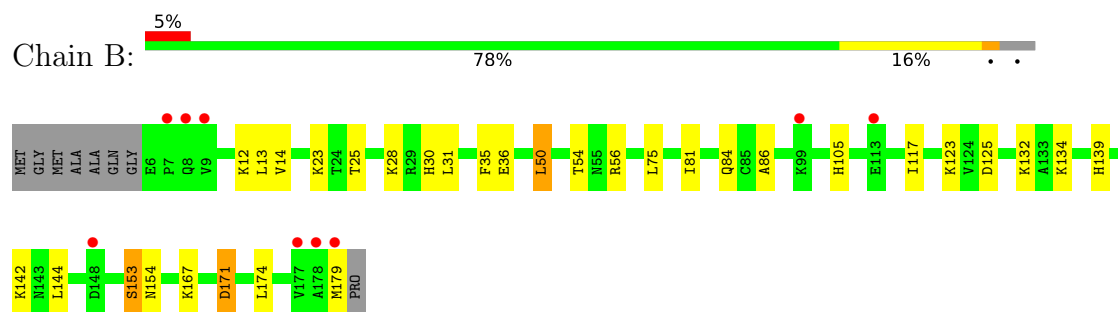
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	25	Total	O	0	0
			25	25		
6	A	111	Total	O	0	0
			111	111		

3 Residue-property plots [i](#)

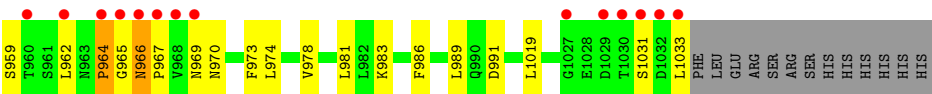
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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



- Molecule 2: Exportin-1





4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	121.11Å 150.59Å 231.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	126.31 – 2.58 126.31 – 2.58	Depositor EDS
% Data completeness (in resolution range)	97.5 (126.31-2.58) 97.5 (126.31-2.58)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.08 (at 2.58Å)	Xtriage
Refinement program	REFMAC 5	Depositor
R, R_{free}	0.214 , 0.250 0.213 , 0.249	Depositor DCC
R_{free} test set	3237 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	63.9	Xtriage
Anisotropy	0.433	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 33.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9786	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.11% 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: GTP, BME, MG

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	B	0.63	0/1449	1.14	2/1957 (0.1%)
2	A	0.61	0/8369	1.19	16/11341 (0.1%)
All	All	0.61	0/9818	1.19	18/13298 (0.1%)

There are no bond length outliers.

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	967	PRO	CB-CA-C	-7.63	100.92	113.06
2	A	487	THR	CA-CB-OG1	-7.38	98.53	109.60
2	A	346	THR	CB-CA-C	6.24	122.66	110.67
1	B	171	ASP	CB-CA-C	5.69	116.14	110.33
2	A	586	ASP	CA-CB-CG	5.66	118.26	112.60
2	A	991	ASP	CB-CA-C	5.58	119.74	110.81
2	A	656	LYS	CA-C-N	5.55	127.99	120.38
2	A	656	LYS	C-N-CA	5.55	127.99	120.38
2	A	849	PHE	CB-CA-C	5.47	120.14	110.85
2	A	20	SER	N-CA-C	-5.46	107.17	113.88
2	A	966	ASN	N-CA-C	-5.44	106.59	113.77
2	A	738	MET	N-CA-C	-5.34	105.46	111.28
2	A	296	GLN	CB-CA-C	-5.29	102.74	110.95
1	B	54	THR	CA-CB-OG1	-5.25	101.73	109.60
2	A	385	PRO	N-CA-C	5.22	121.13	114.92
2	A	839	GLU	CB-CG-CD	5.19	121.43	112.60
2	A	234	ASN	CB-CA-C	-5.10	100.87	110.67
2	A	964	PRO	N-CA-C	5.08	122.39	114.98

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	B	1414	0	1438	20	0
2	A	8199	0	8253	133	0
3	B	32	0	12	1	0
4	B	1	0	0	0	0
5	A	4	0	5	0	0
6	A	111	0	0	10	0
6	B	25	0	0	1	0
All	All	9786	0	9708	148	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 8.

All (148) 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:A:723:CYS:HB3	6:A:1295:HOH:O	1.34	1.26
2:A:30:ASN:HB3	6:A:1281:HOH:O	1.60	1.02
2:A:607:VAL:HA	6:A:1275:HOH:O	1.59	1.01
2:A:303:ASN:OD1	2:A:305:ARG:HG2	1.67	0.94
2:A:916:GLN:HE21	2:A:959:SER:HB2	1.33	0.93
2:A:84:GLU:HG2	2:A:88:LYS:HE3	1.48	0.92
2:A:88:LYS:HE2	2:A:136:GLN:NE2	1.84	0.91
2:A:73:MET:HG3	2:A:123:GLU:CD	1.97	0.89
2:A:607:VAL:HG12	6:A:1275:HOH:O	1.75	0.85
2:A:339:LYS:HE3	6:A:1223:HOH:O	1.76	0.84
2:A:95:PRO:HG2	2:A:98:GLN:HG3	1.63	0.80
2:A:10:ASP:OD2	2:A:14:ARG:HD2	1.83	0.79
2:A:60:TRP:HB3	2:A:86:VAL:HG21	1.64	0.78
2:A:628:GLN:HG3	6:A:1219:HOH:O	1.83	0.78
2:A:288:THR:HG22	2:A:289:LEU:HD12	1.66	0.77
2:A:84:GLU:CG	2:A:88:LYS:HE3	2.16	0.75
2:A:756:LEU:HB3	2:A:803:THR:HG21	1.67	0.75
2:A:172:LYS:HG3	2:A:231:ARG:HG3	1.69	0.73
2:A:219:ALA:HB3	2:A:220:PRO:HD3	1.73	0.71
2:A:962:LEU:HG	2:A:964:PRO:HD2	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:1033:LEU:O	2:A:1033:LEU:HG	1.93	0.69
2:A:545:MET:HE3	2:A:583:MET:HG2	1.75	0.69
1:B:139:HIS:HB2	1:B:144:LEU:HB2	1.73	0.69
2:A:168:MET:HE2	2:A:225:THR:HA	1.74	0.69
2:A:285:THR:HG23	2:A:289:LEU:HD13	1.73	0.69
2:A:303:ASN:OD1	2:A:305:ARG:CG	2.41	0.67
1:B:105:HIS:CE1	1:B:142:LYS:HD2	2.29	0.67
2:A:73:MET:HG3	2:A:123:GLU:OE1	1.95	0.65
1:B:30:HIS:HB3	1:B:50:LEU:HD21	1.78	0.65
2:A:964:PRO:C	2:A:966:ASN:H	2.06	0.64
1:B:12:LYS:H	1:B:84:GLN:NE2	1.96	0.62
2:A:88:LYS:CE	2:A:136:GLN:NE2	2.61	0.62
2:A:402:VAL:HG11	2:A:407:GLN:OE1	1.99	0.61
2:A:781:LEU:O	2:A:786:ILE:HG13	2.01	0.60
1:B:13:LEU:C	1:B:13:LEU:HD23	2.25	0.60
2:A:732:ILE:HD12	2:A:795:ALA:HB2	1.83	0.60
2:A:303:ASN:ND2	2:A:305:ARG:CZ	2.64	0.60
1:B:125:ASP:HB3	1:B:153:SER:OG	2.01	0.59
2:A:485:ASN:OD1	2:A:487:THR:HB	2.02	0.59
2:A:916:GLN:NE2	2:A:959:SER:HB2	2.12	0.59
2:A:55:GLU:HG2	6:A:1253:HOH:O	2.02	0.59
1:B:142:LYS:HG2	6:B:313:HOH:O	2.02	0.58
2:A:545:MET:HE1	2:A:583:MET:HB3	1.83	0.58
2:A:869:THR:O	2:A:873:LEU:HD13	2.03	0.58
2:A:354:MET:HE1	2:A:369:CYS:HA	1.85	0.57
1:B:117:ILE:HB	1:B:144:LEU:HD22	1.87	0.57
2:A:556:ARG:NH1	2:A:594:LYS:O	2.37	0.57
1:B:12:LYS:H	1:B:84:GLN:HE21	1.54	0.56
2:A:545:MET:HE3	2:A:583:MET:CG	2.36	0.56
2:A:986:PHE:HB2	2:A:989:LEU:CD1	2.36	0.55
2:A:70:SER:OG	2:A:75:THR:HB	2.07	0.54
2:A:303:ASN:HD21	2:A:305:ARG:CZ	2.21	0.54
2:A:900:LEU:C	2:A:900:LEU:HD23	2.33	0.54
2:A:263:VAL:HG23	2:A:264:SER:N	2.23	0.54
2:A:88:LYS:HE2	2:A:136:GLN:HE22	1.72	0.54
2:A:964:PRO:C	2:A:966:ASN:N	2.66	0.53
1:B:75:LEU:HD13	2:A:35:LEU:HD21	1.89	0.53
2:A:675:ASN:ND2	2:A:677:ASP:HB2	2.24	0.53
2:A:84:GLU:CD	2:A:88:LYS:HE3	2.34	0.53
2:A:482:ASN:HD22	2:A:487:THR:HB	1.74	0.53
2:A:545:MET:CE	2:A:583:MET:HB3	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:168:MET:HE1	2:A:209:CYS:SG	2.49	0.52
2:A:672:ALA:HA	2:A:678:ILE:HD11	1.91	0.52
2:A:168:MET:HE3	2:A:228:THR:HG21	1.92	0.52
1:B:75:LEU:CD1	2:A:35:LEU:HD21	2.41	0.51
1:B:75:LEU:HD13	2:A:35:LEU:CD2	2.41	0.50
2:A:631:HIS:HB3	2:A:697:ARG:HG3	1.93	0.50
2:A:879:ILE:HA	2:A:882:PHE:CE2	2.47	0.50
2:A:73:MET:HG3	2:A:123:GLU:OE2	2.12	0.50
2:A:67:LEU:HD13	2:A:109:LEU:HD21	1.94	0.50
2:A:856:ASN:HB2	2:A:863:PHE:HE2	1.77	0.49
2:A:986:PHE:HB2	2:A:989:LEU:HD12	1.94	0.49
2:A:249:THR:O	2:A:253:LYS:HB2	2.12	0.49
2:A:607:VAL:CG1	6:A:1275:HOH:O	2.42	0.49
1:B:28:LYS:NZ	1:B:36:GLU:OE2	2.46	0.49
2:A:760:SER:O	2:A:764:SER:OG	2.31	0.49
1:B:56:ARG:HD3	1:B:171:ASP:OD2	2.13	0.48
2:A:573:MET:HB3	2:A:625:LEU:HD21	1.94	0.48
2:A:789:GLN:HB2	2:A:825:ALA:O	2.13	0.48
2:A:782:ASP:OD1	2:A:782:ASP:O	2.31	0.48
2:A:607:VAL:HG23	2:A:608:MET:H	1.78	0.48
2:A:508:MET:HE1	2:A:516:PHE:CD2	2.49	0.48
2:A:978:VAL:O	2:A:981:LEU:HB3	2.13	0.48
2:A:804:MET:HE3	2:A:804:MET:HA	1.95	0.47
2:A:30:ASN:CB	6:A:1281:HOH:O	2.34	0.47
2:A:641:ILE:HD12	2:A:657:TYR:CD2	2.49	0.47
2:A:904:VAL:HG11	2:A:914:PHE:CD2	2.48	0.47
1:B:25:THR:HG21	1:B:35:PHE:CE1	2.49	0.47
2:A:841:TYR:O	2:A:845:ARG:HG3	2.13	0.47
1:B:75:LEU:CD1	2:A:35:LEU:CD2	2.93	0.47
2:A:544:ILE:O	2:A:548:VAL:HG13	2.14	0.47
2:A:285:THR:HG23	2:A:289:LEU:CD1	2.40	0.47
2:A:962:LEU:HB2	2:A:973:PHE:CE1	2.50	0.46
2:A:675:ASN:HD21	2:A:677:ASP:HB2	1.80	0.46
2:A:202:PHE:CZ	2:A:236:ILE:HG21	2.51	0.46
2:A:354:MET:CE	2:A:369:CYS:HA	2.46	0.46
2:A:586:ASP:O	2:A:589:ILE:HG22	2.16	0.46
1:B:123:LYS:HG2	3:B:201:GTP:C6	2.51	0.45
2:A:351:LEU:HD11	2:A:409:TYR:CE1	2.51	0.45
2:A:304:ILE:HD12	2:A:356:LEU:HB3	1.99	0.45
2:A:288:THR:CG2	2:A:289:LEU:HD12	2.43	0.45
2:A:139:LYS:HE3	2:A:186:ILE:HD11	1.97	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:247:ILE:O	2:A:251:ILE:HG13	2.17	0.44
2:A:681:ASP:O	2:A:682:PRO:C	2.61	0.44
2:A:261:ARG:HD2	2:A:318:PHE:CD1	2.52	0.44
2:A:672:ALA:CA	2:A:678:ILE:HD11	2.47	0.44
1:B:14:VAL:O	1:B:86:ALA:HA	2.18	0.43
2:A:109:LEU:O	2:A:113:THR:HG23	2.18	0.43
2:A:789:GLN:OE1	2:A:825:ALA:HA	2.18	0.43
2:A:861:PRO:HA	2:A:864:LEU:HD12	2.00	0.43
2:A:962:LEU:HD23	2:A:965:GLY:HA3	2.00	0.43
2:A:25:ILE:HD11	2:A:65:THR:HG22	2.00	0.43
2:A:660:LEU:HB2	2:A:661:PRO:HD3	2.00	0.43
2:A:517:LEU:O	2:A:521:ILE:HG12	2.19	0.43
2:A:60:TRP:HA	2:A:63:VAL:HG23	2.00	0.42
2:A:904:VAL:HG13	2:A:911:ALA:HA	2.01	0.42
2:A:738:MET:HE3	2:A:738:MET:HB3	1.95	0.42
2:A:263:VAL:CG2	2:A:264:SER:N	2.81	0.42
2:A:603:GLN:O	2:A:606:GLU:HB2	2.19	0.42
2:A:682:PRO:HG2	6:A:1311:HOH:O	2.19	0.42
1:B:81:ILE:HD11	2:A:77:TYR:CD1	2.54	0.42
2:A:930:VAL:HG22	2:A:942:HIS:HB3	2.01	0.42
2:A:887:ARG:HA	2:A:887:ARG:HD2	1.66	0.41
2:A:241:ILE:CG2	2:A:271:ILE:HG12	2.51	0.41
2:A:287:PHE:HB2	2:A:329:PHE:CZ	2.55	0.41
2:A:303:ASN:ND2	2:A:305:ARG:NH1	2.68	0.41
2:A:427:PRO:HB3	2:A:454:TYR:CZ	2.55	0.41
2:A:308:TYR:CE2	2:A:316:GLN:HB3	2.55	0.41
2:A:257:VAL:O	2:A:258:PRO:C	2.64	0.41
2:A:704:HIS:HB3	2:A:705:PRO:HD3	2.02	0.41
2:A:962:LEU:HB2	2:A:973:PHE:CZ	2.56	0.41
2:A:31:VAL:HG12	2:A:50:LEU:HD11	2.03	0.41
2:A:103:LYS:HG2	2:A:146:TRP:CZ3	2.55	0.41
2:A:323:SER:HB3	2:A:357:VAL:HG11	2.03	0.41
2:A:542:SER:HA	2:A:545:MET:HE3	2.03	0.41
2:A:685:VAL:HG12	2:A:747:SER:OG	2.21	0.41
2:A:10:ASP:OD1	2:A:45:MET:HG3	2.21	0.40
2:A:297:MET:H	2:A:297:MET:HG2	1.52	0.40
2:A:676:VAL:O	2:A:679:LEU:HB2	2.21	0.40
2:A:740:THR:HA	2:A:745:ILE:HG21	2.02	0.40
2:A:887:ARG:HH12	2:A:935:HIS:CD2	2.39	0.40
2:A:602:VAL:HG22	2:A:609:PRO:HD3	2.02	0.40
2:A:969:ASN:O	2:A:970:ASN:C	2.64	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:23:LYS:HB2	1:B:23:LYS:HE2	1.94	0.40
2:A:797:GLU:HA	2:A:798:PRO:HD2	1.83	0.40
2:A:382:ARG:O	2:A:383:GLU:C	2.64	0.40
2:A:517:LEU:HD23	2:A:517:LEU:HA	1.85	0.40
2:A:882:PHE:HA	2:A:890:ALA:HA	2.03	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	B	172/182 (94%)	166 (96%)	6 (4%)	0	100	100
2	A	1009/1060 (95%)	979 (97%)	30 (3%)	0	100	100
All	All	1181/1242 (95%)	1145 (97%)	36 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	B	153/157 (98%)	144 (94%)	9 (6%)	18	36
2	A	921/960 (96%)	881 (96%)	40 (4%)	26	49
All	All	1074/1117 (96%)	1025 (95%)	49 (5%)	24	47

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	31	LEU
1	B	50	LEU
1	B	132	LYS
1	B	134	LYS
1	B	153	SER
1	B	154	ASN
1	B	167	LYS
1	B	174	LEU
1	B	179	MET
2	A	8	LEU
2	A	33	ASN
2	A	39	GLU
2	A	62	ARG
2	A	133	ILE
2	A	140	GLN
2	A	141	GLU
2	A	162	SER
2	A	163	LEU
2	A	198	MET
2	A	278	GLN
2	A	288	THR
2	A	297	MET
2	A	312	LYS
2	A	341	LEU
2	A	363	THR
2	A	387	SER
2	A	441	VAL
2	A	446	LYS
2	A	487	THR
2	A	548	VAL
2	A	555	LEU
2	A	590	LYS
2	A	678	ILE
2	A	733	GLN
2	A	739	VAL
2	A	764	SER
2	A	781	LEU
2	A	786	ILE
2	A	792	VAL
2	A	818	GLU
2	A	824	ASP
2	A	832	ASN

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Mol	Chain	Res	Type
2	A	840	GLU
2	A	887	ARG
2	A	895	GLN
2	A	974	LEU
2	A	983	LYS
2	A	1019	LEU
2	A	1031	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (35) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	30	HIS
1	B	84	GLN
1	B	105	HIS
1	B	143	ASN
2	A	26	ASN
2	A	165	GLN
2	A	204	GLN
2	A	215	ASN
2	A	278	GLN
2	A	293	GLN
2	A	310	ASN
2	A	320	GLN
2	A	321	ASN
2	A	333	HIS
2	A	352	HIS
2	A	374	ASN
2	A	481	HIS
2	A	482	ASN
2	A	530	GLN
2	A	543	ASN
2	A	619	ASN
2	A	663	GLN
2	A	675	ASN
2	A	727	ASN
2	A	767	ASN
2	A	775	ASN
2	A	832	ASN
2	A	856	ASN
2	A	916	GLN
2	A	924	GLN
2	A	935	HIS

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Mol	Chain	Res	Type
2	A	963	ASN
2	A	966	ASN
2	A	988	HIS
2	A	1006	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 1 is monoatomic - leaving 2 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	$\# Z > 2$
3	GTP	B	201	4	33,34,34	0.56	0	50,54,54	0.74	1 (2%)
5	BME	A	1101	2	3,3,3	0.19	0	2,2,2	0.33	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
3	GTP	B	201	4	-	2/22/38/38	0/3/3/3
5	BME	A	1101	2	-	1/1/1/1	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	201	GTP	O3A-PA-O1A	-2.34	103.66	110.70

There are no chirality outliers.

All (3) torsion outliers are listed below:

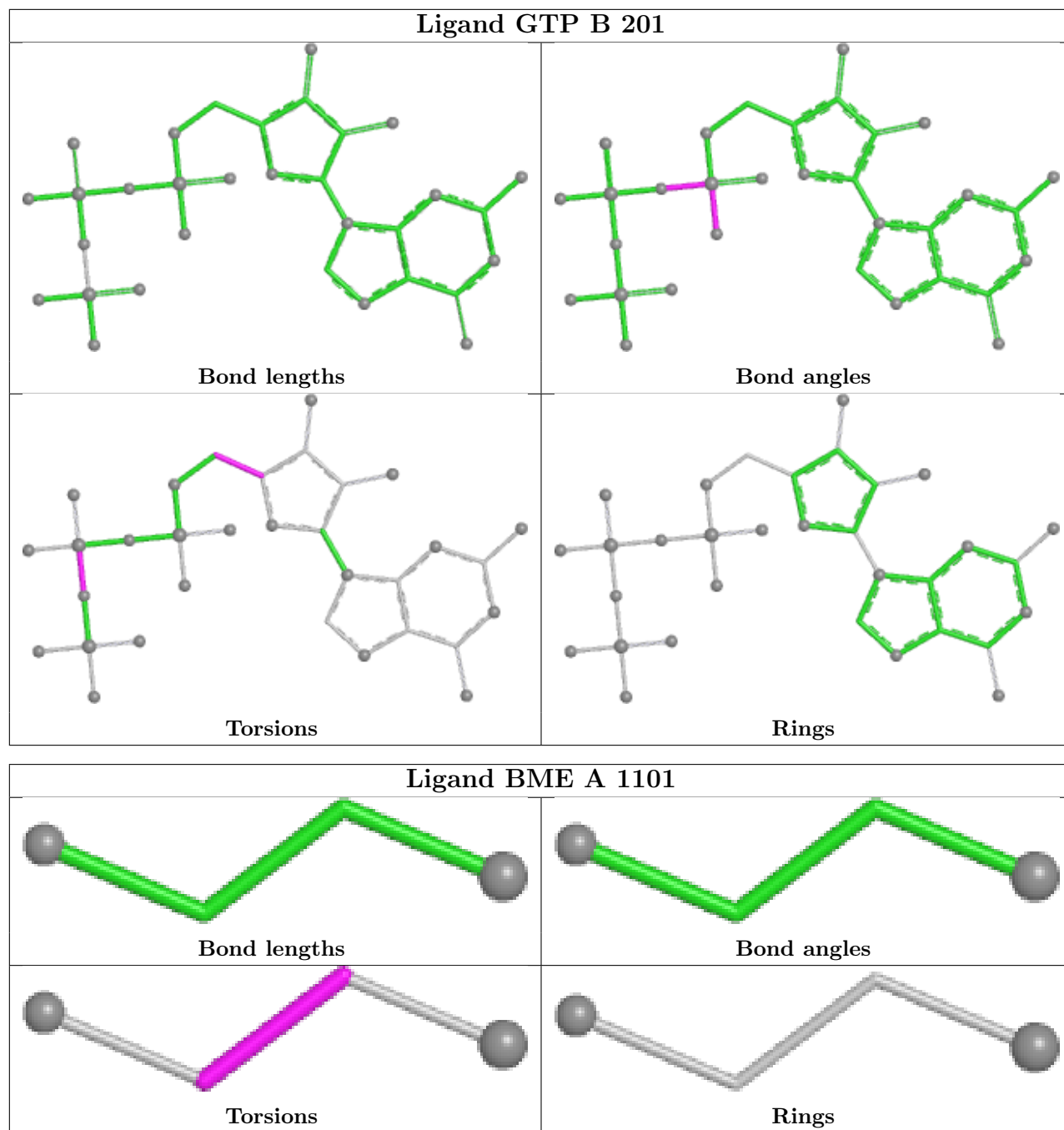
Mol	Chain	Res	Type	Atoms
5	A	1101	BME	O1-C1-C2-S2
3	B	201	GTP	PG-O3B-PB-O2B
3	B	201	GTP	O4'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	201	GTP	1	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	B	174/182 (95%)	0.08	9 (5%) 33 28	35, 51, 85, 159	0
2	A	1013/1060 (95%)	0.17	66 (6%) 25 20	36, 60, 89, 191	0
All	All	1187/1242 (95%)	0.16	75 (6%) 26 21	35, 58, 89, 191	0

All (75) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	1033	LEU	5.6
1	B	7	PRO	5.6
2	A	965	GLY	5.0
2	A	964	PRO	5.0
2	A	740	THR	4.9
1	B	178	ALA	4.6
2	A	967	PRO	4.6
2	A	1031	SER	4.5
1	B	179	MET	4.5
2	A	738	MET	4.5
2	A	388	THR	4.2
2	A	8	LEU	4.2
2	A	749	ARG	4.2
2	A	966	ASN	4.2
2	A	958	ILE	4.1
2	A	962	LEU	4.1
2	A	1032	ASP	4.1
2	A	956	GLY	3.9
2	A	608	MET	3.9
2	A	1030	THR	3.8
2	A	143	PRO	3.8
2	A	43	GLN	3.7
2	A	739	VAL	3.6
2	A	968	VAL	3.6

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Mol	Chain	Res	Type	RSRZ
2	A	736	GLY	3.6
2	A	957	LYS	3.5
2	A	429	GLU	3.4
2	A	61	THR	3.4
2	A	305	ARG	3.4
2	A	90	ARG	3.3
2	A	443	GLU	3.2
2	A	737	GLU	3.1
1	B	9	VAL	3.1
2	A	907	GLU	3.0
2	A	142	TRP	3.0
2	A	735	ASN	2.9
1	B	148	ASP	2.9
1	B	8	GLN	2.9
1	B	177	VAL	2.8
2	A	604	VAL	2.8
2	A	969	ASN	2.7
2	A	123	GLU	2.7
2	A	909	ALA	2.6
2	A	341	LEU	2.6
2	A	741	LYS	2.6
2	A	1027	GLY	2.5
2	A	72	ASN	2.5
2	A	71	GLN	2.5
2	A	34	CYS	2.4
2	A	104	LYS	2.4
2	A	382	ARG	2.4
2	A	141	GLU	2.4
2	A	532	ARG	2.3
2	A	446	LYS	2.3
2	A	873	LEU	2.3
2	A	469	TYR	2.2
2	A	906	GLN	2.2
2	A	960	THR	2.2
2	A	868	PRO	2.2
2	A	22	LYS	2.2
2	A	481	HIS	2.1
2	A	344	ARG	2.1
2	A	339	LYS	2.1
2	A	276	VAL	2.1
2	A	440	VAL	2.1
2	A	607	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
2	A	887	ARG	2.1
1	B	99	LYS	2.1
2	A	64	ASP	2.1
2	A	782	ASP	2.1
2	A	1029	ASP	2.1
2	A	792	VAL	2.0
2	A	430	ALA	2.0
2	A	904	VAL	2.0
1	B	113	GLU	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

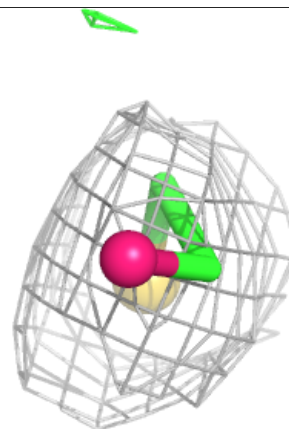
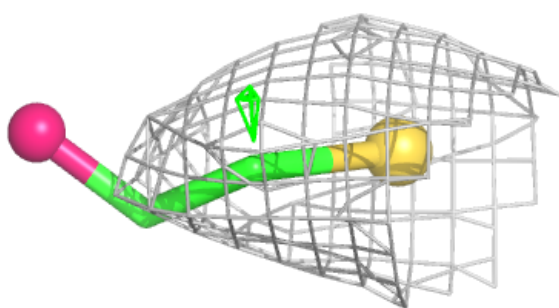
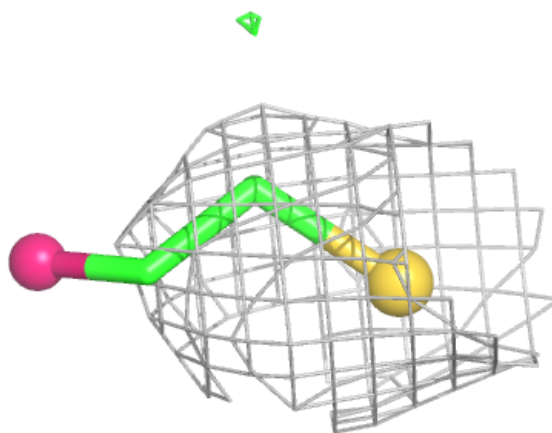
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	MG	B	202	1/1	0.87	0.17	52,52,52,52	0
5	BME	A	1101	4/4	0.87	0.21	96,97,99,106	0
3	GTP	B	201	32/32	0.98	0.05	37,42,51,54	0

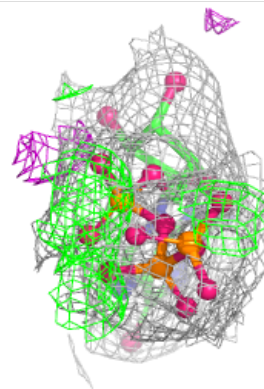
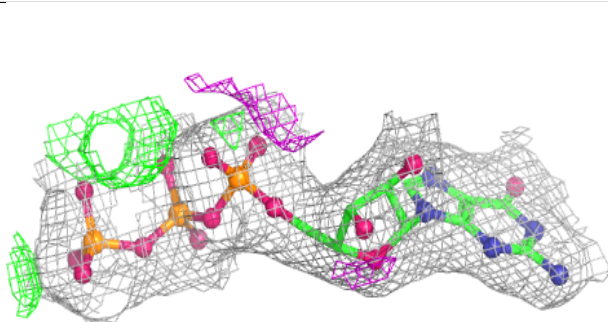
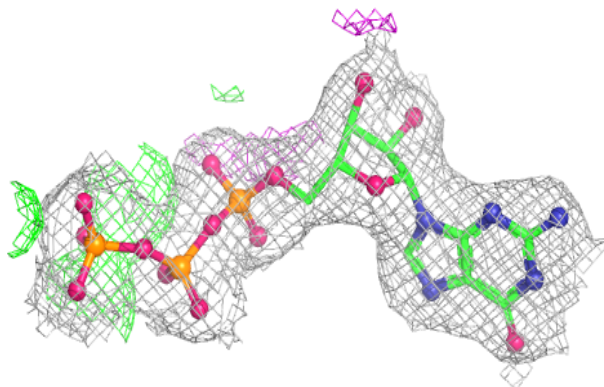
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around BME A 1101:

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

**Electron density around GTP B 201:**

$2mF_o - DF_c$ (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.