Full wwPDB X-ray Structure Validation Report (i)

Nov 20, 2023 – 10:33 PM JST

PDB ID	:	7DLW
Title	:	Crystal structure of Arabidopsis ACS7 in complex with PPG
Authors	:	Hao, B.; Zhang, Y.; Li, X.; Rao, Z.
Deposited on	:	2020-11-30
Resolution	:	2.19 Å(reported)

The following versions of software and data (see references (i)) were used in the production of this report:

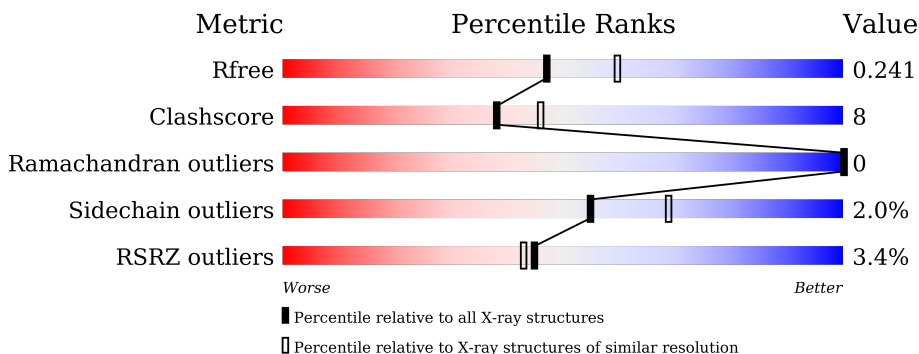|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.19 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	Percentile Ranks	Value
Rfree		0.241
Clashscore		8
Ramachandran outliers		0
Sidechain outliers		2.0%
RSRZ outliers		3.4%

Worse ⬛ *Better*

⬛ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (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 <=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	447	2% / 77% / 15% / 8%
1	B	447	2% / 80% / 13% / 6%
1	C	447	5% / 71% / 20% / 8%
1	D	447	4% / 75% / 17% / 7%

2 Entry composition ⓘ

There are 4 unique types of molecules in this entry. The entry contains 13595 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 1-aminocyclopropane-1-carboxylate synthase 7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	410	Total 3270	C 2067	N 566	O 621	S 16	0	0	0
1	B	419	Total 3354	C 2116	N 588	O 634	S 16	0	0	0
1	C	411	Total 3278	C 2071	N 568	O 623	S 16	0	0	0
1	D	414	Total 3304	C 2088	N 572	O 628	S 16	0	0	0

- Molecule 2 is (2E,3E)-4-(2-aminoethoxy)-2-[({3-hydroxy-2-methyl-5-[(phosphonooxy)methyl]pyridin-4-yl}methyl)imino]but-3-enoic acid (three-letter code: PPG) (formula: $C_{14}H_{20}N_3O_8P$) (labeled as "Ligand of Interest" by depositor).
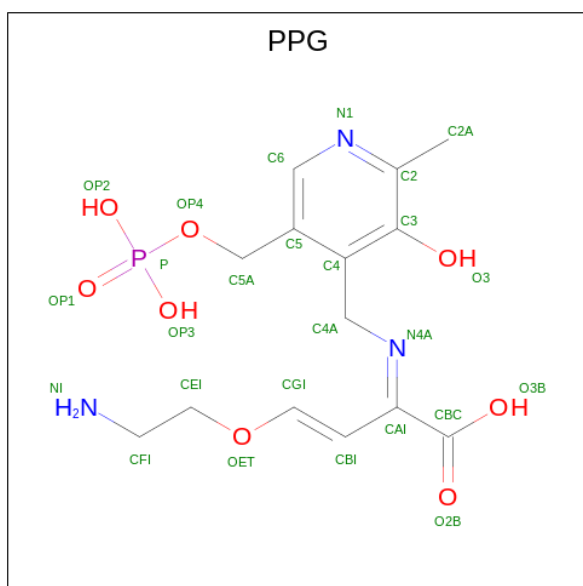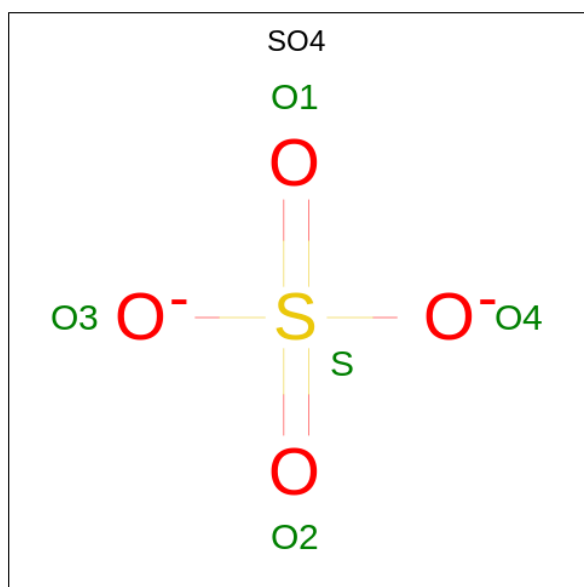

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 26	C 14	N 3	O 8	P 1	0	0

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total 26	C 14	N 3	O 8	P 1	0	0
2	C	1	Total 26	C 14	N 3	O 8	P 1	0	0
2	D	1	Total 26	C 14	N 3	O 8	P 1	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).

SO4

O1

O

O3 O⁻ — S — O⁻ O4

S

O

O2

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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	76	Total 76	O 76	0	0
4	B	81	Total 81	O 81	0	0
4	C	59	Total 59	O 59	0	0
4	D	64	Total 64	O 64	0	0

3 Residue-property plots ⓘ

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.
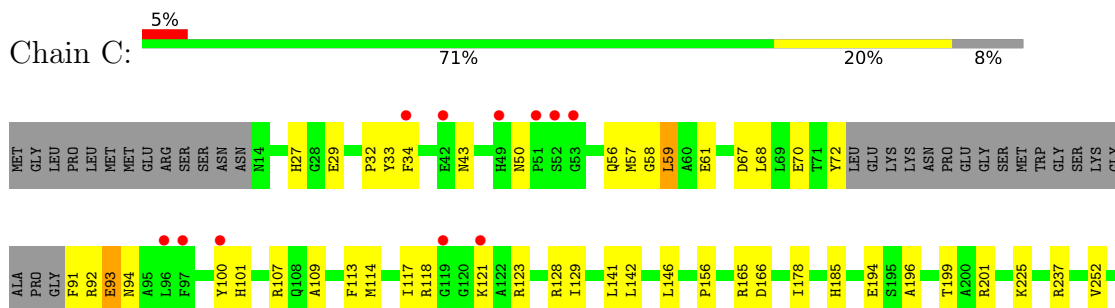
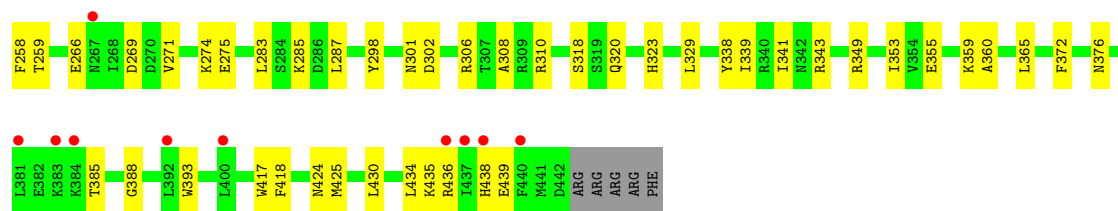- Molecule 1: 1-aminocyclopropane-1-carboxylate synthase 7
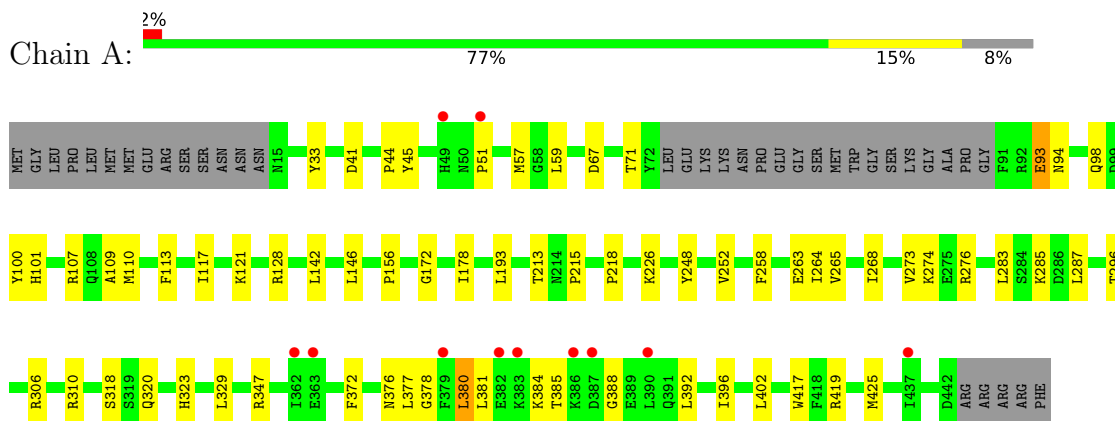
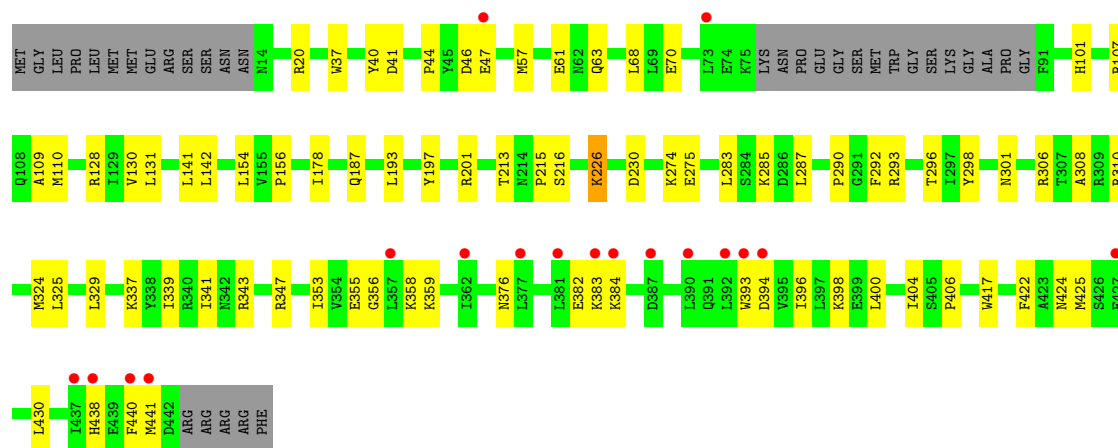- Molecule 1: 1-aminocyclopropane-1-carboxylate synthase 7
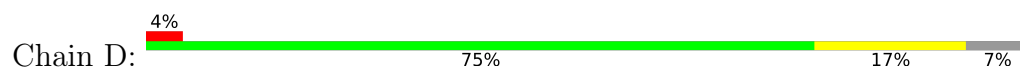

- Molecule 1: 1-aminocyclopropane-1-carboxylate synthase 7

• Molecule 1: 1-aminocyclopropane-1-carboxylate synthase 7

Chain D:
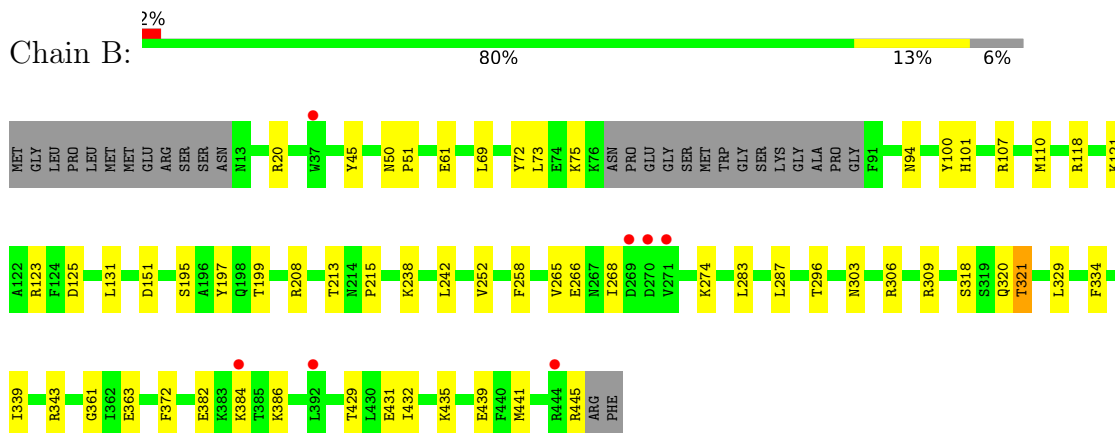
4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	66.88Å 69.35Å 85.40Å 97.70° 94.97° 106.50°	Depositor
Resolution (Å)	45.20 – 2.19 45.20 – 2.19	Depositor EDS
% Data completeness (in resolution range)	95.4 (45.20-2.19) 95.4 (45.20-2.19)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.38 (at 2.18Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.193 , 0.241 0.193 , 0.241	Depositor DCC
R_{free} test set	2142 reflections (3.01%)	wwPDB-VP
Wilson B-factor (Å^2)	42.3	Xtriage
Anisotropy	0.125	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 36.3	EDS
L-test for twinning[2]	$< |L| > = 0.49, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.012 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	13595	wwPDB-VP
Average B, all atoms (Å^2)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.91% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: PPG, SO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$|Z|$>5	RMSZ	#$|Z|$>5
1	A	0.44	0/3338	0.64	0/4518
1	B	0.46	0/3422	0.66	0/4627
1	C	0.44	0/3346	0.66	0/4529
1	D	0.45	0/3372	0.65	0/4563
All	All	0.45	0/13478	0.65	0/18237

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	3270	0	3202	52	0
1	B	3354	0	3296	41	0
1	C	3278	0	3208	60	0
1	D	3304	0	3238	53	0
2	A	26	0	17	2	0
2	B	26	0	17	1	0
2	C	26	0	17	4	0
2	D	26	0	17	0	0
3	A	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	76	0	0	4	0
4	B	81	0	0	2	0
4	C	59	0	0	2	0
4	D	64	0	0	4	0
All	All	13595	0	13012	201	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 (201) 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:C:68:LEU:HD11	1:C:341:ILE:HG21	1.55	0.88
1:A:385:THR:HG23	1:A:388:GLY:H	1.41	0.85
1:C:29:GLU:HA	1:C:34:PHE:HD2	1.42	0.83
1:A:57:MET:HG2	1:A:425:MET:HE1	1.66	0.77
1:A:380:LEU:HD12	1:A:380:LEU:N	1.99	0.76
1:B:361:GLY:HA3	4:B:1113:HOH:O	1.86	0.74
1:C:56:GLN:HE22	1:C:59:LEU:HD12	1.52	0.74
1:C:353:ILE:HD13	1:C:430:LEU:HD11	1.71	0.72
1:B:265:VAL:HG13	1:B:274:LYS:HG2	1.71	0.72
1:C:33:TYR:OH	2:C:1001:PPG:HGI	1.90	0.71
1:A:380:LEU:HD12	1:A:380:LEU:H	1.58	0.69
1:C:57:MET:HG2	1:C:425:MET:HE1	1.73	0.69
1:C:101:HIS:O	1:C:107:ARG:HD3	1.92	0.68
4:C:1101:HOH:O	1:D:20:ARG:HD2	1.92	0.68
1:A:94:ASN:HD21	1:A:323:HIS:CG	2.12	0.67
1:C:29:GLU:HA	1:C:34:PHE:CD2	2.27	0.67
1:B:303:ASN:OD1	1:B:306:ARG:NH2	2.27	0.66
1:A:110:MET:HG2	1:A:296:THR:HG21	1.78	0.64
1:D:110:MET:HG2	1:D:296:THR:HG21	1.77	0.64
1:C:56:GLN:NE2	1:C:59:LEU:HD12	2.11	0.64
1:D:356:GLY:HA2	1:D:359:LYS:HE2	1.80	0.64
1:A:378:GLY:O	1:A:384:LYS:NZ	2.30	0.64
1:B:123:ARG:NH1	1:C:302:ASP:OD2	2.32	0.63
1:A:265:VAL:HG13	1:A:274:LYS:HG2	1.80	0.63
1:A:287:LEU:HD11	1:A:329:LEU:HD11	1.81	0.63
1:C:32:PRO:HB3	1:C:393:TRP:CH2	2.33	0.62
1:A:378:GLY:C	1:A:381:LEU:HD23	2.19	0.62
1:C:355:GLU:O	1:C:359:LYS:HG3	1.99	0.62
1:B:101:HIS:O	1:B:107:ARG:HD3	1.98	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:378:GLY:HA2	1:A:381:LEU:HD23	1.82	0.62
1:A:378:GLY:CA	1:A:381:LEU:HD23	2.30	0.61
1:C:306:ARG:HD3	1:C:310:ARG:CZ	2.30	0.61
1:C:353:ILE:HD12	1:C:434:LEU:HD21	1.83	0.61
1:D:131:LEU:HD23	1:D:296:THR:HG22	1.84	0.60
1:C:91:PHE:N	1:C:93:GLU:OE2	2.34	0.59
1:D:37:TRP:O	1:D:40:TYR:HB3	2.02	0.59
1:C:56:GLN:NE2	1:C:59:LEU:CD1	2.65	0.59
1:B:195:SER:O	1:B:199:THR:HG23	2.02	0.58
1:D:128:ARG:HB2	1:D:298:TYR:CE1	2.39	0.58
1:D:216:SER:HB2	4:D:1139:HOH:O	2.03	0.58
1:A:101:HIS:O	1:A:107:ARG:HD3	2.03	0.58
1:C:320:GLN:NE2	1:D:324:MET:SD	2.77	0.57
1:C:393:TRP:HB2	1:C:418:PHE:HE2	1.68	0.57
1:B:431:GLU:O	1:B:435:LYS:HG2	2.05	0.56
1:B:118:ARG:O	1:B:121:LYS:HG3	2.05	0.56
1:C:58:GLY:HA2	4:C:1131:HOH:O	2.04	0.56
1:C:68:LEU:HD11	1:C:341:ILE:CG2	2.34	0.56
1:D:57:MET:HG2	1:D:425:MET:HE1	1.87	0.56
1:B:110:MET:HG2	1:B:296:THR:HG21	1.87	0.56
1:A:109:ALA:HB1	1:A:329:LEU:HB3	1.88	0.56
1:C:194:GLU:OE2	1:C:237:ARG:NH2	2.38	0.56
1:B:69:LEU:HD23	1:B:334:PHE:HZ	1.71	0.55
1:D:61:GLU:OE1	1:D:285:LYS:NZ	2.40	0.55
1:D:353:ILE:HD12	1:D:430:LEU:HD11	1.88	0.55
1:B:101:HIS:NE2	1:B:309:ARG:NH1	2.54	0.55
1:D:41:ASP:HA	1:D:44:PRO:HG3	1.88	0.55
1:A:98:GLN:NE2	1:B:61:GLU:OE2	2.41	0.54
1:A:264:ILE:O	1:A:268:ILE:HG12	2.07	0.54
1:B:441:MET:O	1:B:445:ARG:HG3	2.08	0.54
1:C:271:VAL:HG22	1:C:274:LYS:HE2	1.88	0.54
1:D:274:LYS:HE2	4:D:1111:HOH:O	2.08	0.54
1:D:396:ILE:HG23	1:D:400:LEU:HD12	1.91	0.53
1:C:118:ARG:O	1:C:121:LYS:HD3	2.08	0.53
1:A:172:GLY:N	4:A:1105:HOH:O	2.41	0.53
1:B:123:ARG:HH12	1:B:125:ASP:HB2	1.74	0.53
1:A:283:LEU:HB3	1:A:287:LEU:HD12	1.90	0.52
1:A:347:ARG:HB3	1:A:347:ARG:HH11	1.74	0.52
1:D:400:LEU:HD21	1:D:440:PHE:HB2	1.91	0.52
1:A:347:ARG:HH11	1:A:347:ARG:CG	2.23	0.52
1:B:363:GLU:HB2	4:B:1150:HOH:O	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:43:ASN:OD1	1:C:50:ASN:ND2	2.42	0.52
1:B:287:LEU:HD11	1:B:329:LEU:HD11	1.91	0.52
1:A:377:LEU:O	1:A:380:LEU:HD13	2.08	0.51
1:C:385:THR:HG23	1:C:388:GLY:H	1.75	0.51
1:A:378:GLY:HA2	1:A:381:LEU:CD2	2.41	0.51
1:D:178:ILE:HD13	1:D:193:LEU:HD23	1.93	0.51
1:B:94:ASN:HD22	1:B:320:GLN:HA	1.76	0.51
1:C:435:LYS:O	1:C:439:GLU:HG3	2.11	0.51
1:B:283:LEU:HD22	1:B:287:LEU:HD12	1.93	0.51
1:C:92:ARG:HB2	1:D:70:GLU:OE2	2.10	0.51
1:A:318:SER:OG	1:B:321:THR:HG21	2.11	0.50
1:B:131:LEU:HD23	1:B:296:THR:HG22	1.93	0.50
1:C:339:ILE:O	1:C:343:ARG:HG3	2.11	0.50
1:D:394:ASP:O	1:D:398:LYS:HG2	2.12	0.50
1:C:72:TYR:CD1	1:C:72:TYR:C	2.85	0.50
1:C:196:ALA:O	1:C:199:THR:OG1	2.27	0.50
1:C:275:GLU:O	1:C:301:ASN:HB2	2.11	0.50
1:A:380:LEU:N	1:A:380:LEU:CD1	2.72	0.50
1:D:306:ARG:HD3	1:D:310:ARG:NH1	2.27	0.50
1:D:63:GLN:NE2	1:D:424:ASN:OD1	2.41	0.50
1:C:318:SER:HB2	4:D:1145:HOH:O	2.11	0.49
1:B:94:ASN:ND2	1:B:320:GLN:HA	2.28	0.49
1:B:268:ILE:O	1:B:274:LYS:HE2	2.13	0.49
1:B:101:HIS:HA	1:B:309:ARG:HD3	1.94	0.48
1:A:252:VAL:HG21	1:A:258:PHE:HB2	1.95	0.48
1:A:113:PHE:CE2	1:A:117:ILE:HD11	2.49	0.48
1:D:275:GLU:O	1:D:301:ASN:HB2	2.14	0.47
1:A:218:PRO:HB3	1:A:419:ARG:HD3	1.97	0.47
1:A:396:ILE:HG22	1:A:402:LEU:HB2	1.96	0.47
1:C:113:PHE:CE2	1:C:117:ILE:HD11	2.50	0.47
1:D:290:PRO:O	1:D:293:ARG:HD2	2.15	0.46
1:A:67:ASP:O	1:A:71:THR:HG23	2.15	0.46
1:A:226:LYS:HB3	1:A:226:LYS:HE2	1.73	0.46
1:C:285:LYS:HZ1	2:C:1001:PPG:HBI	1.80	0.46
1:A:376:ASN:HB2	1:A:417:TRP:CZ3	2.50	0.46
1:B:72:TYR:HD1	1:B:73:LEU:HD23	1.81	0.46
1:C:156:PRO:HA	1:C:178:ILE:HB	1.97	0.46
1:D:376:ASN:HB2	1:D:417:TRP:CZ3	2.50	0.46
1:C:128:ARG:HB2	1:C:298:TYR:CE1	2.51	0.46
1:B:213:THR:HG22	1:B:215:PRO:O	2.16	0.46
1:D:101:HIS:O	1:D:107:ARG:HD3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:347:ARG:CG	1:A:347:ARG:NH1	2.73	0.46
1:D:339:ILE:O	1:D:343:ARG:HG3	2.15	0.46
1:C:360:ALA:HA	1:C:438:HIS:CE1	2.52	0.45
1:A:128:ARG:HD2	4:A:1170:HOH:O	2.16	0.45
1:A:156:PRO:HA	1:A:178:ILE:HB	1.99	0.45
1:A:273:VAL:O	1:A:276:ARG:HG2	2.17	0.45
1:A:347:ARG:NH1	1:A:347:ARG:HG2	2.31	0.45
1:B:20:ARG:NE	1:B:20:ARG:HA	2.31	0.45
1:A:142:LEU:O	1:A:146:LEU:HG	2.16	0.45
1:A:178:ILE:HD13	1:A:193:LEU:HD23	1.98	0.45
1:D:154:LEU:HB3	1:D:178:ILE:HD11	1.98	0.45
1:D:383:LYS:HB3	1:D:384:LYS:H	1.55	0.45
1:C:94:ASN:HD21	1:C:323:HIS:HB2	1.80	0.45
1:D:353:ILE:HD13	1:D:422:PHE:HB3	1.96	0.45
1:D:324:MET:HG3	1:D:325:LEU:N	2.32	0.45
1:A:33:TYR:OH	2:A:1001:PPG:HGI	2.16	0.45
1:B:435:LYS:O	1:B:439:GLU:HB2	2.17	0.45
1:A:377:LEU:HB3	1:A:380:LEU:HD13	1.99	0.45
1:C:27:HIS:ND1	1:C:29:GLU:HG3	2.32	0.45
1:D:283:LEU:HD22	1:D:287:LEU:HD23	1.99	0.45
1:D:57:MET:HG2	1:D:425:MET:CE	2.47	0.44
1:D:393:TRP:NE1	1:D:404:ILE:O	2.44	0.44
1:A:213:THR:HG22	1:A:215:PRO:O	2.17	0.44
1:D:109:ALA:HB1	1:D:329:LEU:HB3	1.99	0.44
1:B:45:TYR:CE1	1:B:51:PRO:HA	2.52	0.44
1:C:109:ALA:HB1	1:C:329:LEU:HB3	1.99	0.44
1:C:360:ALA:HA	1:C:438:HIS:ND1	2.33	0.44
1:A:215:PRO:HG2	1:A:248:TYR:HB2	2.00	0.44
1:D:156:PRO:HA	1:D:178:ILE:HB	2.00	0.44
1:B:123:ARG:NH1	1:B:125:ASP:HB2	2.32	0.44
1:C:376:ASN:HB2	1:C:417:TRP:CZ3	2.53	0.44
1:D:142:LEU:HD23	1:D:142:LEU:HA	1.83	0.44
1:A:380:LEU:H	1:A:380:LEU:CD1	2.26	0.43
1:D:130:VAL:O	1:D:296:THR:HA	2.18	0.43
1:C:320:GLN:HB2	1:D:292:PHE:CE1	2.53	0.43
1:A:121:LYS:HE2	1:A:263:GLU:OE2	2.18	0.43
1:C:61:GLU:HB2	1:C:424:ASN:CG	2.39	0.43
1:C:349:ARG:HD2	1:C:430:LEU:HD22	2.01	0.43
1:C:393:TRP:HB2	1:C:418:PHE:CE2	2.52	0.43
1:D:187:GLN:NE2	4:D:1107:HOH:O	2.37	0.43
1:B:50:ASN:N	1:B:51:PRO:HD3	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:252:VAL:HG11	1:C:258:PHE:HB2	1.99	0.43
2:A:1001:PPG:H4A1	2:A:1001:PPG:H5A1	1.76	0.43
1:B:318:SER:HB3	1:B:321:THR:HG23	2.01	0.43
1:B:429:THR:HA	1:B:432:ILE:HG22	1.99	0.43
1:C:285:LYS:HE3	2:C:1001:PPG:H4A2	1.99	0.43
4:A:1153:HOH:O	1:B:318:SER:HB2	2.18	0.43
1:A:377:LEU:O	1:A:380:LEU:CD1	2.67	0.42
1:C:114:MET:HE1	1:C:129:ILE:CD1	2.49	0.42
1:A:41:ASP:O	1:A:44:PRO:HD3	2.19	0.42
1:B:151:ASP:OD2	1:B:208:ARG:HD3	2.20	0.42
1:B:431:GLU:HG3	1:B:435:LYS:HE2	2.00	0.42
1:D:398:LYS:N	1:D:398:LYS:HD2	2.35	0.42
1:B:252:VAL:HG11	1:B:258:PHE:HB2	2.01	0.42
1:B:339:ILE:O	1:B:343:ARG:HG3	2.19	0.42
1:D:441:MET:HE3	1:D:441:MET:HB3	1.82	0.42
1:C:283:LEU:HD22	1:C:287:LEU:HD12	2.02	0.42
1:A:45:TYR:CE2	1:A:51:PRO:HA	2.55	0.42
1:A:306:ARG:HD3	1:A:310:ARG:CZ	2.49	0.42
1:D:213:THR:HG22	1:D:215:PRO:O	2.20	0.42
1:A:93:GLU:HG2	4:A:1166:HOH:O	2.19	0.42
1:C:165:ARG:HD2	1:C:166:ASP:OD1	2.19	0.42
1:D:61:GLU:OE2	1:D:61:GLU:HA	2.19	0.42
1:D:226:LYS:HE3	1:D:230:ASP:OD2	2.19	0.42
1:D:337:LYS:HB3	1:D:337:LYS:HE2	1.76	0.42
1:C:185:HIS:HB3	1:C:365:LEU:HD11	2.01	0.41
1:D:46:ASP:OD1	1:D:47:GLU:N	2.53	0.41
1:B:197:TYR:CD2	1:B:238:LYS:HE3	2.56	0.41
1:C:225:LYS:HB2	1:C:259:THR:HG21	2.02	0.41
1:D:359:LYS:HB2	1:D:359:LYS:HE3	1.65	0.41
1:B:386:LYS:HE2	1:B:386:LYS:HB3	1.98	0.41
1:C:68:LEU:HD12	1:C:338:TYR:HD1	1.84	0.41
1:D:197:TYR:O	1:D:201:ARG:HG2	2.20	0.41
1:C:68:LEU:HD12	1:C:338:TYR:CD1	2.55	0.41
1:C:141:LEU:HD21	1:C:308:ALA:HA	2.02	0.41
1:C:285:LYS:CE	2:C:1001:PPG:H4A2	2.51	0.41
1:A:320:GLN:OE1	1:B:321:THR:HG22	2.21	0.41
1:A:392:LEU:O	1:A:396:ILE:HD12	2.21	0.41
1:B:101:HIS:HB3	1:B:107:ARG:NH1	2.36	0.41
2:B:1001:PPG:HBI	2:B:1001:PPG:H4A1	1.98	0.41
1:C:271:VAL:HA	1:C:274:LYS:HE2	2.03	0.41
1:D:141:LEU:HD21	1:D:308:ALA:HA	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:248:TYR:CE1	1:A:285:LYS:HG3	2.57	0.40
1:D:306:ARG:HD3	1:D:310:ARG:CZ	2.51	0.40
1:D:393:TRP:NE1	1:D:406:PRO:HD3	2.37	0.40
1:D:393:TRP:CD1	1:D:406:PRO:HD3	2.56	0.40
1:C:142:LEU:O	1:C:146:LEU:HG	2.22	0.40
1:C:67:ASP:OD1	1:C:68:LEU:HD23	2.21	0.40
1:D:37:TRP:CD1	1:D:37:TRP:C	2.94	0.40
1:D:68:LEU:HD11	1:D:341:ILE:HG21	2.02	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	406/447 (91%)	398 (98%)	8 (2%)	0	100	100
1	B	415/447 (93%)	407 (98%)	8 (2%)	0	100	100
1	C	407/447 (91%)	399 (98%)	8 (2%)	0	100	100
1	D	410/447 (92%)	401 (98%)	9 (2%)	0	100	100
All	All	1638/1788 (92%)	1605 (98%)	33 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	359/390 (92%)	354 (99%)	5 (1%)	67	80
1	B	368/390 (94%)	360 (98%)	8 (2%)	52	65
1	C	360/390 (92%)	350 (97%)	10 (3%)	43	56
1	D	363/390 (93%)	357 (98%)	6 (2%)	60	74
All	All	1450/1560 (93%)	1421 (98%)	29 (2%)	55	69

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	59	LEU
1	A	93	GLU
1	A	100	TYR
1	A	372	PHE
1	A	380	LEU
1	B	75	LYS
1	B	100	TYR
1	B	242	LEU
1	B	266	GLU
1	B	321	THR
1	B	372	PHE
1	B	382	GLU
1	B	384	LYS
1	C	59	LEU
1	C	70	GLU
1	C	93	GLU
1	C	100	TYR
1	C	123	ARG
1	C	201	ARG
1	C	266	GLU
1	C	269	ASP
1	C	372	PHE
1	C	436	ARG
1	D	226	LYS
1	D	347	ARG
1	D	355	GLU
1	D	358	LYS
1	D	382	GLU
1	D	438	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	15	ASN
1	A	94	ASN
1	B	267	ASN
1	B	428	ASN
1	C	116	GLN
1	C	204	ASN
1	C	224	GLN
1	D	204	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 ⓘ

There are no monosaccharides in this entry.

5.6　Ligand geometry ⓘ

5 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	$\#|Z| > 2$
3	SO4	A	1002	-	4,4,4	0.56	0	6,6,6	0.11	0
2	PPG	D	1001	-	25,26,26	1.71	4 (16%)	26,35,35	1.60	6 (23%)
2	PPG	C	1001	-	25,26,26	1.70	4 (16%)	26,35,35	1.62	7 (26%)
2	PPG	A	1001	-	25,26,26	1.77	4 (16%)	26,35,35	2.03	7 (26%)
2	PPG	B	1001	-	25,26,26	1.66	4 (16%)	26,35,35	1.46	6 (23%)

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	PPG	D	1001	-	-	11/20/21/21	0/1/1/1
2	PPG	C	1001	-	-	8/20/21/21	0/1/1/1
2	PPG	A	1001	-	-	11/20/21/21	0/1/1/1
2	PPG	B	1001	-	-	11/20/21/21	0/1/1/1

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1001	PPG	CAI-CBC	5.07	1.53	1.48
2	C	1001	PPG	CAI-CBC	4.89	1.53	1.48
2	B	1001	PPG	CAI-CBC	4.68	1.52	1.48
2	D	1001	PPG	CAI-CBC	4.64	1.52	1.48
2	A	1001	PPG	CBI-CAI	3.47	1.54	1.43
2	D	1001	PPG	C3-C2	-3.46	1.37	1.40
2	D	1001	PPG	CBI-CAI	3.27	1.53	1.43
2	A	1001	PPG	C5-C4	-3.13	1.36	1.40
2	B	1001	PPG	CBI-CAI	3.11	1.53	1.43
2	C	1001	PPG	CBI-CAI	2.99	1.52	1.43
2	B	1001	PPG	C5-C4	-2.87	1.36	1.40
2	C	1001	PPG	C5-C4	-2.81	1.36	1.40
2	B	1001	PPG	C3-C2	-2.43	1.38	1.40
2	C	1001	PPG	C3-C2	-2.16	1.38	1.40
2	D	1001	PPG	C5-C4	-2.09	1.37	1.40
2	A	1001	PPG	C3-C2	-2.01	1.38	1.40

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1001	PPG	C6-C5-C4	4.67	121.42	118.12
2	A	1001	PPG	CBC-CAI-N4A	-4.53	116.70	121.84
2	C	1001	PPG	C6-C5-C4	3.81	120.82	118.12
2	A	1001	PPG	C4A-C4-C5	-3.74	115.21	119.73
2	D	1001	PPG	CBC-CAI-N4A	-3.52	117.85	121.84
2	C	1001	PPG	CBC-CAI-N4A	-3.25	118.16	121.84
2	B	1001	PPG	C6-C5-C4	3.24	120.41	118.12
2	A	1001	PPG	OP4-C5A-C5	-3.14	103.37	109.35
2	A	1001	PPG	C5-C6-N1	-3.10	118.65	123.82
2	A	1001	PPG	O3B-CBC-CAI	3.08	118.49	113.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	1001	PPG	O3B-CBC-CAI	2.97	118.31	113.42
2	D	1001	PPG	O3-C3-C4	2.70	126.06	118.13
2	D	1001	PPG	C4A-C4-C5	-2.68	116.49	119.73
2	C	1001	PPG	O3B-CBC-CAI	2.65	117.79	113.42
2	B	1001	PPG	O3B-CBC-CAI	2.62	117.73	113.42
2	D	1001	PPG	C6-C5-C4	2.56	119.93	118.12
2	C	1001	PPG	C5-C6-N1	-2.51	119.64	123.82
2	B	1001	PPG	O3-C3-C4	2.48	125.41	118.13
2	B	1001	PPG	C4A-C4-C5	-2.39	116.84	119.73
2	C	1001	PPG	C4A-C4-C5	-2.38	116.86	119.73
2	B	1001	PPG	CBC-CAI-N4A	-2.34	119.19	121.84
2	C	1001	PPG	O3-C3-C4	2.33	124.95	118.13
2	D	1001	PPG	C5-C6-N1	-2.25	120.07	123.82
2	C	1001	PPG	C2A-C2-C3	-2.24	118.12	120.89
2	B	1001	PPG	C5-C6-N1	-2.09	120.34	123.82
2	A	1001	PPG	O3-C3-C4	2.04	124.11	118.13

There are no chirality outliers.

All (41) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1001	PPG	C3-C4-C4A-N4A
2	A	1001	PPG	C5-C4-C4A-N4A
2	A	1001	PPG	C5A-OP4-P-OP1
2	A	1001	PPG	C5A-OP4-P-OP2
2	A	1001	PPG	C5A-OP4-P-OP3
2	A	1001	PPG	N4A-CAI-CBI-CGI
2	A	1001	PPG	CBC-CAI-CBI-CGI
2	B	1001	PPG	C3-C4-C4A-N4A
2	B	1001	PPG	C5-C4-C4A-N4A
2	B	1001	PPG	C5A-OP4-P-OP2
2	B	1001	PPG	C5A-OP4-P-OP3
2	B	1001	PPG	N4A-CAI-CBC-O3B
2	B	1001	PPG	CBI-CAI-CBC-O2B
2	B	1001	PPG	CBI-CAI-CBC-O3B
2	B	1001	PPG	CBI-CGI-OET-CEI
2	C	1001	PPG	C3-C4-C4A-N4A
2	C	1001	PPG	C5-C4-C4A-N4A
2	C	1001	PPG	C5A-OP4-P-OP1
2	C	1001	PPG	C5A-OP4-P-OP2
2	C	1001	PPG	C5A-OP4-P-OP3
2	C	1001	PPG	CBI-CGI-OET-CEI

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Mol	Chain	Res	Type	Atoms
2	C	1001	PPG	OET-CEI-CFI-NI
2	D	1001	PPG	C3-C4-C4A-N4A
2	D	1001	PPG	C5-C4-C4A-N4A
2	D	1001	PPG	C5A-OP4-P-OP2
2	D	1001	PPG	C5A-OP4-P-OP3
2	D	1001	PPG	N4A-CAI-CBC-O3B
2	D	1001	PPG	CBI-CAI-CBC-O2B
2	D	1001	PPG	CBI-CAI-CBC-O3B
2	D	1001	PPG	CBI-CGI-OET-CEI
2	D	1001	PPG	OET-CEI-CFI-NI
2	A	1001	PPG	CFI-CEI-OET-CGI
2	B	1001	PPG	C5A-OP4-P-OP1
2	D	1001	PPG	C5A-OP4-P-OP1
2	B	1001	PPG	CBC-CAI-CBI-CGI
2	A	1001	PPG	C4-C5-C5A-OP4
2	B	1001	PPG	N4A-CAI-CBC-O2B
2	C	1001	PPG	N4A-CAI-CBC-O2B
2	D	1001	PPG	N4A-CAI-CBC-O2B
2	A	1001	PPG	OET-CEI-CFI-NI
2	A	1001	PPG	C6-C5-C5A-OP4

There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1001	PPG	4	0
2	A	1001	PPG	2	0
2	B	1001	PPG	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 then 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.

Ligand PPG D 1001

Bond lengths

Bond angles

Torsions

Rings

Ligand PPG C 1001

Bond lengths

Bond angles

Torsions

Rings

Ligand PPG A 1001

Bond lengths

Bond angles

Torsions

Rings

Ligand PPG B 1001

Bond lengths

Bond angles

Torsions

Rings
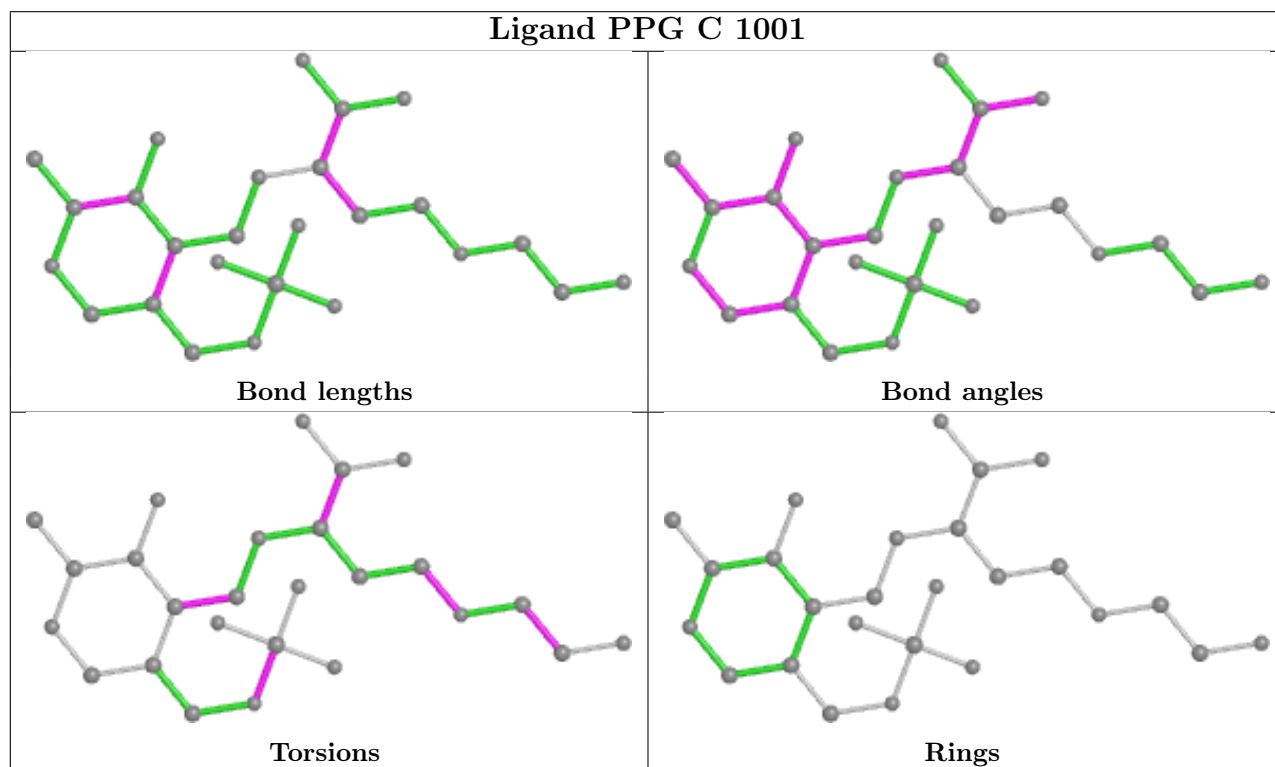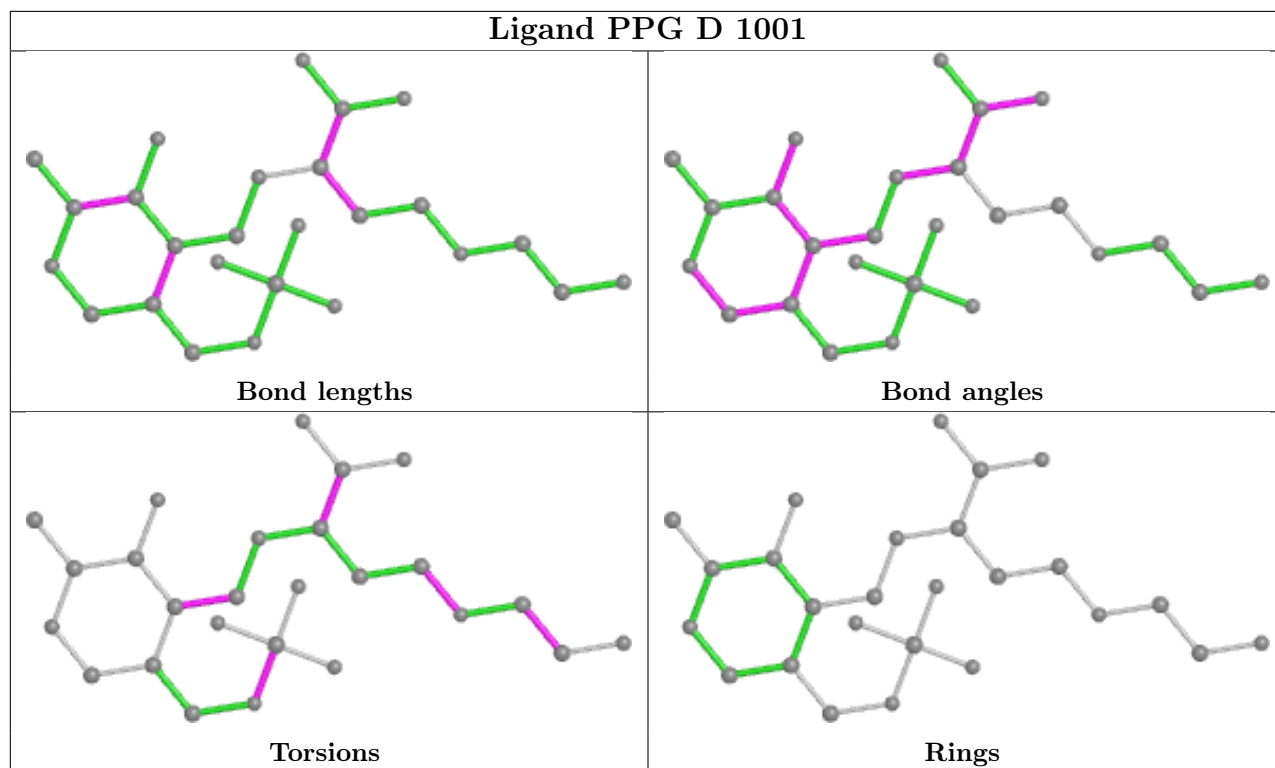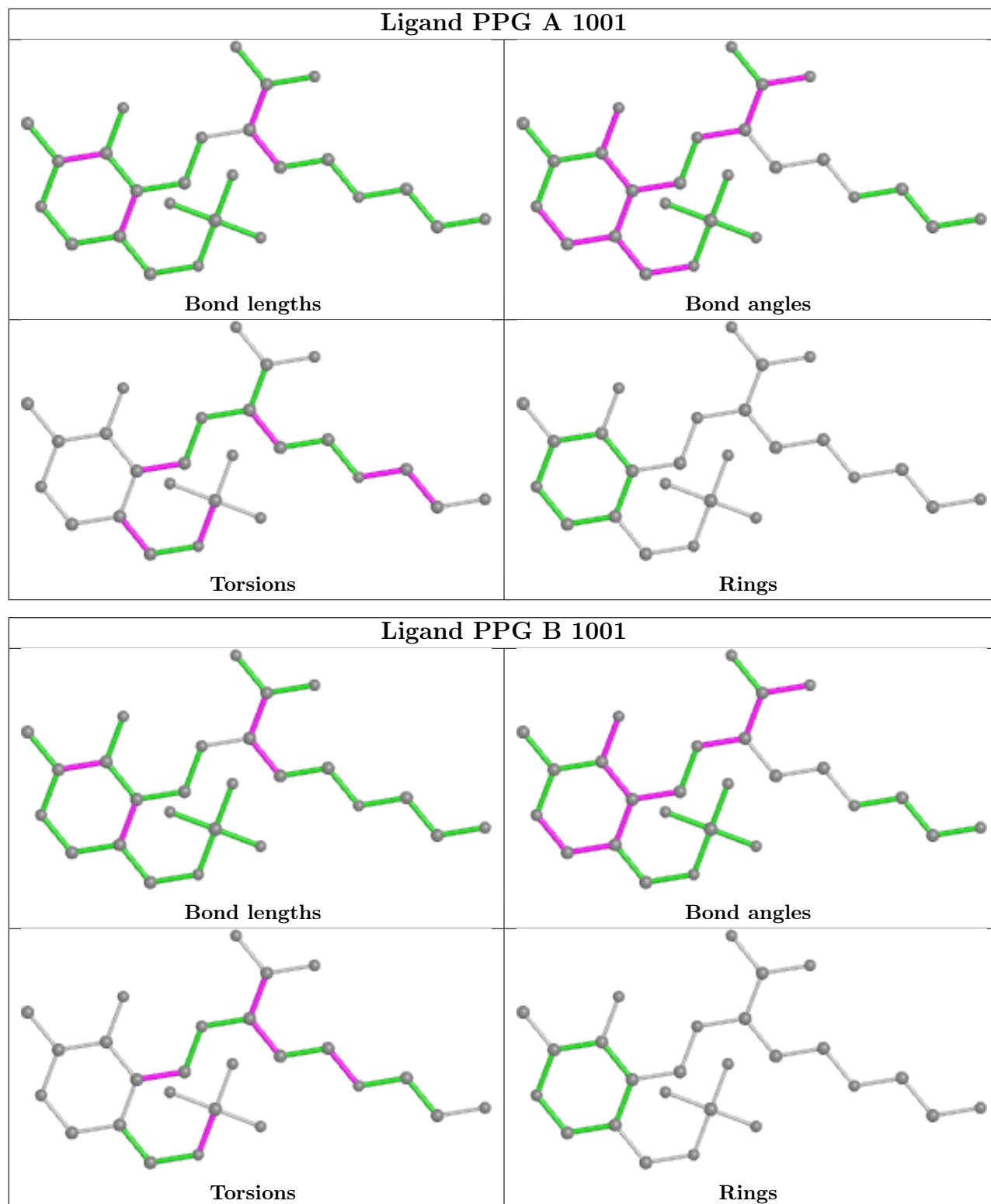
5.7　Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	410/447 (91%)	0.07	11 (2%)	54	52	28, 46, 66, 90	0
1	B	419/447 (93%)	-0.05	7 (1%)	70	68	29, 44, 64, 78	0
1	C	411/447 (91%)	0.26	21 (5%)	28	26	33, 51, 77, 91	0
1	D	414/447 (92%)	0.24	18 (4%)	35	33	33, 50, 78, 96	0
All	All	1654/1788 (92%)	0.13	57 (3%)	45	43	28, 48, 74, 96	0

All (57) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	440	PHE	5.0
1	B	271	VAL	4.9
1	D	383	LYS	4.3
1	C	49	HIS	4.3
1	D	357	LEU	4.2
1	C	400	LEU	3.9
1	C	383	LYS	3.7
1	A	386	LYS	3.7
1	C	384	LYS	3.7
1	D	441	MET	3.6
1	A	382	GLU	3.5
1	C	96	LEU	3.5
1	C	51	PRO	3.5
1	A	49	HIS	3.2
1	C	121	LYS	3.2
1	D	390	LEU	3.2
1	A	379	PHE	3.1
1	C	34	PHE	3.1
1	D	384	LYS	3.1
1	A	387	ASP	3.0
1	D	393	TRP	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	52	SER	3.0
1	D	381	LEU	3.0
1	A	383	LYS	2.9
1	B	269	ASP	2.9
1	C	119	GLY	2.9
1	D	438	HIS	2.9
1	C	42	GLU	2.8
1	D	437	ILE	2.7
1	B	392	LEU	2.7
1	D	394	ASP	2.7
1	B	444	ARG	2.7
1	A	362	ILE	2.7
1	C	97	PHE	2.6
1	D	47	GLU	2.6
1	C	392	LEU	2.6
1	D	392	LEU	2.4
1	C	267	ASN	2.4
1	C	440	PHE	2.4
1	A	51	PRO	2.4
1	B	384	LYS	2.4
1	B	37	TRP	2.4
1	D	73	LEU	2.3
1	D	377	LEU	2.3
1	C	436	ARG	2.3
1	A	363	GLU	2.3
1	C	53	GLY	2.3
1	C	100	TYR	2.3
1	D	387	ASP	2.3
1	A	437	ILE	2.2
1	B	270	ASP	2.2
1	C	437	ILE	2.1
1	D	362	ILE	2.1
1	C	381	LEU	2.0
1	D	427	GLU	2.0
1	C	438	HIS	2.0
1	A	390	LEU	2.0

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

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

6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

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
3	SO4	A	1002	5/5	0.84	0.16	59,63,68,84	0
2	PPG	B	1001	26/26	0.96	0.13	28,37,54,61	0
2	PPG	C	1001	26/26	0.96	0.14	32,39,61,71	0
2	PPG	D	1001	26/26	0.96	0.15	35,41,63,66	0
2	PPG	A	1001	26/26	0.96	0.15	31,40,63,69	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.
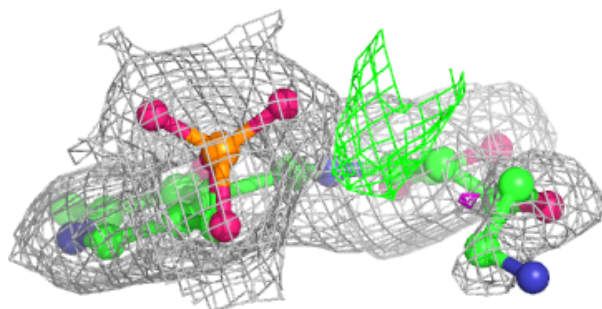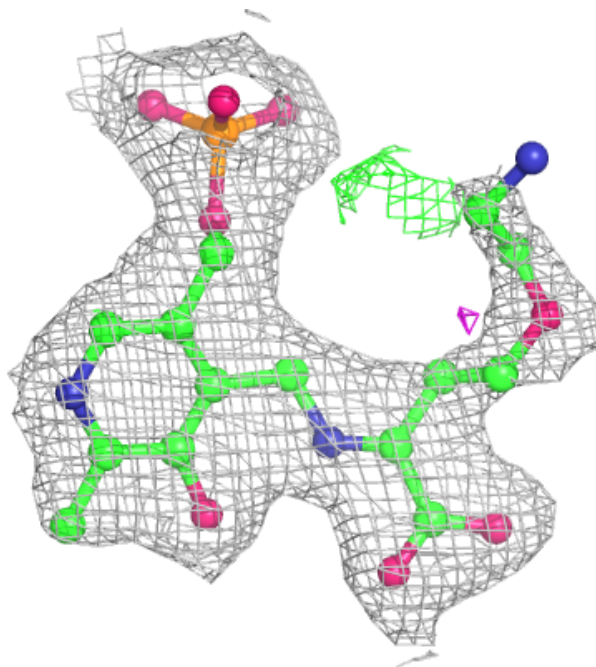
Electron density around PPG B 1001:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)
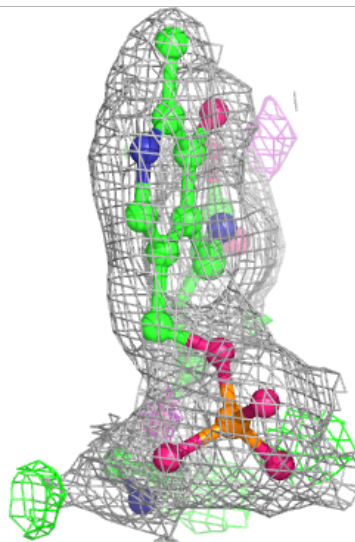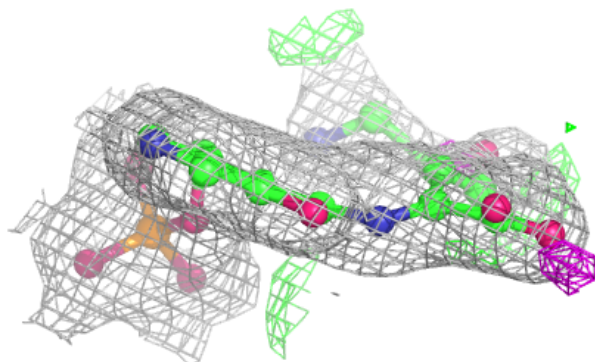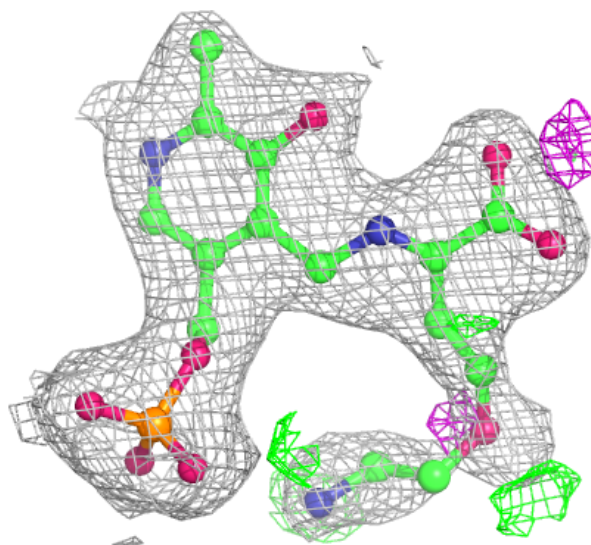
Electron density around PPG C 1001:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
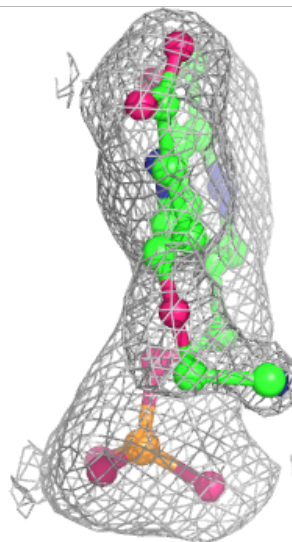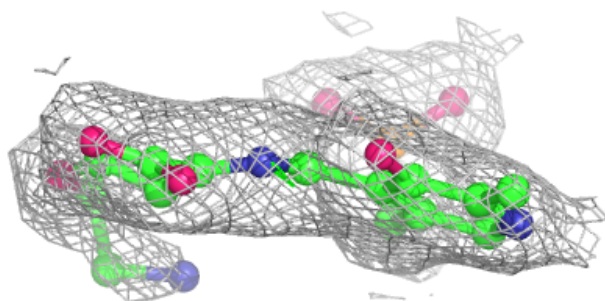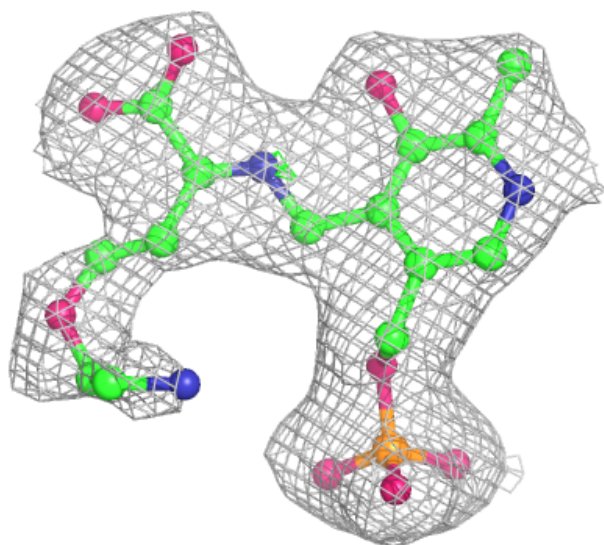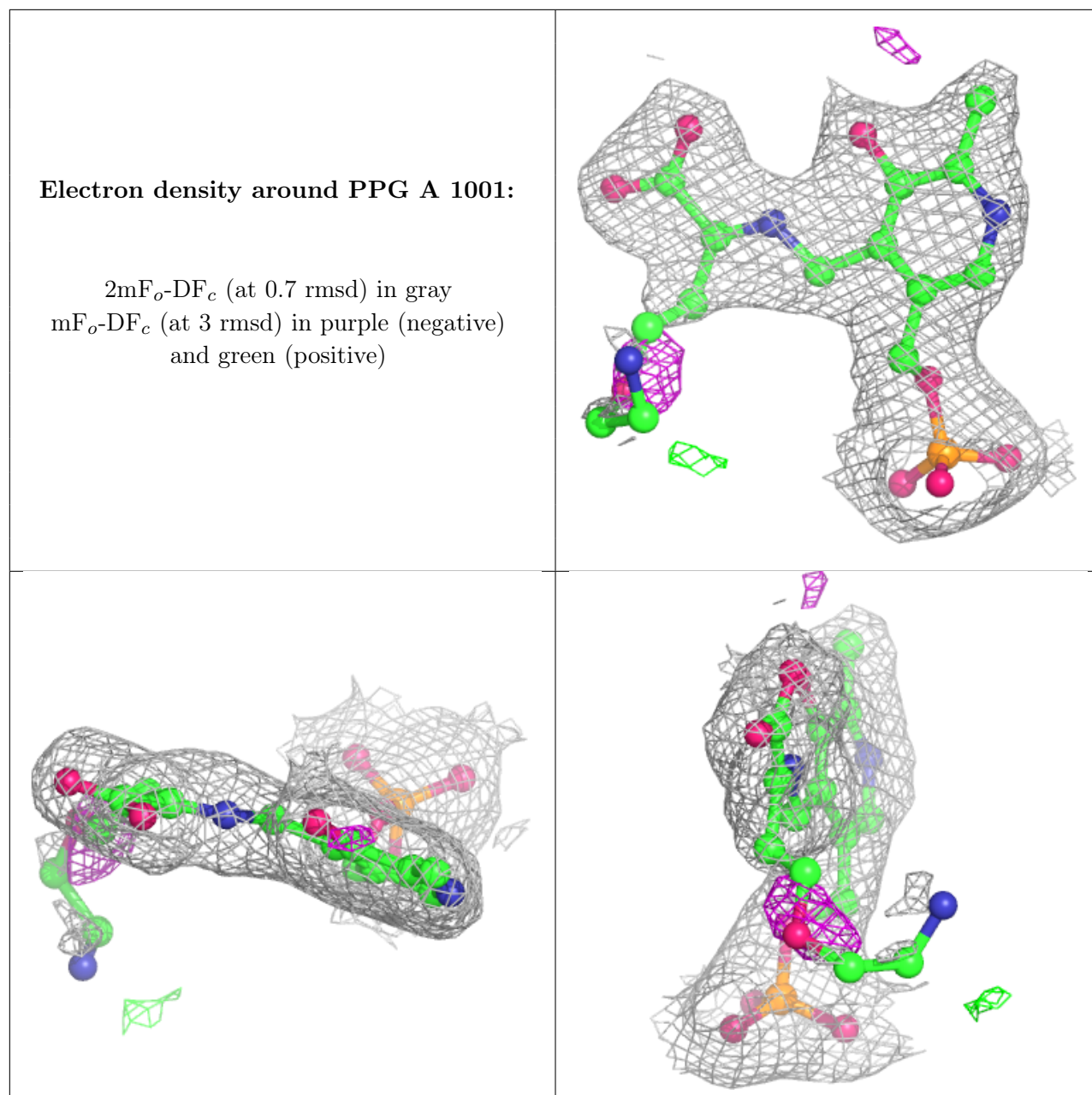$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)
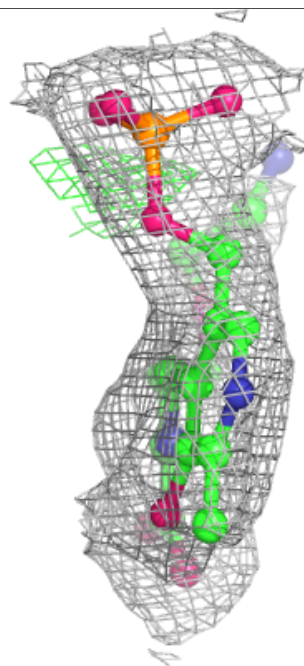
Electron density around PPG D 1001:

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

Electron density around PPG A 1001:

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

6.5　Other polymers ⓘ

There are no such residues in this entry.