



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 03:24 PM UTC

PDB ID : 2WMC / pdb_00002wmc
Title : Crystal structure of eukaryotic initiation factor 4E from *Pisum sativum*
Authors : Ashby, J.A.; Stevenson, C.E.M.; Maule, A.J.; Lawson, D.M.
Deposited on : 2009-06-30
Resolution : 2.20 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

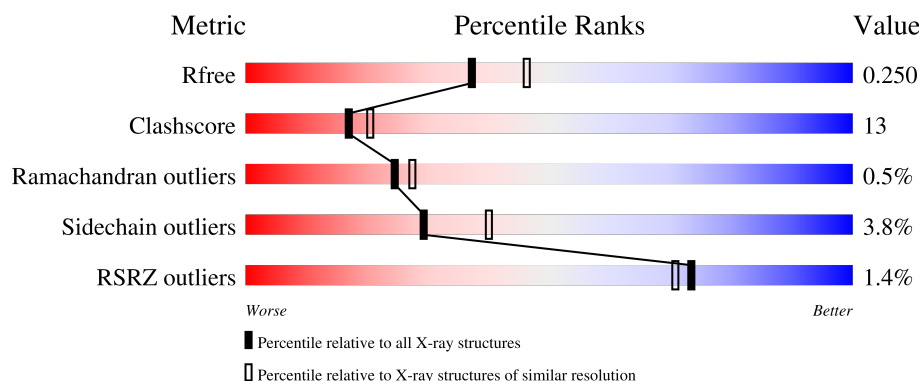
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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

Mol	Chain	Length	Quality of chain
1	A	178	% 72% 23% ..
1	B	178	2% 62% 25% • 11%
1	C	178	% 67% 26% ..
1	D	178	% 76% 14% • 8%
1	E	178	% 71% 20% • 6%

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Mol	Chain	Length	Quality of chain
1	F	178	2% 63% 26% • 9%
1	G	178	3% 68% 24% • 5%
1	H	178	% 70% 25% • •

2 Entry composition

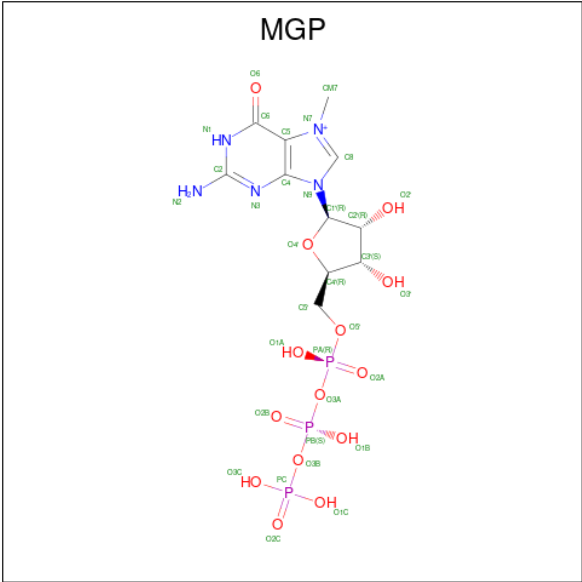
There are 3 unique types of molecules in this entry. The entry contains 11810 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 EUKARYOTIC TRANSLATION INITIATION FACTOR 4E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	174	Total	C	N	O	S	0	0	0
			1408	907	238	257	6			
1	B	159	Total	C	N	O	S	0	0	0
			1304	844	216	238	6			
1	C	172	Total	C	N	O	S	0	0	0
			1383	894	229	254	6			
1	D	163	Total	C	N	O	S	0	0	0
			1326	860	219	241	6			
1	E	167	Total	C	N	O	S	0	0	0
			1349	874	222	247	6			
1	F	162	Total	C	N	O	S	0	0	0
			1302	843	213	240	6			
1	G	169	Total	C	N	O	S	0	0	0
			1350	877	217	250	6			
1	H	171	Total	C	N	O	S	0	0	0
			1366	884	223	253	6			

- Molecule 2 is 7-METHYL-GUANOSINE-5'-TRIPHOSPHATE (CCD ID: MGP) (formula: $C_{11}H_{19}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			29	11	5	11	2		
2	B	1	Total	C	N	O	P	0	0
			29	11	5	11	2		
2	C	1	Total	C	N	O	P	0	0
			29	11	5	11	2		
2	D	1	Total	C	N	O	P	0	0
			29	11	5	11	2		
2	E	1	Total	C	N	O	P	0	0
			29	11	5	11	2		
2	F	1	Total	C	N	O	P	0	0
			29	11	5	11	2		
2	G	1	Total	C	N	O	P	0	0
			29	11	5	11	2		
2	H	1	Total	C	N	O	P	0	0
			29	11	5	11	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	125	Total	O	0	0
			125	125		
3	B	111	Total	O	0	0
			111	111		
3	C	95	Total	O	0	0
			95	95		
3	D	122	Total	O	0	0
			122	122		

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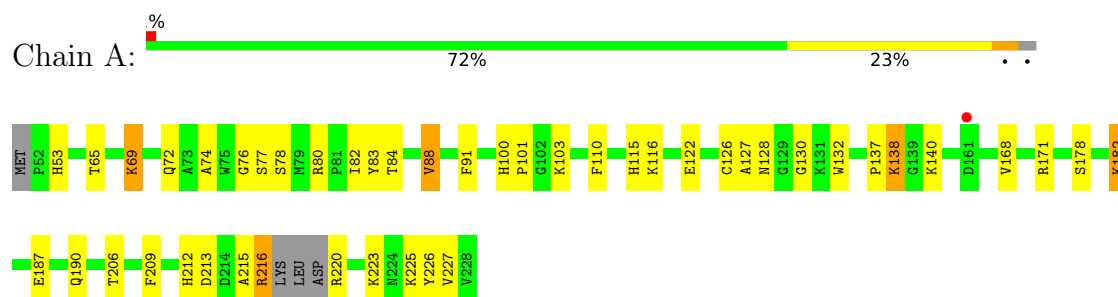
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	E	93	Total 93	O 93	0	0
3	F	66	Total 66	O 66	0	0
3	G	90	Total 90	O 90	0	0
3	H	88	Total 88	O 88	0	0

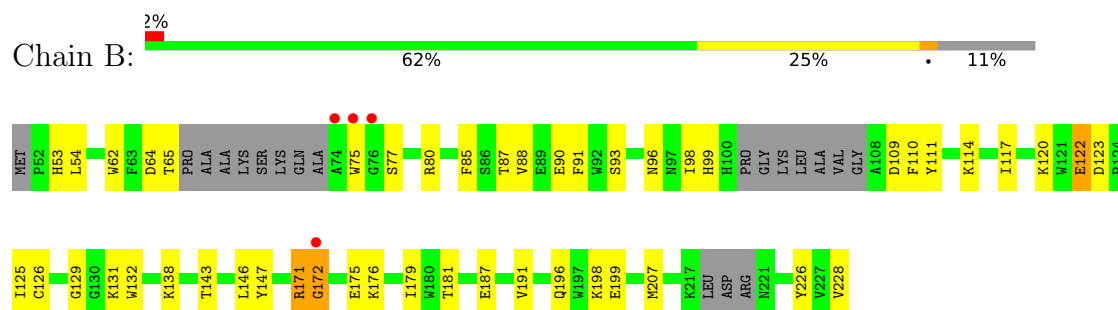
3 Residue-property plots [i](#)

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.

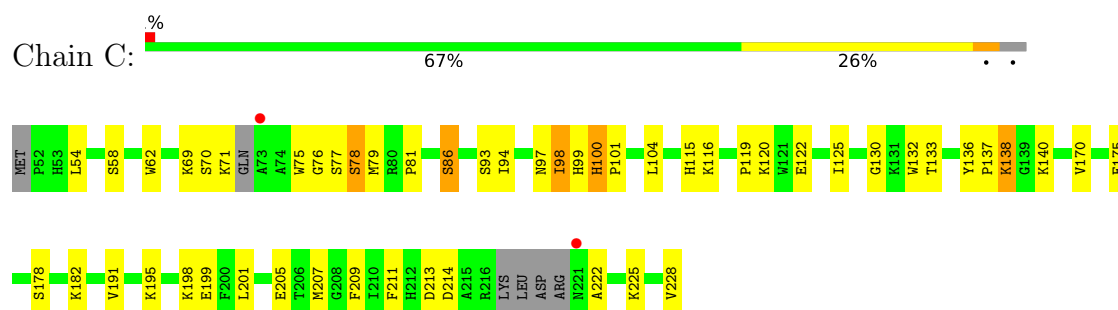
• Molecule 1: EUKARYOTIC TRANSLATION INITIATION FACTOR 4E



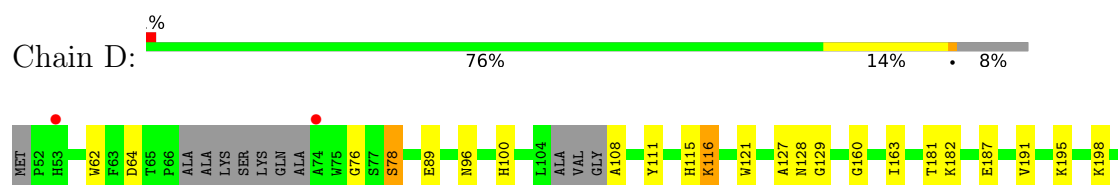
• Molecule 1: EUKARYOTIC TRANSLATION INITIATION FACTOR 4E

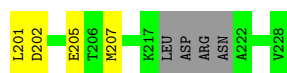


• Molecule 1: EUKARYOTIC TRANSLATION INITIATION FACTOR 4E



• Molecule 1: EUKARYOTIC TRANSLATION INITIATION FACTOR 4E

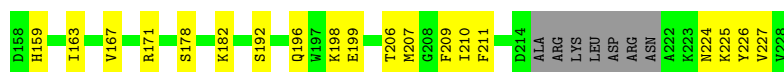
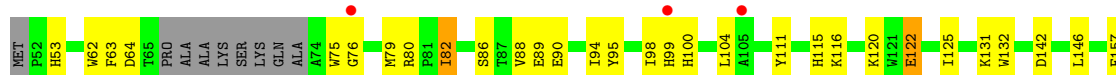




• Molecule 1: EUKARYOTIC TRANSLATION INITIATION FACTOR 4E



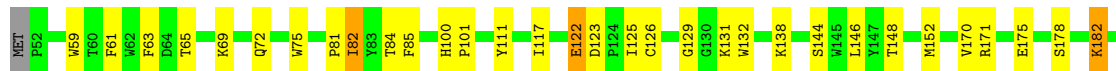
• Molecule 1: EUKARYOTIC TRANSLATION INITIATION FACTOR 4E



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4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	73.61Å 136.32Å 74.42Å 90.00° 92.65° 90.00°	Depositor
Resolution (Å)	136.08 – 2.20 74.33 – 2.20	Depositor EDS
% Data completeness (in resolution range)	97.2 (136.08-2.20) 97.2 (74.33-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.23 (at 2.19Å)	Xtriage
Refinement program	REFMAC 5.4.0067	Depositor
R, R_{free}	0.180 , 0.250 0.183 , 0.250	Depositor DCC
R_{free} test set	3642 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	21.0	Xtriage
Anisotropy	0.569	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 43.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.024 for l,k,-h 0.047 for h,-k,-l 0.039 for l,-k,h	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	11810	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.40% 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: MGP

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	0.76	0/1454	1.07	4/1971 (0.2%)
1	B	0.77	0/1346	1.04	1/1821 (0.1%)
1	C	0.71	0/1428	1.03	3/1936 (0.2%)
1	D	0.74	0/1370	1.01	2/1856 (0.1%)
1	E	0.70	0/1394	1.06	1/1891 (0.1%)
1	F	0.64	0/1345	1.02	3/1827 (0.2%)
1	G	0.67	0/1395	1.08	4/1894 (0.2%)
1	H	0.71	0/1412	1.02	1/1919 (0.1%)
All	All	0.71	0/11144	1.04	19/15115 (0.1%)

There are no bond length outliers.

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	65	THR	CA-C-N	8.86	128.60	119.56
1	G	65	THR	C-N-CA	8.86	128.60	119.56
1	A	77	SER	N-CA-C	-7.39	104.26	113.20
1	G	173	ARG	N-CA-C	-7.05	105.03	112.93
1	C	77	SER	N-CA-C	-6.89	104.84	113.18
1	G	68	ALA	N-CA-C	-6.38	105.36	113.01
1	C	100	HIS	CA-C-N	6.37	127.80	119.84
1	C	100	HIS	C-N-CA	6.37	127.80	119.84
1	A	215	ALA	N-CA-C	-6.14	104.67	111.36
1	D	121	TRP	N-CA-C	-5.95	104.87	111.71
1	E	202	ASP	N-CA-C	-5.59	104.20	111.74
1	A	69	LYS	N-CA-C	-5.55	106.01	112.89
1	B	131	LYS	N-CA-C	5.48	117.42	108.76
1	A	88	VAL	N-CA-C	-5.26	105.41	110.72
1	F	80	ARG	CA-C-N	-5.25	113.90	120.51
1	F	80	ARG	C-N-CA	-5.25	113.90	120.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	182	LYS	CB-CA-C	-5.19	101.47	110.45
1	F	76	GLY	N-CA-C	-5.15	104.49	113.76
1	H	213	ASP	N-CA-C	-5.13	105.76	112.23

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	1408	0	1321	25	0
1	B	1304	0	1206	36	0
1	C	1383	0	1290	40	0
1	D	1326	0	1234	17	0
1	E	1349	0	1254	38	0
1	F	1302	0	1190	44	0
1	G	1350	0	1243	32	0
1	H	1366	0	1260	37	0
2	A	29	0	15	2	0
2	B	29	0	15	0	0
2	C	29	0	15	0	0
2	D	29	0	15	0	0
2	E	29	0	15	4	0
2	F	29	0	15	1	0
2	G	29	0	15	3	0
2	H	29	0	15	1	0
3	A	125	0	0	0	0
3	B	111	0	0	1	0
3	C	95	0	0	1	0
3	D	122	0	0	1	0
3	E	93	0	0	0	0
3	F	66	0	0	1	0
3	G	90	0	0	1	0
3	H	88	0	0	0	0
All	All	11810	0	10118	268	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 13.

All (268) 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:H:63:PHE:CD1	1:H:82:ILE:HD11	1.82	1.13
1:H:129:GLY:HA2	1:H:182:LYS:O	1.54	1.07
1:C:75:TRP:HZ3	1:C:120:LYS:HG2	1.27	0.95
1:E:198:LYS:HG2	1:E:207:MET:HE3	1.49	0.93
1:E:115:HIS:CE1	1:E:116:LYS:HE2	2.05	0.92
1:C:115:HIS:O	1:C:116:LYS:HB2	1.69	0.92
1:E:63:PHE:CE2	1:E:65:THR:HG22	2.07	0.88
1:H:63:PHE:CE1	1:H:82:ILE:HD11	2.07	0.88
1:C:198:LYS:HG2	1:C:207:MET:HE3	1.55	0.87
1:E:122:GLU:OE2	2:E:500:MGP:N1	2.07	0.87
1:E:114:LYS:HB2	1:E:117:ILE:HD12	1.57	0.86
1:H:63:PHE:HD1	1:H:82:ILE:HD11	1.30	0.86
1:A:72:GLN:HG2	1:A:74:ALA:O	1.75	0.84
1:H:129:GLY:CA	1:H:182:LYS:O	2.24	0.84
1:A:206:THR:HG22	1:A:227:VAL:HG13	1.57	0.83
1:F:94:ILE:HD11	1:F:98:ILE:CD1	2.10	0.81
1:C:79:MET:SD	1:C:119:PRO:HG2	2.21	0.80
1:G:149:LEU:O	1:G:153:ILE:HG23	1.84	0.77
1:A:138:LYS:HE2	1:A:171:ARG:O	1.83	0.77
1:E:216:ARG:HG3	1:E:216:ARG:HH11	1.49	0.76
1:E:63:PHE:HE2	1:E:65:THR:HG22	1.50	0.75
1:G:132:TRP:CZ3	1:G:228:VAL:HG22	2.22	0.74
1:B:171:ARG:HH11	1:B:171:ARG:CG	2.01	0.74
1:E:97:ASN:HB3	1:H:146:LEU:HD22	1.69	0.73
1:E:216:ARG:HG3	1:E:216:ARG:NH1	2.02	0.73
1:F:94:ILE:HD11	1:F:98:ILE:HD11	1.70	0.73
1:G:87:THR:OG1	1:G:90:GLU:HB2	1.89	0.72
1:E:128:ASN:OD1	1:E:182:LYS:O	2.06	0.72
1:G:115:HIS:O	1:G:116:LYS:HB2	1.87	0.71
1:G:176:LYS:NZ	2:G:500:MGP:O3B	2.23	0.71
1:C:75:TRP:CZ3	1:C:120:LYS:HG2	2.18	0.70
1:A:206:THR:CG2	1:A:227:VAL:HG13	2.21	0.70
1:H:198:LYS:HD3	1:H:228:VAL:HG23	1.74	0.69
1:B:143:THR:HG22	1:B:147:TYR:CE2	2.28	0.69
1:G:100:HIS:HB3	1:G:101:PRO:HD2	1.76	0.68
1:E:198:LYS:CG	1:E:207:MET:HE3	2.24	0.68
1:E:98:ILE:HG22	1:E:99:HIS:N	2.07	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:206:THR:CG2	1:A:227:VAL:CG1	2.73	0.67
1:E:63:PHE:CE2	1:E:65:THR:CG2	2.78	0.67
1:B:171:ARG:HH11	1:B:171:ARG:CB	2.08	0.66
1:C:100:HIS:HB3	1:C:101:PRO:HD2	1.76	0.66
1:E:61:PHE:HE2	1:E:94:ILE:HD13	1.60	0.66
1:E:65:THR:HB	1:E:66:PRO:HD2	1.77	0.66
1:G:66:PRO:CG	1:G:106:VAL:O	2.44	0.66
1:F:75:TRP:CH2	1:F:79:MET:HE1	2.31	0.66
1:E:216:ARG:HH11	1:E:216:ARG:CG	2.09	0.65
1:F:62:TRP:HB2	1:F:111:TYR:HB2	1.78	0.65
1:B:138:LYS:NZ	1:B:175:GLU:OE2	2.29	0.65
2:E:500:MGP:O2B	2:E:500:MGP:O1A	2.15	0.65
1:G:66:PRO:HG3	1:G:106:VAL:O	1.95	0.65
1:C:75:TRP:HZ3	1:C:120:LYS:CG	2.05	0.65
1:E:115:HIS:HE1	1:E:116:LYS:HE2	1.63	0.64
1:B:171:ARG:NH1	1:B:171:ARG:HG2	2.12	0.64
1:B:187:GLU:HG3	1:B:226:TYR:CE1	2.34	0.62
1:E:189:ALA:O	1:E:193:ILE:HG13	2.00	0.62
1:G:173:ARG:O	1:G:174:ALA:HB2	2.01	0.61
1:B:75:TRP:HZ3	1:B:120:LYS:HG2	1.65	0.61
1:D:116:LYS:HE2	1:D:116:LYS:HA	1.83	0.61
1:G:62:TRP:HB2	1:G:111:TYR:HB2	1.83	0.60
1:G:105:ALA:O	1:G:170:VAL:HG11	2.01	0.60
1:E:61:PHE:CE2	1:E:94:ILE:HD13	2.37	0.60
1:F:159:HIS:HD2	1:F:192:SER:OG	1.85	0.60
1:E:63:PHE:HE2	1:E:65:THR:CG2	2.15	0.60
1:E:98:ILE:HG22	1:E:99:HIS:O	2.02	0.60
1:D:62:TRP:HB2	1:D:111:TYR:HB2	1.84	0.59
1:G:210:ILE:HG13	1:G:224:ASN:HD22	1.66	0.59
1:E:98:ILE:CG2	1:E:99:HIS:N	2.65	0.59
1:F:94:ILE:HD11	1:F:98:ILE:HD12	1.85	0.59
1:C:198:LYS:CG	1:C:207:MET:HE3	2.30	0.58
1:F:132:TRP:O	1:F:178:SER:HA	2.03	0.58
1:H:214:ASP:O	1:H:222:ALA:HB2	2.03	0.58
1:A:187:GLU:HG3	1:A:226:TYR:CE1	2.38	0.58
1:H:65:THR:O	1:H:69:LYS:HG3	2.03	0.58
1:C:94:ILE:HD11	1:C:98:ILE:CD1	2.34	0.57
1:B:143:THR:HG21	1:C:99:HIS:CE1	2.39	0.57
1:C:125:ILE:HD12	3:C:2040:HOH:O	2.03	0.57
1:B:138:LYS:HD3	1:B:172:GLY:O	2.03	0.57
1:H:198:LYS:CD	1:H:228:VAL:HG23	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:138:LYS:HD3	1:G:172:GLY:O	2.04	0.57
1:G:65:THR:O	1:G:69:LYS:HG3	2.04	0.57
1:B:187:GLU:HG3	1:B:226:TYR:CD1	2.40	0.57
1:D:129:GLY:HA3	1:D:181:THR:O	2.05	0.56
1:B:196:GLN:O	1:B:199:GLU:HG2	2.04	0.56
1:C:136:TYR:OH	1:C:201:LEU:HD13	2.06	0.56
1:E:114:LYS:CB	1:E:117:ILE:HD12	2.33	0.56
1:F:90:GLU:O	1:F:94:ILE:HG22	2.04	0.56
1:F:64:ASP:HB2	1:F:79:MET:HG3	1.85	0.56
1:F:125:ILE:CG2	1:F:182:LYS:HE2	2.36	0.56
2:G:500:MGP:O2B	2:G:500:MGP:O1A	2.23	0.56
1:C:99:HIS:HB3	1:C:104:LEU:HD21	1.88	0.56
1:F:95:TYR:CZ	1:F:146:LEU:HD13	2.42	0.55
1:H:198:LYS:NZ	1:H:203:TYR:O	2.39	0.55
1:B:171:ARG:CG	1:B:171:ARG:NH1	2.62	0.55
1:H:198:LYS:HG2	1:H:207:MET:HE3	1.89	0.55
1:A:127:ALA:O	1:A:216:ARG:NH2	2.36	0.55
1:F:115:HIS:O	1:F:116:LYS:CB	2.54	0.55
1:A:137:PRO:HB2	1:A:140:LYS:HG3	1.88	0.55
1:G:74:ALA:HB1	3:G:2010:HOH:O	2.06	0.54
1:C:94:ILE:HD11	1:C:98:ILE:HD13	1.89	0.54
1:H:82:ILE:HD13	1:H:82:ILE:N	2.21	0.54
1:C:130:GLY:HA3	1:C:209:PHE:CZ	2.43	0.54
1:A:213:ASP:HA	1:A:216:ARG:NH1	2.23	0.53
1:A:76:GLY:C	1:A:78:SER:H	2.17	0.53
1:G:75:TRP:CZ3	2:G:500:MGP:C6	2.92	0.52
1:B:62:TRP:HB2	1:B:111:TYR:HB2	1.92	0.52
1:D:116:LYS:HA	1:D:116:LYS:CE	2.39	0.52
1:F:94:ILE:CD1	1:F:98:ILE:HD12	2.40	0.52
1:E:87:THR:OG1	1:E:90:GLU:HB2	2.09	0.51
1:G:67:ALA:O	1:G:70:SER:HB3	2.10	0.51
1:C:198:LYS:HG2	1:C:207:MET:CE	2.34	0.51
1:C:198:LYS:HE2	1:C:228:VAL:OXT	2.11	0.51
1:B:198:LYS:HG2	1:B:207:MET:HE3	1.93	0.51
1:A:115:HIS:O	1:A:116:LYS:HB2	2.10	0.51
1:F:99:HIS:HB2	1:F:104:LEU:HD21	1.93	0.51
1:C:132:TRP:O	1:C:178:SER:HA	2.11	0.51
1:H:59:TRP:HB2	1:H:85:PHE:CZ	2.46	0.51
1:B:64:ASP:OD1	1:B:65:THR:N	2.44	0.51
1:H:123:ASP:HB3	1:H:126:CYS:HB2	1.93	0.51
1:D:198:LYS:NZ	1:D:205:GLU:O	2.30	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:100:HIS:HB3	1:H:101:PRO:HD2	1.93	0.50
1:B:143:THR:HG21	1:C:99:HIS:ND1	2.25	0.50
1:B:143:THR:CG2	1:B:147:TYR:CE2	2.94	0.50
1:D:89:GLU:CD	1:D:89:GLU:H	2.20	0.50
1:F:206:THR:CG2	1:F:227:VAL:HG13	2.42	0.50
1:A:128:ASN:OD1	1:A:182:LYS:O	2.29	0.50
1:C:104:LEU:HB2	1:C:170:VAL:HG21	1.94	0.50
1:G:65:THR:HB	1:G:66:PRO:CD	2.42	0.50
1:B:129:GLY:HA3	1:B:181:THR:O	2.12	0.50
1:B:132:TRP:CZ3	1:B:228:VAL:HG22	2.47	0.50
1:E:115:HIS:O	1:E:116:LYS:HB2	2.12	0.49
1:E:59:TRP:HB2	1:E:85:PHE:CZ	2.47	0.49
1:B:125:ILE:HD12	3:B:2033:HOH:O	2.11	0.49
1:D:128:ASN:OD1	1:D:128:ASN:C	2.55	0.49
1:G:107:GLY:N	1:G:170:VAL:O	2.41	0.49
2:E:500:MGP:O2B	2:E:500:MGP:C5'	2.61	0.49
1:B:120:LYS:HB3	1:B:122:GLU:HG2	1.94	0.48
1:G:203:TYR:CD1	1:G:207:MET:HE2	2.48	0.48
1:G:52:PRO:HB3	1:G:89:GLU:CD	2.38	0.48
1:H:148:THR:O	1:H:152:MET:HG3	2.14	0.48
2:A:500:MGP:O2B	2:A:500:MGP:O1A	2.31	0.48
1:A:220:ARG:NH2	2:A:500:MGP:H5'A	2.28	0.48
1:C:198:LYS:CE	1:C:228:VAL:OXT	2.61	0.48
1:D:160:GLY:HA2	1:D:163:ILE:HD12	1.96	0.48
1:C:198:LYS:NZ	1:C:228:VAL:OXT	2.43	0.48
1:E:167:VAL:HG22	1:E:168:VAL:N	2.28	0.48
1:D:76:GLY:C	1:D:78:SER:H	2.20	0.47
1:F:206:THR:HG23	1:F:227:VAL:HG13	1.96	0.47
1:H:75:TRP:CD1	1:H:75:TRP:C	2.92	0.47
1:H:144:SER:HB3	1:H:201:LEU:HD22	1.97	0.47
1:B:85:PHE:HB2	1:B:90:GLU:HB3	1.96	0.47
1:F:225:LYS:O	1:F:226:TYR:CD1	2.68	0.47
1:F:120:LYS:HB3	1:F:122:GLU:HG2	1.96	0.47
1:G:61:PHE:HA	1:G:111:TYR:O	2.14	0.47
1:E:186:ASN:O	1:E:189:ALA:HB3	2.14	0.47
1:G:223:LYS:HA	1:G:223:LYS:HD3	1.77	0.47
1:B:143:THR:CG2	1:B:147:TYR:CZ	2.98	0.47
1:E:120:LYS:HB3	1:E:122:GLU:HG2	1.96	0.47
1:C:99:HIS:HB3	1:C:104:LEU:CD2	2.45	0.46
1:C:195:LYS:O	1:C:199:GLU:HG3	2.14	0.46
1:G:98:ILE:CG2	1:G:99:HIS:N	2.78	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:146:LEU:HD22	1:C:97:ASN:CB	2.46	0.46
1:F:95:TYR:CD1	1:F:95:TYR:C	2.93	0.46
1:H:138:LYS:HD2	1:H:175:GLU:OE2	2.15	0.46
1:B:53:HIS:O	1:B:87:THR:HB	2.16	0.46
1:F:125:ILE:HG23	1:F:182:LYS:HE2	1.97	0.46
1:G:61:PHE:HE2	1:G:94:ILE:HG23	1.80	0.46
1:C:93:SER:O	1:C:97:ASN:ND2	2.45	0.46
1:D:96:ASN:O	1:D:100:HIS:HB2	2.16	0.46
1:H:63:PHE:HD1	1:H:82:ILE:CD1	2.14	0.46
1:C:138:LYS:HA	1:C:175:GLU:HG3	1.97	0.46
1:H:61:PHE:HA	1:H:111:TYR:O	2.16	0.46
1:H:117:ILE:HG12	1:H:125:ILE:HD12	1.98	0.46
1:C:214:ASP:HB3	1:C:222:ALA:HB1	1.98	0.46
1:C:76:GLY:C	1:C:78:SER:H	2.23	0.45
1:F:157:PHE:CD2	1:F:163:ILE:CD1	2.99	0.45
1:F:210:ILE:HG13	1:F:224:ASN:HD22	1.81	0.45
1:A:53:HIS:O	1:A:88:VAL:HG23	2.16	0.45
1:C:137:PRO:HG2	1:C:140:LYS:HG3	1.98	0.45
1:E:88:VAL:O	1:E:91:PHE:HB3	2.17	0.45
1:H:170:VAL:O	1:H:171:ARG:HD3	2.16	0.45
1:A:69:LYS:O	1:A:72:GLN:HB2	2.16	0.45
1:A:110:PHE:HB3	1:A:168:VAL:CG1	2.46	0.45
1:B:171:ARG:HH11	1:B:171:ARG:CA	2.29	0.45
1:A:65:THR:O	1:A:69:LYS:HG3	2.17	0.45
1:F:211:PHE:CE1	1:F:225:LYS:HB3	2.52	0.45
1:C:133:THR:O	1:C:207:MET:HB2	2.16	0.45
1:D:127:ALA:HB3	3:D:2038:HOH:O	2.16	0.45
1:F:159:HIS:HD2	1:F:192:SER:CB	2.29	0.45
1:B:171:ARG:HH11	1:B:171:ARG:HG2	1.69	0.45
1:F:122:GLU:HG2	1:F:122:GLU:H	1.65	0.45
1:E:213:ASP:O	1:E:216:ARG:HG2	2.15	0.45
1:F:157:PHE:CG	1:F:163:ILE:HD11	2.52	0.45
1:H:132:TRP:CH2	1:H:228:VAL:HG13	2.51	0.45
1:B:77:SER:O	1:B:80:ARG:NH1	2.38	0.45
1:B:88:VAL:O	1:B:91:PHE:HB3	2.17	0.45
1:G:105:ALA:O	1:G:170:VAL:CG1	2.65	0.45
1:G:114:LYS:HB2	1:G:117:ILE:HD12	1.99	0.45
1:D:64:ASP:O	1:D:108:ALA:HA	2.18	0.44
1:E:100:HIS:HB3	1:E:101:PRO:HD2	2.00	0.44
1:F:157:PHE:CD2	1:F:163:ILE:HD11	2.52	0.44
1:H:131:LYS:O	1:H:209:PHE:HA	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:96:ASN:HD22	1:B:96:ASN:HA	1.69	0.44
1:F:131:LYS:O	1:F:209:PHE:HA	2.18	0.44
1:H:59:TRP:O	1:H:84:THR:HA	2.18	0.44
1:C:138:LYS:HZ2	1:C:138:LYS:HB3	1.83	0.44
1:D:115:HIS:O	1:D:116:LYS:HB2	2.17	0.44
2:E:500:MGP:O2B	2:E:500:MGP:H5'	2.18	0.44
1:E:213:ASP:O	1:E:217:LYS:HG3	2.17	0.44
1:F:111:TYR:CD2	1:F:167:VAL:HB	2.53	0.44
1:C:94:ILE:CD1	1:C:98:ILE:HD13	2.48	0.43
1:G:210:ILE:CG1	1:G:224:ASN:HD22	2.30	0.43
1:C:69:LYS:C	1:C:71:LYS:H	2.26	0.43
1:F:100:HIS:CB	1:F:142:ASP:OD2	2.66	0.43
1:F:206:THR:HG23	1:F:227:VAL:CG1	2.47	0.43
1:E:104:LEU:HD23	1:E:104:LEU:HA	1.90	0.43
1:F:53:HIS:HB3	1:F:88:VAL:HB	2.01	0.43
1:C:191:VAL:CG1	1:C:195:LYS:HZ3	2.31	0.43
1:F:63:PHE:CB	1:F:82:ILE:HD13	2.48	0.43
1:F:157:PHE:HB2	3:F:2048:HOH:O	2.19	0.43
1:A:130:GLY:HA3	1:A:209:PHE:CZ	2.54	0.43
1:C:62:TRP:CZ3	1:C:81:PRO:HD3	2.54	0.43
1:A:88:VAL:O	1:A:91:PHE:HB3	2.19	0.43
1:F:206:THR:CG2	1:F:207:MET:N	2.81	0.43
1:A:132:TRP:O	1:A:178:SER:HA	2.19	0.42
1:C:58:SER:OG	1:C:86:SER:OG	2.37	0.42
1:D:201:LEU:O	1:D:202:ASP:HB2	2.19	0.42
1:A:132:TRP:CZ2	1:A:190:GLN:O	2.72	0.42
1:F:206:THR:HG22	1:F:207:MET:N	2.33	0.42
1:F:211:PHE:CE1	1:F:225:LYS:CB	3.02	0.42
1:F:89:GLU:OE1	1:F:89:GLU:N	2.44	0.42
1:H:132:TRP:O	1:H:178:SER:HA	2.19	0.42
1:E:94:ILE:O	1:E:98:ILE:HG12	2.20	0.42
1:H:81:PRO:C	1:H:82:ILE:HD13	2.45	0.42
1:E:65:THR:HG21	1:H:202:ASP:OD2	2.20	0.42
1:H:170:VAL:HA	1:H:175:GLU:HG2	2.02	0.42
1:B:123:ASP:HB3	1:B:126:CYS:HB2	2.02	0.42
1:H:122:GLU:OE2	2:H:500:MGP:N1	2.49	0.42
1:B:146:LEU:HD22	1:C:97:ASN:HB3	2.02	0.41
1:H:227:VAL:HG12	1:H:228:VAL:N	2.35	0.41
1:E:186:ASN:CG	1:E:189:ALA:CB	2.93	0.41
1:F:120:LYS:C	1:F:122:GLU:N	2.77	0.41
1:A:126:CYS:O	1:A:212:HIS:HD2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:98:ILE:HD12	1:B:110:PHE:CE1	2.54	0.41
1:F:159:HIS:CD2	1:F:192:SER:CB	3.03	0.41
1:G:171:ARG:HB3	1:G:172:GLY:H	1.69	0.41
1:E:186:ASN:CG	1:E:189:ALA:HB2	2.46	0.41
1:H:69:LYS:O	1:H:72:GLN:HG2	2.20	0.41
1:B:114:LYS:HB2	1:B:117:ILE:HD12	2.03	0.41
1:D:187:GLU:O	1:D:191:VAL:HG23	2.21	0.41
1:A:83:TYR:CD1	1:A:84:THR:N	2.89	0.41
1:F:206:THR:CG2	1:F:227:VAL:CG1	2.98	0.41
1:G:101:PRO:HG2	1:G:142:ASP:HA	2.02	0.41
1:B:75:TRP:CZ3	1:B:120:LYS:HG2	2.52	0.41
1:B:109:ASP:OD1	1:B:171:ARG:NH2	2.54	0.41
1:C:211:PHE:CZ	1:C:225:LYS:HG2	2.55	0.41
1:D:76:GLY:C	1:D:78:SER:N	2.76	0.41
1:F:122:GLU:OE2	2:F:500:MGP:N1	2.49	0.41
1:F:196:GLN:O	1:F:199:GLU:HB2	2.20	0.41
1:H:210:ILE:HG22	1:H:211:PHE:O	2.21	0.41
1:C:76:GLY:C	1:C:78:SER:N	2.78	0.40
1:D:207:MET:HE2	1:D:207:MET:HB3	1.76	0.40
1:G:113:PHE:O	1:G:114:LYS:C	2.64	0.40
1:A:80:ARG:CZ	1:A:82:ILE:HD13	2.51	0.40
1:G:59:TRP:O	1:G:84:THR:HA	2.21	0.40
1:H:187:GLU:O	1:H:191:VAL:HG23	2.21	0.40
1:H:63:PHE:CE1	1:H:82:ILE:CD1	2.93	0.40
1:A:100:HIS:O	1:A:101:PRO:C	2.64	0.40
1:F:171:ARG:HD3	1:F:171:ARG:HA	1.81	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	170/178 (96%)	167 (98%)	3 (2%)	0	100	100
1	B	151/178 (85%)	145 (96%)	5 (3%)	1 (1%)	18	19
1	C	166/178 (93%)	159 (96%)	6 (4%)	1 (1%)	21	23
1	D	155/178 (87%)	151 (97%)	4 (3%)	0	100	100
1	E	161/178 (90%)	155 (96%)	5 (3%)	1 (1%)	21	23
1	F	156/178 (88%)	151 (97%)	5 (3%)	0	100	100
1	G	163/178 (92%)	155 (95%)	6 (4%)	2 (1%)	10	8
1	H	167/178 (94%)	164 (98%)	2 (1%)	1 (1%)	21	23
All	All	1289/1424 (90%)	1247 (97%)	36 (3%)	6 (0%)	24	27

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	172	GLY
1	C	70	SER
1	G	79	MET
1	G	105	ALA
1	H	182	LYS
1	E	172	GLY

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	144/150 (96%)	137 (95%)	7 (5%)	22	29
1	B	134/150 (89%)	126 (94%)	8 (6%)	17	21
1	C	141/150 (94%)	132 (94%)	9 (6%)	16	19
1	D	137/150 (91%)	134 (98%)	3 (2%)	45	61
1	E	138/150 (92%)	131 (95%)	7 (5%)	21	27
1	F	131/150 (87%)	127 (97%)	4 (3%)	35	48
1	G	136/150 (91%)	134 (98%)	2 (2%)	57	73

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	H	138/150 (92%)	136 (99%)	2 (1%)	59 75
All	All	1099/1200 (92%)	1057 (96%)	42 (4%)	29 40

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	103	LYS
1	A	122	GLU
1	A	138	LYS
1	A	182	LYS
1	A	216	ARG
1	A	223	LYS
1	A	225	LYS
1	B	54	LEU
1	B	93	SER
1	B	99	HIS
1	B	122	GLU
1	B	171	ARG
1	B	176	LYS
1	B	179	ILE
1	B	191	VAL
1	C	54	LEU
1	C	78	SER
1	C	86	SER
1	C	98	ILE
1	C	122	GLU
1	C	138	LYS
1	C	182	LYS
1	C	205	GLU
1	C	213	ASP
1	D	78	SER
1	D	116	LYS
1	D	195	LYS
1	E	78	SER
1	E	86	SER
1	E	94	ILE
1	E	122	GLU
1	E	163	ILE
1	E	202	ASP
1	E	216	ARG
1	F	82	ILE
1	F	86	SER

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Mol	Chain	Res	Type
1	F	122	GLU
1	F	198	LYS
1	G	138	LYS
1	G	171	ARG
1	H	82	ILE
1	H	122	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	135	ASN
1	A	156	GLN
1	A	224	ASN
1	B	221	ASN
1	C	96	ASN
1	C	183	ASN
1	C	224	ASN
1	D	53	HIS
1	E	135	ASN
1	E	224	ASN
1	F	57	ASN
1	F	224	ASN
1	G	97	ASN
1	G	224	ASN
1	H	57	ASN
1	H	72	GLN
1	H	135	ASN
1	H	156	GLN
1	H	224	ASN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

8 ligands are modelled in this entry.

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
2	MGP	G	500	-	30,31,35	1.42	4 (13%)	47,49,56	1.76	11 (23%)
2	MGP	D	500	-	30,31,35	1.93	6 (20%)	47,49,56	1.70	12 (25%)
2	MGP	B	500	-	30,31,35	1.37	3 (10%)	47,49,56	1.84	12 (25%)
2	MGP	E	500	-	30,31,35	1.57	5 (16%)	47,49,56	1.66	9 (19%)
2	MGP	C	500	-	30,31,35	1.35	4 (13%)	47,49,56	1.72	9 (19%)
2	MGP	F	500	-	30,31,35	1.56	5 (16%)	47,49,56	1.81	11 (23%)
2	MGP	H	500	-	30,31,35	1.54	4 (13%)	47,49,56	1.62	8 (17%)
2	MGP	A	500	-	30,31,35	1.72	5 (16%)	47,49,56	1.56	9 (19%)

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
2	MGP	G	500	-	-	7/16/32/38	0/3/3/3
2	MGP	D	500	-	-	6/16/32/38	0/3/3/3
2	MGP	B	500	-	-	3/16/32/38	0/3/3/3
2	MGP	E	500	-	-	6/16/32/38	0/3/3/3
2	MGP	C	500	-	-	1/16/32/38	0/3/3/3
2	MGP	F	500	-	-	7/16/32/38	0/3/3/3
2	MGP	H	500	-	-	3/16/32/38	0/3/3/3
2	MGP	A	500	-	-	0/16/32/38	0/3/3/3

All (36) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	500	MGP	PA-O3A	5.98	1.66	1.59
2	A	500	MGP	C5-N7	-5.72	1.32	1.39
2	H	500	MGP	C5-N7	-4.79	1.33	1.39
2	D	500	MGP	PB-O2B	4.75	1.65	1.50
2	E	500	MGP	C5-N7	-4.73	1.33	1.39
2	A	500	MGP	PA-O3A	4.50	1.64	1.59
2	D	500	MGP	C5-N7	-4.41	1.34	1.39
2	B	500	MGP	PB-O2B	4.32	1.63	1.50
2	G	500	MGP	PB-O2B	4.31	1.63	1.50
2	H	500	MGP	PB-O2B	4.29	1.63	1.50
2	F	500	MGP	C5-N7	-4.25	1.34	1.39
2	E	500	MGP	PB-O2B	4.21	1.63	1.50
2	G	500	MGP	C5-N7	-4.05	1.34	1.39
2	F	500	MGP	PB-O2B	3.94	1.62	1.50
2	C	500	MGP	C5-N7	-3.94	1.34	1.39
2	B	500	MGP	C5-N7	-3.83	1.34	1.39
2	C	500	MGP	PB-O2B	3.60	1.61	1.50
2	A	500	MGP	PB-O2B	3.43	1.61	1.50
2	F	500	MGP	PA-O3A	3.31	1.63	1.59
2	E	500	MGP	PA-O3A	3.11	1.62	1.59
2	H	500	MGP	PA-O3A	3.05	1.62	1.59
2	D	500	MGP	PB-O1B	2.85	1.65	1.54
2	A	500	MGP	C4-N9	-2.59	1.31	1.38
2	D	500	MGP	O4'-C1'	2.43	1.47	1.42
2	C	500	MGP	O4'-C1'	2.38	1.47	1.42
2	E	500	MGP	PB-O1B	2.30	1.63	1.54
2	D	500	MGP	C4-N9	-2.28	1.32	1.38
2	F	500	MGP	PB-O1B	2.18	1.62	1.54
2	G	500	MGP	PB-O1B	2.12	1.62	1.54
2	G	500	MGP	C4-N9	-2.11	1.32	1.38
2	H	500	MGP	PB-O1B	2.07	1.62	1.54
2	A	500	MGP	C5-C6	-2.04	1.37	1.43
2	C	500	MGP	PB-O1B	2.04	1.62	1.54
2	E	500	MGP	O4'-C1'	2.04	1.46	1.42
2	B	500	MGP	PB-O1B	2.02	1.62	1.54
2	F	500	MGP	C4-N9	-2.01	1.33	1.38

All (81) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	500	MGP	C2-N3-C4	5.39	121.59	112.30
2	G	500	MGP	C2-N3-C4	5.31	121.45	112.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	500	MGP	C2-N3-C4	5.19	121.23	112.30
2	H	500	MGP	C2-N3-C4	4.97	120.86	112.30
2	E	500	MGP	C2-N3-C4	4.78	120.54	112.30
2	F	500	MGP	C2-N3-C4	4.77	120.51	112.30
2	D	500	MGP	C2-N3-C4	4.61	120.25	112.30
2	F	500	MGP	O4'-C1'-N9	4.06	117.56	108.36
2	A	500	MGP	C2-N3-C4	3.89	119.00	112.30
2	E	500	MGP	C5-C4-N3	-3.87	120.84	128.15
2	H	500	MGP	C5-C4-N3	-3.66	121.23	128.15
2	D	500	MGP	C6-C5-N7	3.64	136.74	132.17
2	F	500	MGP	C2'-C3'-C4'	-3.63	95.59	102.61
2	B	500	MGP	CM7-N7-C8	-3.62	119.30	124.79
2	C	500	MGP	C5-C6-N1	3.61	119.29	111.84
2	B	500	MGP	C6-C5-N7	3.59	136.67	132.17
2	C	500	MGP	C5-C4-N3	-3.53	121.48	128.15
2	B	500	MGP	C5-C4-N3	-3.50	121.53	128.15
2	G	500	MGP	C5-C4-N3	-3.48	121.56	128.15
2	C	500	MGP	C6-C5-N7	3.41	136.45	132.17
2	B	500	MGP	C5-C6-N1	3.41	118.88	111.84
2	H	500	MGP	C5-C6-N1	3.34	118.75	111.84
2	A	500	MGP	C2'-C3'-C4'	-3.34	96.16	102.61
2	E	500	MGP	C5-C6-N1	3.18	118.42	111.84
2	G	500	MGP	C6-C5-N7	3.17	136.15	132.17
2	G	500	MGP	C2-N1-C6	-3.12	119.46	125.11
2	F	500	MGP	C5-C4-N3	-3.09	122.31	128.15
2	E	500	MGP	C2-N1-C6	-3.02	119.62	125.11
2	B	500	MGP	O3B-PB-O3A	3.00	114.69	104.64
2	D	500	MGP	C5-C6-N1	2.99	118.02	111.84
2	G	500	MGP	C5-C6-N1	2.98	118.01	111.84
2	H	500	MGP	O6-C6-C5	-2.95	121.44	128.01
2	F	500	MGP	C5-C6-N1	2.94	117.91	111.84
2	B	500	MGP	CM7-N7-C5	2.93	130.45	126.80
2	D	500	MGP	C5-C4-N3	-2.93	122.62	128.15
2	C	500	MGP	C2-N1-C6	-2.90	119.86	125.11
2	E	500	MGP	O3B-PB-O3A	2.88	114.30	104.64
2	B	500	MGP	C2-N1-C6	-2.87	119.90	125.11
2	E	500	MGP	O6-C6-C5	-2.87	121.60	128.01
2	A	500	MGP	C5-C4-N3	-2.86	122.74	128.15
2	H	500	MGP	C2-N1-C6	-2.85	119.94	125.11
2	E	500	MGP	N9-C4-N3	2.84	131.63	125.95
2	F	500	MGP	C2-N1-C6	-2.78	120.07	125.11
2	F	500	MGP	O6-C6-C5	-2.72	121.94	128.01

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	500	MGP	O4'-C1'-N9	2.69	114.45	108.36
2	H	500	MGP	N9-C4-N3	2.66	131.28	125.95
2	A	500	MGP	C5-C6-N1	2.66	117.33	111.84
2	A	500	MGP	O3B-PB-O3A	2.65	113.53	104.64
2	G	500	MGP	O6-C6-C5	-2.56	122.29	128.01
2	F	500	MGP	O3B-PB-O3A	2.56	113.23	104.64
2	C	500	MGP	O6-C6-C5	-2.52	122.38	128.01
2	G	500	MGP	O4'-C1'-N9	2.49	114.00	108.36
2	F	500	MGP	C2'-C1'-N9	-2.46	106.41	113.25
2	E	500	MGP	C5'-C4'-C3'	-2.45	106.40	115.21
2	A	500	MGP	C2'-C1'-N9	-2.42	106.52	113.25
2	F	500	MGP	O4'-C4'-C5'	-2.41	101.61	109.33
2	D	500	MGP	C2-N1-C6	-2.41	120.75	125.11
2	H	500	MGP	C6-C5-N7	2.40	135.18	132.17
2	C	500	MGP	O3B-PB-O3A	2.40	112.68	104.64
2	D	500	MGP	C2'-C3'-C4'	-2.38	98.01	102.61
2	G	500	MGP	O3B-PB-O3A	2.35	112.52	104.64
2	D	500	MGP	O6-C6-C5	-2.32	122.83	128.01
2	B	500	MGP	O6-C6-C5	-2.28	122.92	128.01
2	B	500	MGP	N9-C4-N3	2.26	130.48	125.95
2	F	500	MGP	C6-C5-N7	2.25	135.00	132.17
2	C	500	MGP	N9-C4-N3	2.24	130.44	125.95
2	A	500	MGP	O6-C6-C5	-2.21	123.07	128.01
2	G	500	MGP	C3'-C2'-C1'	-2.21	97.28	101.46
2	H	500	MGP	O1A-PA-O3A	2.20	113.22	107.27
2	G	500	MGP	N2-C2-N1	2.19	121.38	116.76
2	D	500	MGP	O2'-C2'-C1'	-2.17	102.65	110.10
2	C	500	MGP	O4'-C4'-C3'	-2.16	100.87	105.15
2	E	500	MGP	C6-C5-N7	2.13	134.85	132.17
2	D	500	MGP	N2-C2-N1	2.13	121.25	116.76
2	B	500	MGP	C5'-C4'-C3'	-2.10	107.64	115.21
2	A	500	MGP	N9-C8-N7	-2.10	107.38	112.48
2	D	500	MGP	N9-C8-N7	-2.09	107.40	112.48
2	D	500	MGP	C8-N7-C5	2.08	110.39	107.78
2	A	500	MGP	C4'-O4'-C1'	-2.05	104.93	109.47
2	B	500	MGP	O1B-PB-O2B	-2.05	102.84	110.83
2	G	500	MGP	C2'-C3'-C4'	-2.04	98.67	102.61

There are no chirality outliers.

All (33) torsion outliers are listed below:

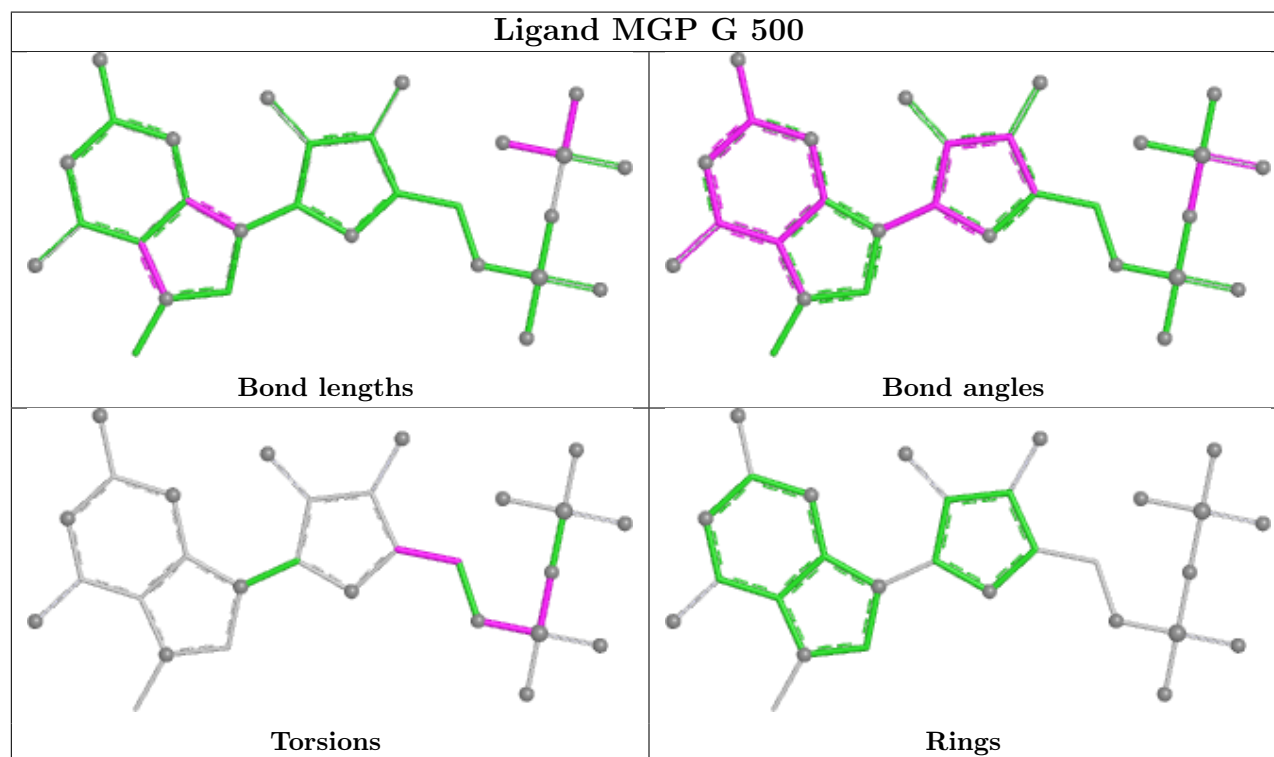
Mol	Chain	Res	Type	Atoms
2	B	500	MGP	C5'-O5'-PA-O3A
2	D	500	MGP	C5'-O5'-PA-O1A
2	D	500	MGP	C5'-O5'-PA-O2A
2	D	500	MGP	C5'-O5'-PA-O3A
2	E	500	MGP	C5'-O5'-PA-O1A
2	F	500	MGP	O4'-C4'-C5'-O5'
2	G	500	MGP	C5'-O5'-PA-O1A
2	G	500	MGP	C5'-O5'-PA-O2A
2	G	500	MGP	C5'-O5'-PA-O3A
2	G	500	MGP	O4'-C4'-C5'-O5'
2	E	500	MGP	C3'-C4'-C5'-O5'
2	F	500	MGP	C3'-C4'-C5'-O5'
2	G	500	MGP	C3'-C4'-C5'-O5'
2	E	500	MGP	O4'-C4'-C5'-O5'
2	G	500	MGP	PB-O3A-PA-O1A
2	B	500	MGP	C5'-O5'-PA-O1A
2	B	500	MGP	C5'-O5'-PA-O2A
2	F	500	MGP	C5'-O5'-PA-O1A
2	F	500	MGP	C5'-O5'-PA-O2A
2	F	500	MGP	C5'-O5'-PA-O3A
2	H	500	MGP	PA-O3A-PB-O2B
2	D	500	MGP	PA-O3A-PB-O2B
2	E	500	MGP	PA-O3A-PB-O2B
2	D	500	MGP	PA-O3A-PB-O1B
2	D	500	MGP	PA-O3A-PB-O3B
2	E	500	MGP	PA-O3A-PB-O1B
2	E	500	MGP	PA-O3A-PB-O3B
2	H	500	MGP	PA-O3A-PB-O1B
2	H	500	MGP	PA-O3A-PB-O3B
2	C	500	MGP	PB-O3A-PA-O2A
2	F	500	MGP	PB-O3A-PA-O2A
2	F	500	MGP	PB-O3A-PA-O1A
2	G	500	MGP	PB-O3A-PA-O2A

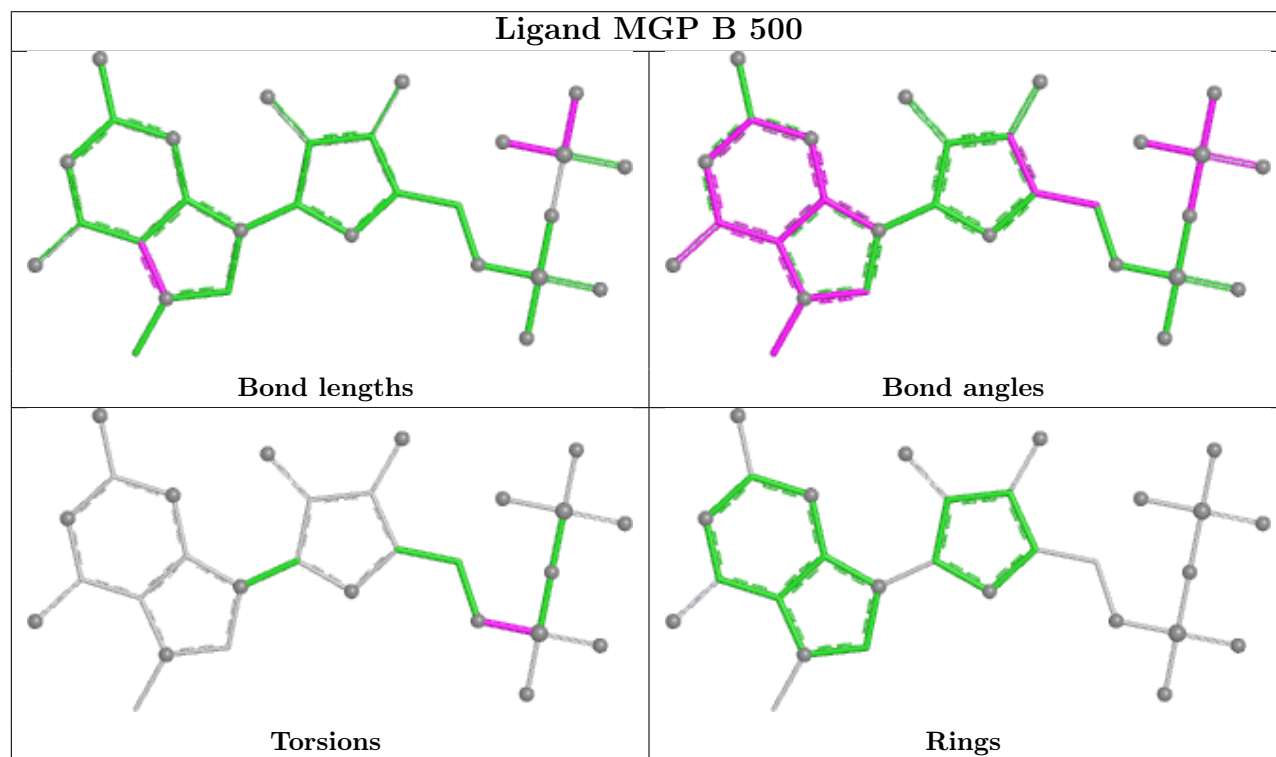
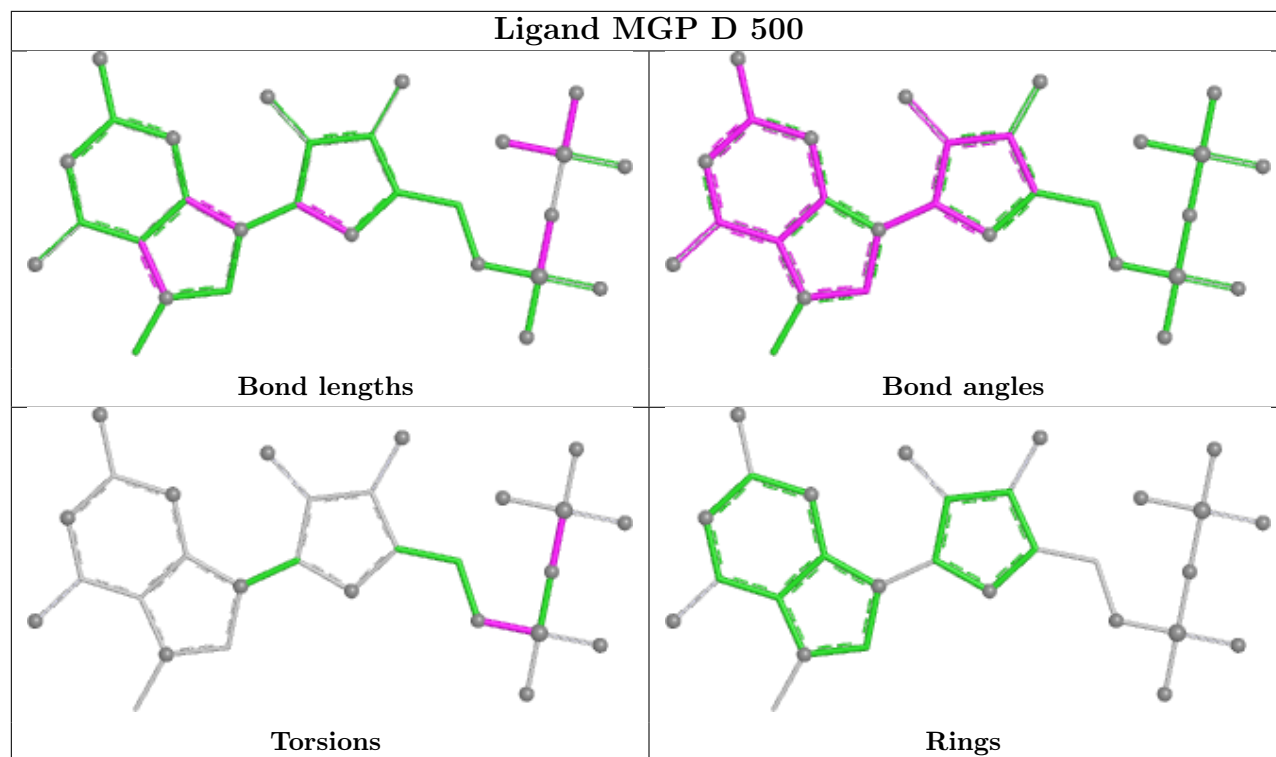
There are no ring outliers.

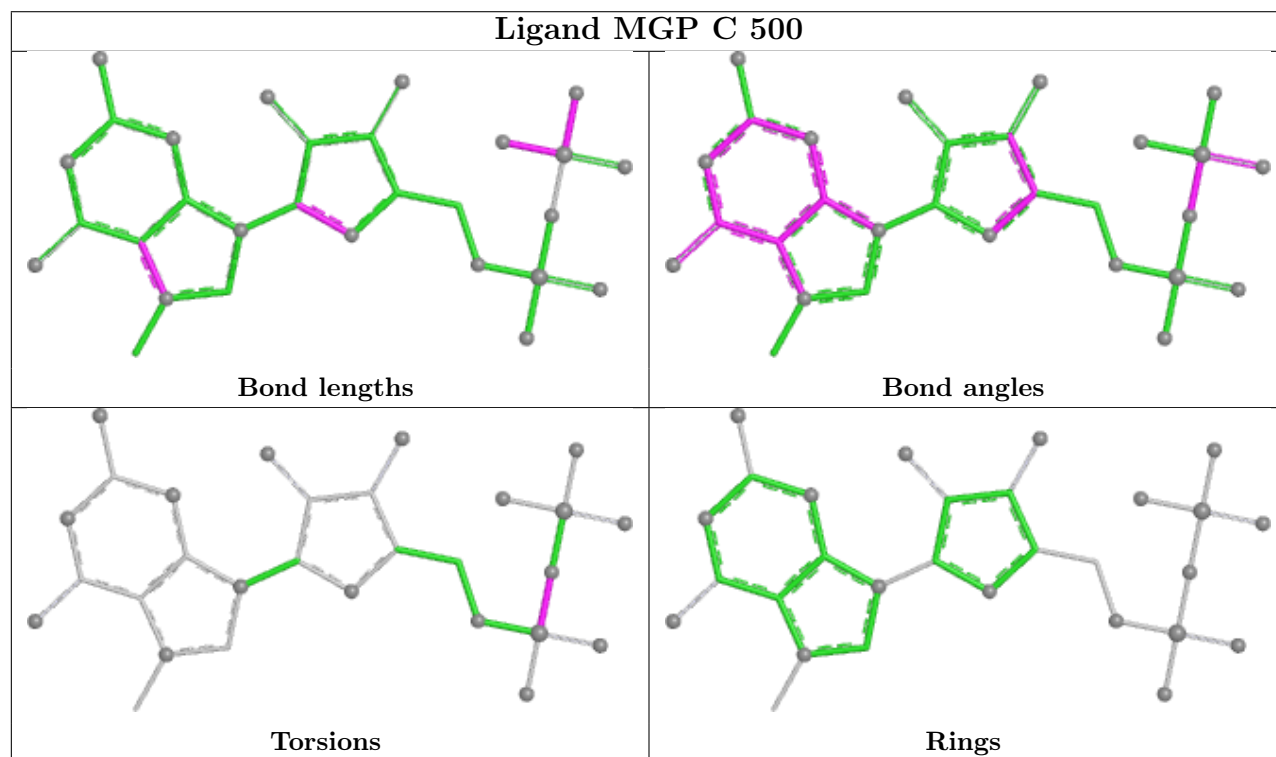
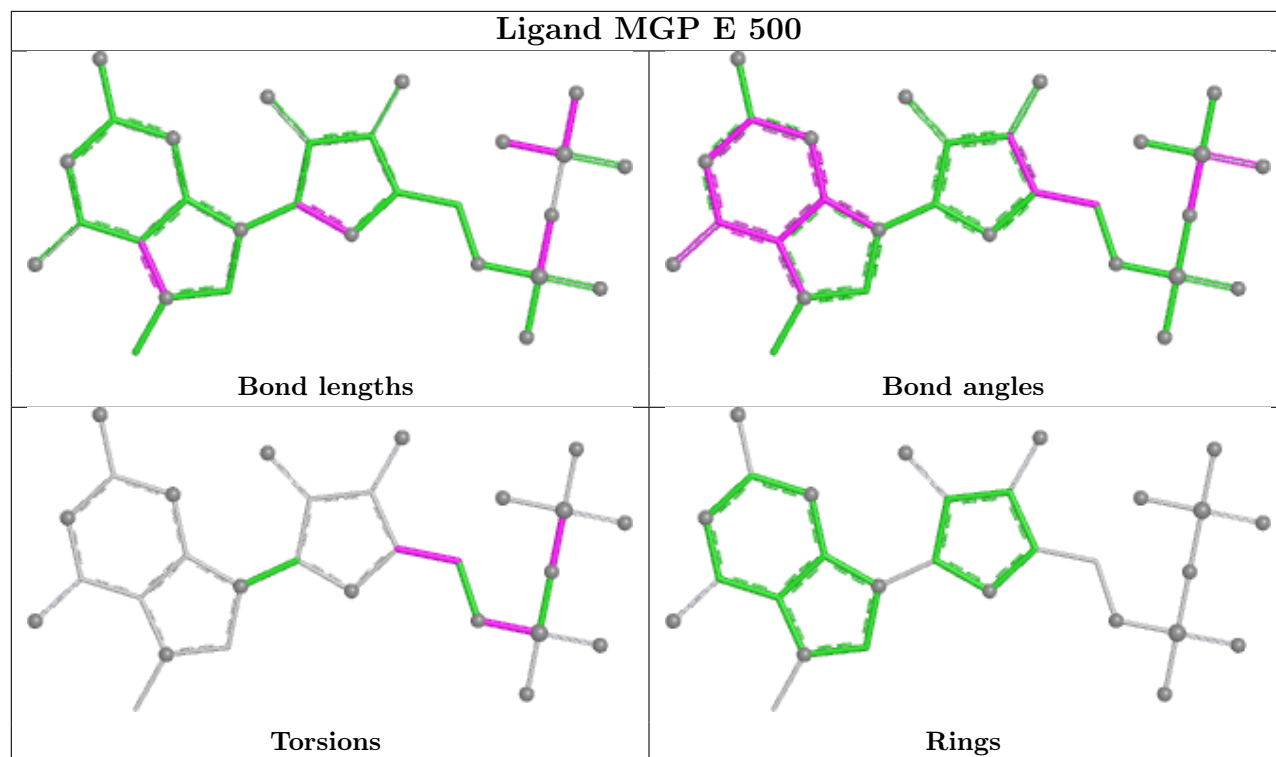
5 monomers are involved in 11 short contacts:

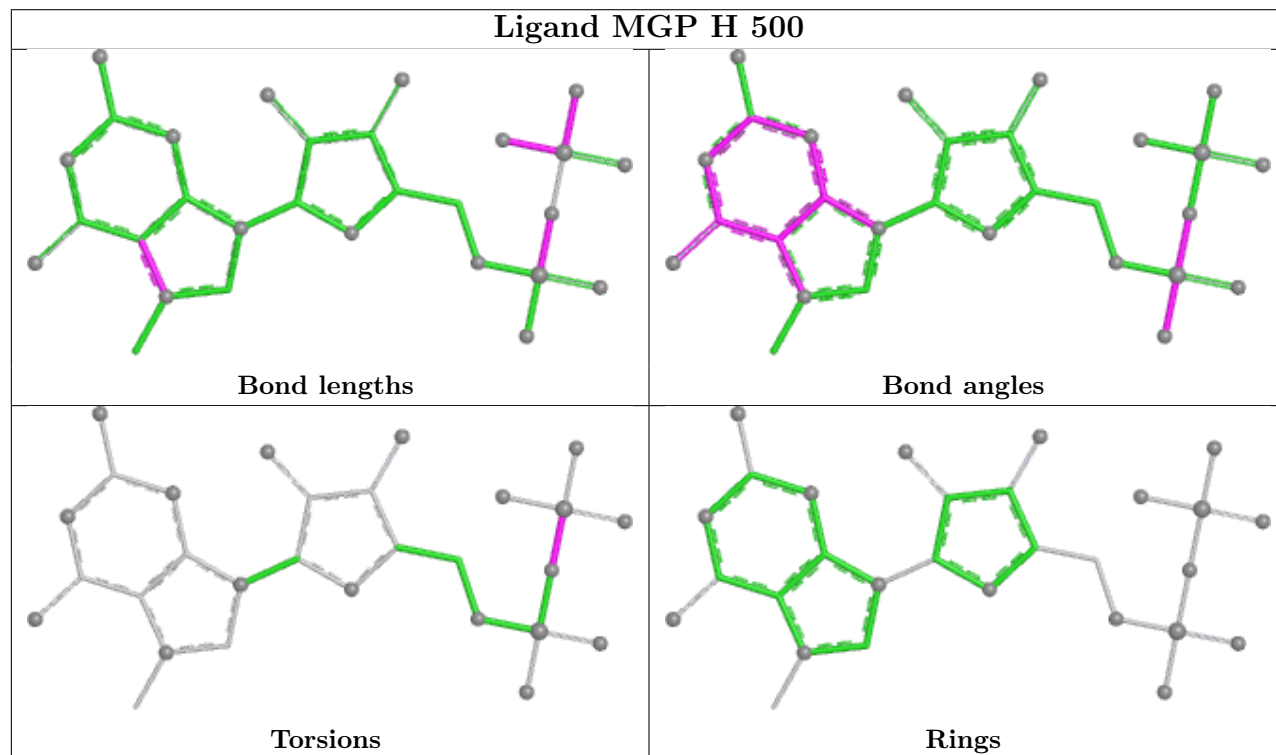
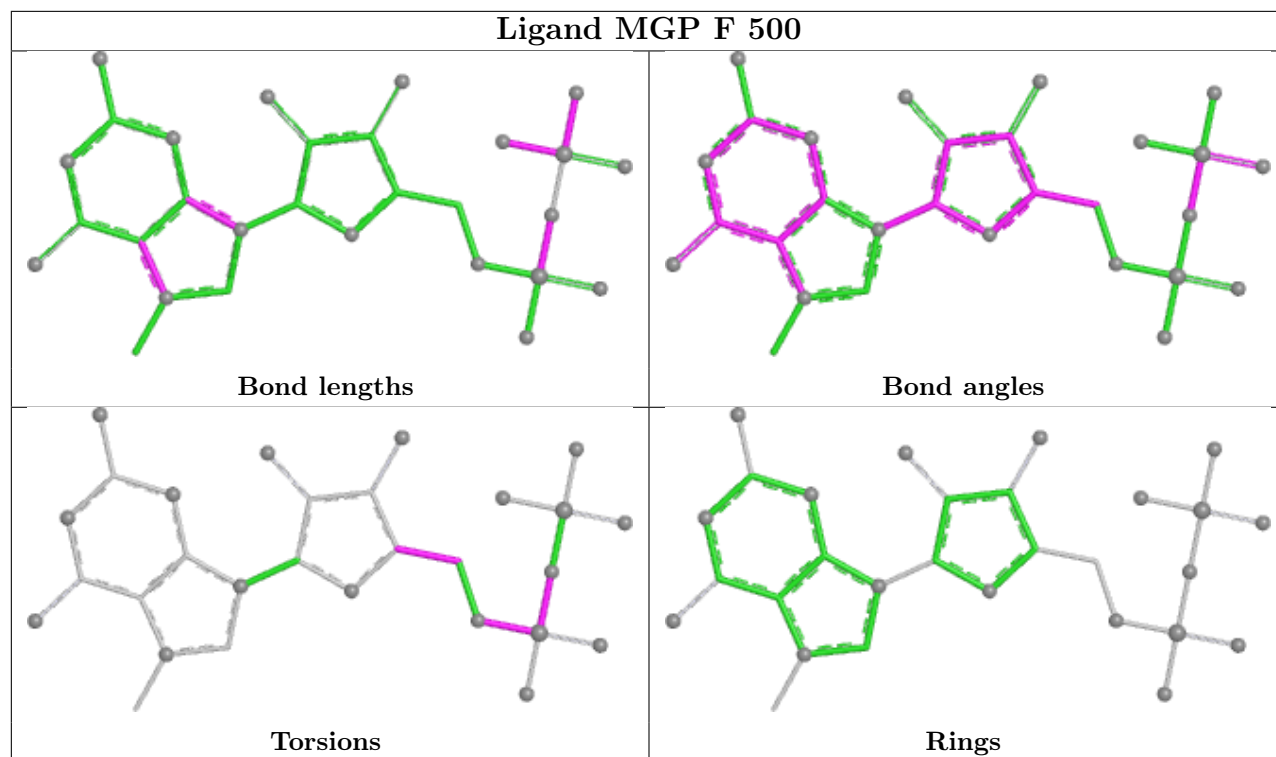
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	500	MGP	3	0
2	E	500	MGP	4	0
2	F	500	MGP	1	0
2	H	500	MGP	1	0
2	A	500	MGP	2	0

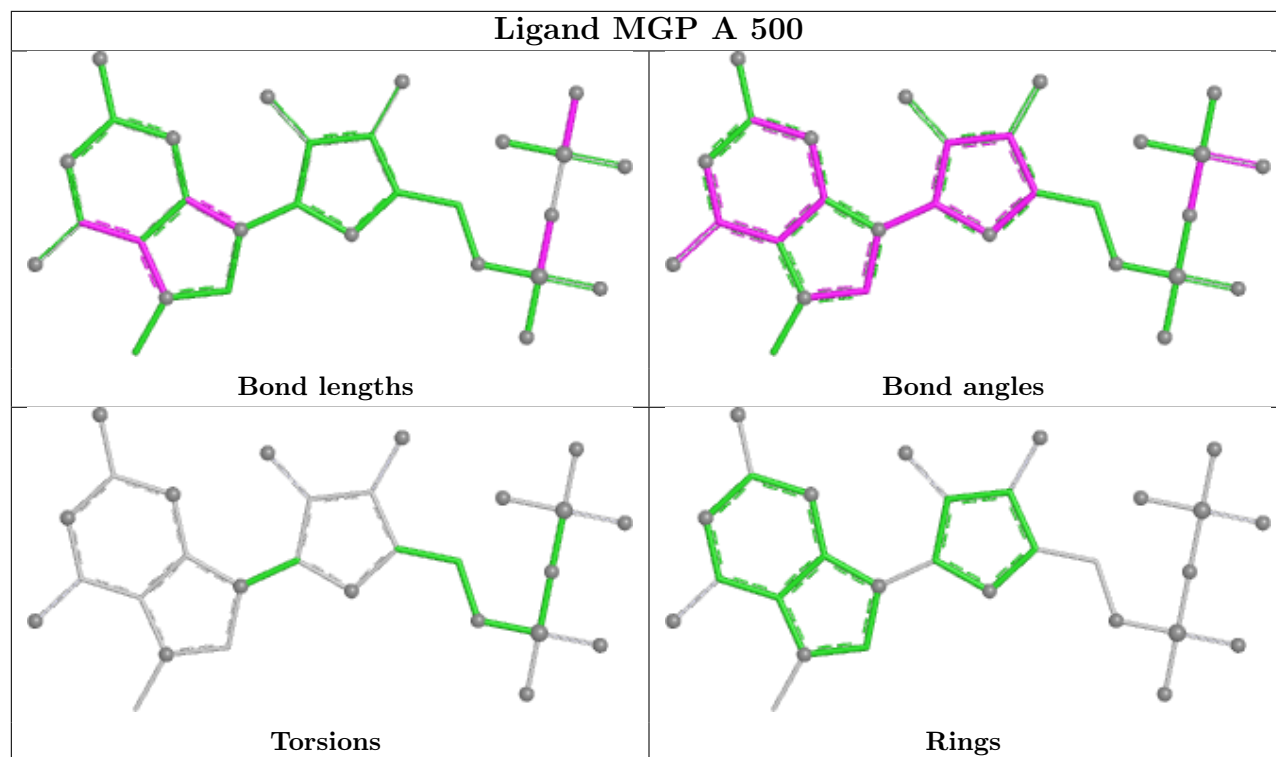
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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	174/178 (97%)	-0.14	1 (0%) 85 83	17, 22, 31, 38	0
1	B	159/178 (89%)	0.05	4 (2%) 58 55	18, 22, 31, 35	0
1	C	172/178 (96%)	-0.09	2 (1%) 76 74	17, 23, 30, 36	0
1	D	163/178 (91%)	-0.04	2 (1%) 76 74	18, 23, 28, 31	0
1	E	167/178 (93%)	-0.09	1 (0%) 85 83	18, 22, 31, 35	0
1	F	162/178 (91%)	0.12	3 (1%) 66 63	18, 24, 31, 37	0
1	G	169/178 (94%)	0.12	5 (2%) 52 49	17, 23, 35, 37	0
1	H	171/178 (96%)	-0.01	1 (0%) 85 83	18, 23, 28, 31	0
All	All	1337/1424 (93%)	-0.01	19 (1%) 73 71	17, 23, 31, 38	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	76	GLY	3.9
1	B	74	ALA	3.7
1	G	107	GLY	3.1
1	D	53	HIS	2.8
1	E	67	ALA	2.7
1	F	76	GLY	2.7
1	D	74	ALA	2.6
1	G	102	GLY	2.6
1	F	105	ALA	2.5
1	C	73	ALA	2.4
1	G	70	SER	2.4
1	F	99	HIS	2.4
1	B	172	GLY	2.4
1	G	66	PRO	2.3
1	A	161	ASP	2.2
1	G	76	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	75	TRP	2.2
1	H	185	SER	2.1
1	C	221	ASN	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](#)

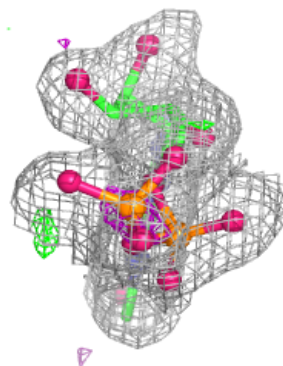
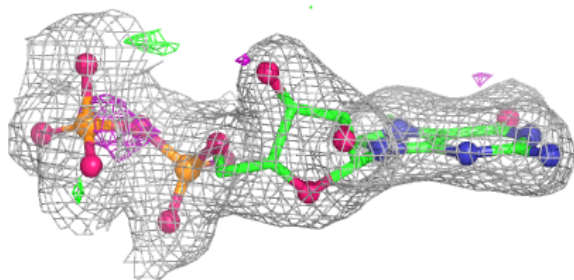
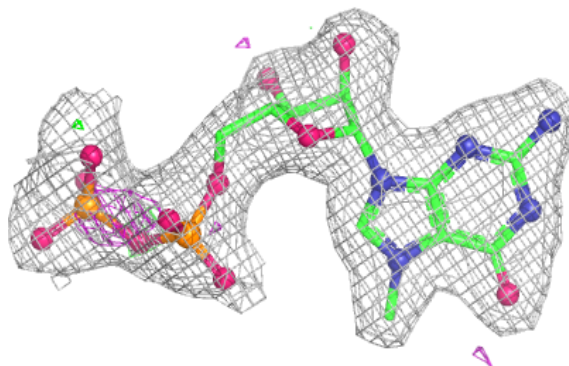
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	MGP	D	500	29/33	0.89	0.09	14,24,48,50	0
2	MGP	F	500	29/33	0.89	0.08	36,43,52,53	0
2	MGP	G	500	29/33	0.89	0.08	24,29,52,52	0
2	MGP	H	500	29/33	0.89	0.09	24,31,44,45	0
2	MGP	E	500	29/33	0.91	0.08	17,29,46,47	0
2	MGP	B	500	29/33	0.91	0.07	18,29,48,49	0
2	MGP	C	500	29/33	0.94	0.06	22,29,40,41	0
2	MGP	A	500	29/33	0.94	0.07	15,23,38,40	0

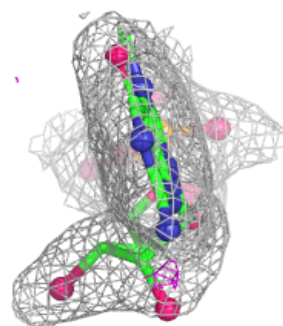
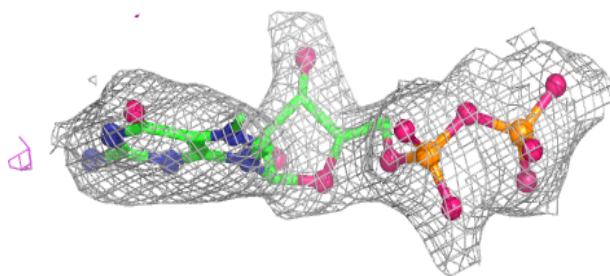
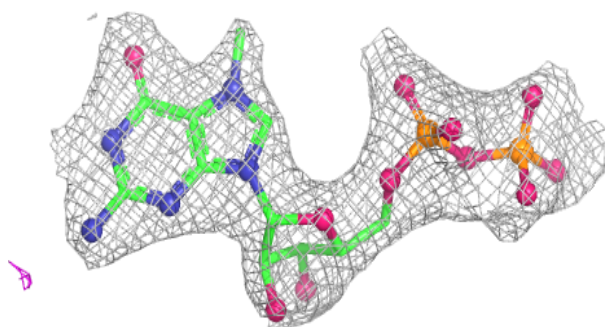
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around MGP D 500:

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

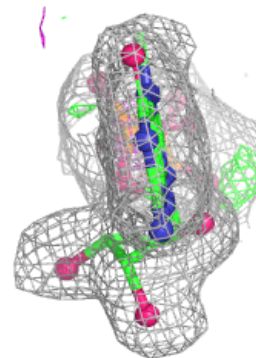
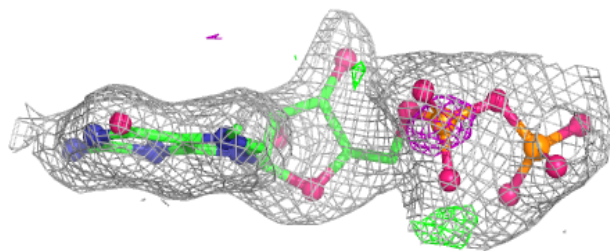
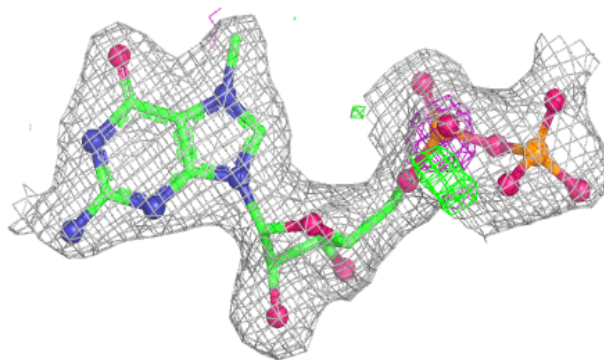
**Electron density around MGP F 500:**

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

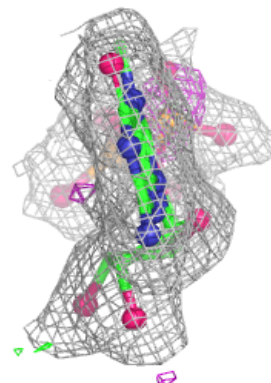
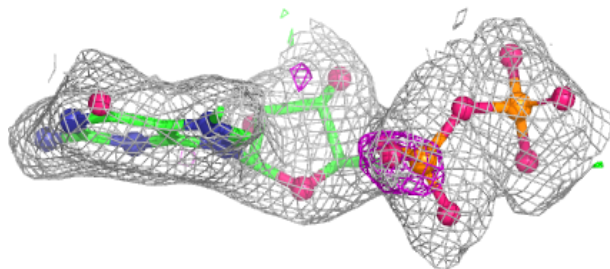
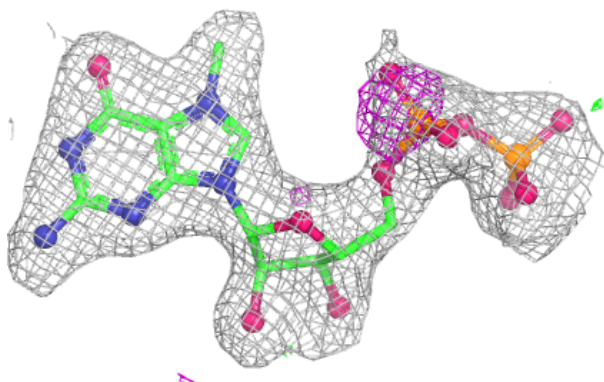


Electron density around MGP G 500:

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

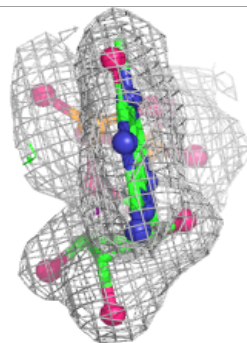
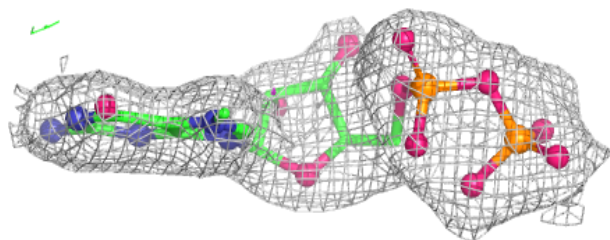
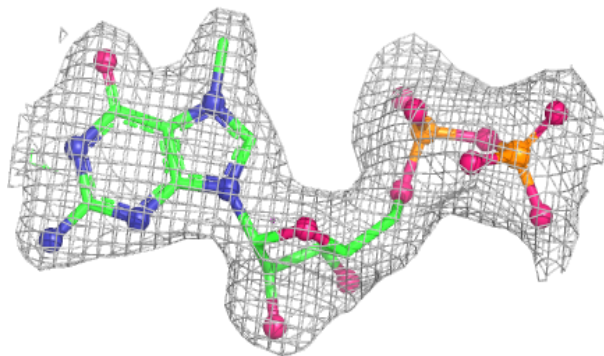
**Electron density around MGP H 500:**

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

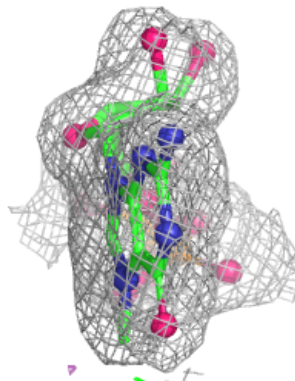
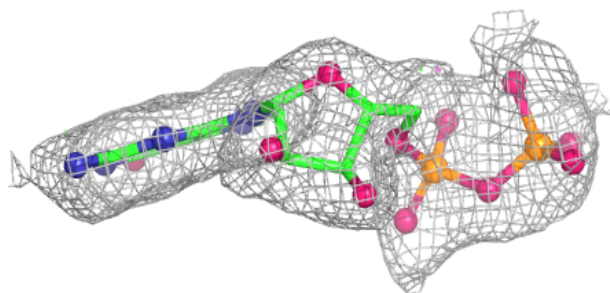
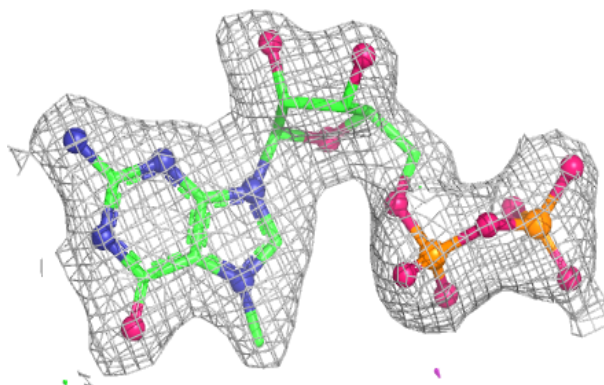


Electron density around MGP E 500:

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

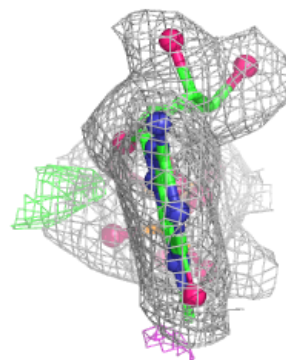
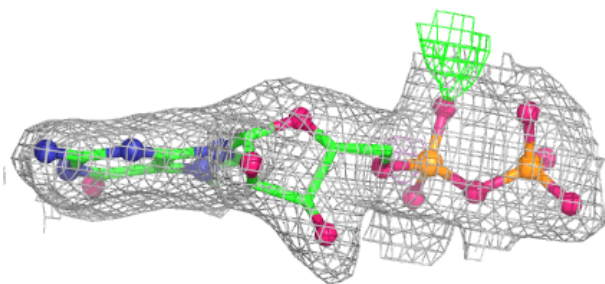
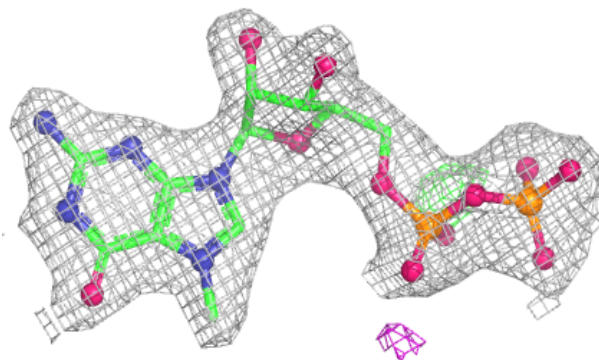
**Electron density around MGP B 500:**

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

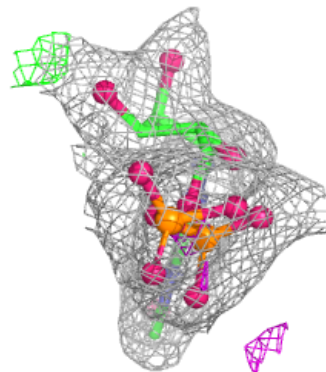
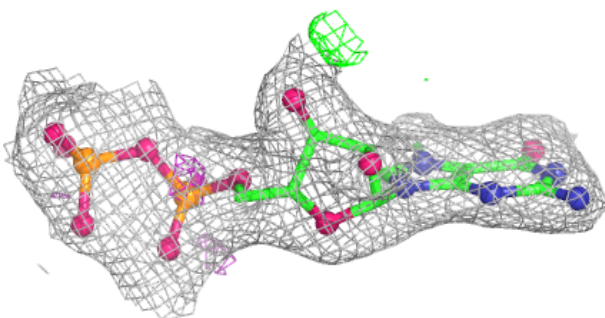
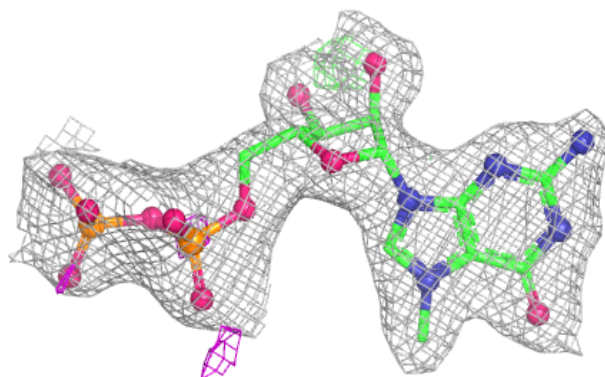


Electron density around MGP C 500:

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

**Electron density around MGP A 500:**

$2mF_o-DF_c$ (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.