



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 10:54 AM UTC

PDB ID : 4B98 / pdb_00004b98
Title : The structure of the omega aminotransferase from Pseudomonas aeruginosa
Authors : Sayer, C.; Isupov, M.N.; Westlake, A.; Littlechild, J.A.
Deposited on : 2012-09-03
Resolution : 1.65 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

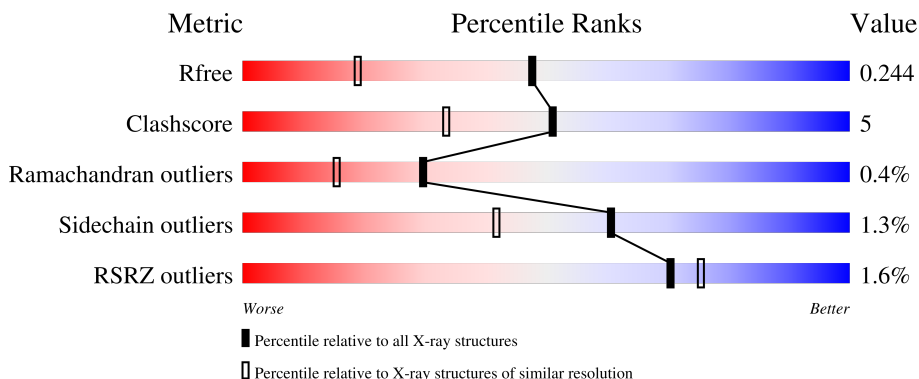
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.65 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	2563 (1.66-1.66)
Clashscore	190562	2662 (1.66-1.66)
Ramachandran outliers	187476	2621 (1.66-1.66)
Sidechain outliers	187428	2621 (1.66-1.66)
RSRZ outliers	180081	2564 (1.66-1.66)

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	448	2% 92% 7%
1	B	448	% 90% 8%
1	C	448	2% 91% 7%
1	D	448	2% 86% 12%

2 Entry composition [i](#)

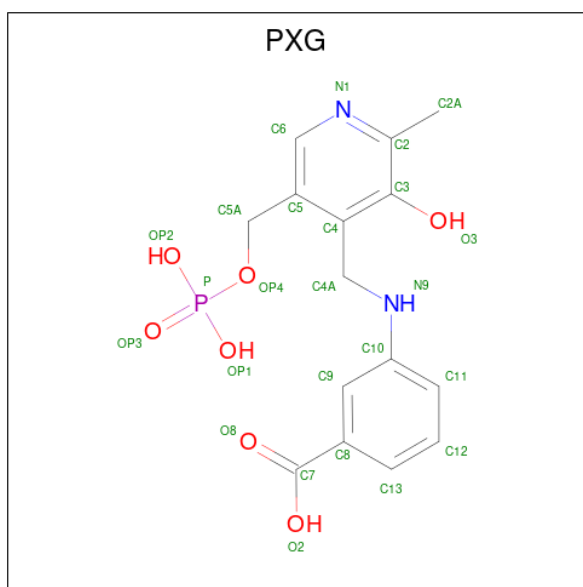
There are 6 unique types of molecules in this entry. The entry contains 15751 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 BETA-ALANINE--PYRUVATE TRANSAMINASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	441	Total	C	N	O	S	0	24	0
			3497	2224	612	643	18			
1	B	440	Total	C	N	O	S	0	27	0
			3503	2228	615	643	17			
1	C	441	Total	C	N	O	S	0	25	0
			3504	2229	615	641	19			
1	D	441	Total	C	N	O	S	0	27	0
			3511	2232	615	646	18			

- Molecule 2 is 3-[O-PHOSPHONOPYRIDOXYL]--AMINO-BENZOIC ACID (CCD ID: PXG) (formula: C₁₅H₁₇N₂O₇P).



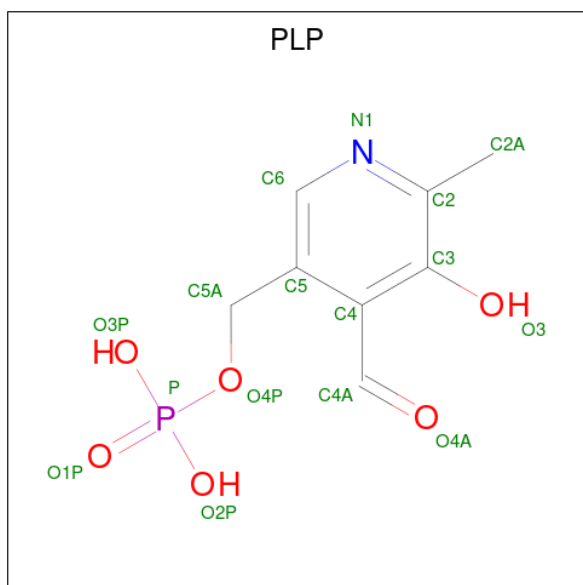
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	1
			50	30	4	14	2		
2	B	1	Total	C	N	O	P	0	1
			50	30	4	14	2		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	N	O	P	0	1
			50	30	4	14	2		
2	D	1	Total	C	N	O	P	0	1
			50	30	4	14	2		

- Molecule 3 is PYRIDOXAL-5'-PHOSPHATE (CCD ID: PLP) (formula: $C_8H_{10}NO_6P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			16	8	1	6	1		
3	B	1	Total	C	N	O	P	0	0
			16	8	1	6	1		
3	C	1	Total	C	N	O	P	0	0
			16	8	1	6	1		
3	D	1	Total	C	N	O	P	0	0
			16	8	1	6	1		

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Ca	0	0
			1	1		
4	B	1	Total	Ca	0	0
			1	1		

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Cl 1 1	0	0
5	B	1	Total Cl 1 1	0	0
5	C	1	Total Cl 1 1	0	0
5	D	1	Total Cl 1 1	0	0

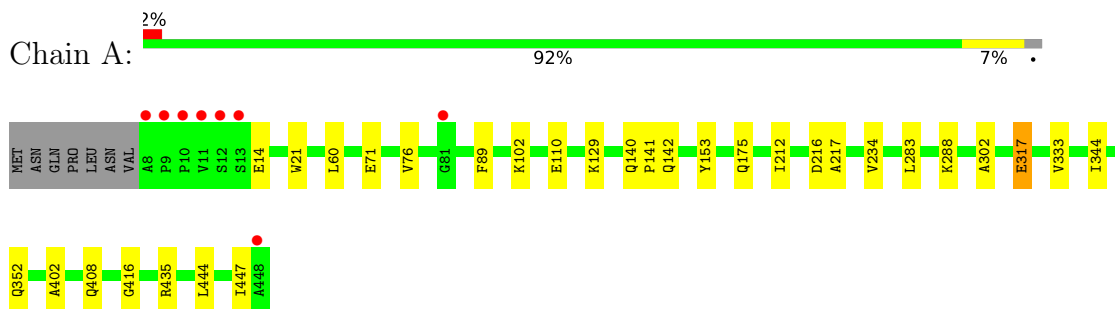
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	410	Total O 410 410	0	0
6	B	367	Total O 367 367	0	0
6	C	390	Total O 390 390	0	0
6	D	299	Total O 299 299	0	0

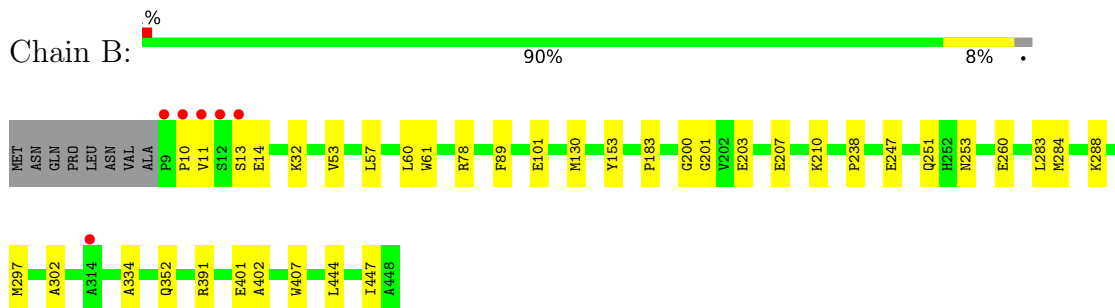
3 Residue-property plots [i](#)

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.

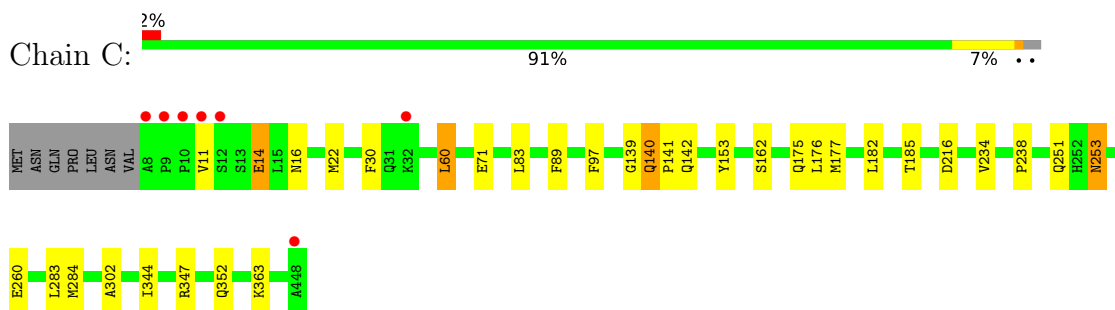
• Molecule 1: BETA-ALANINE--PYRUVATE TRANSAMINASE



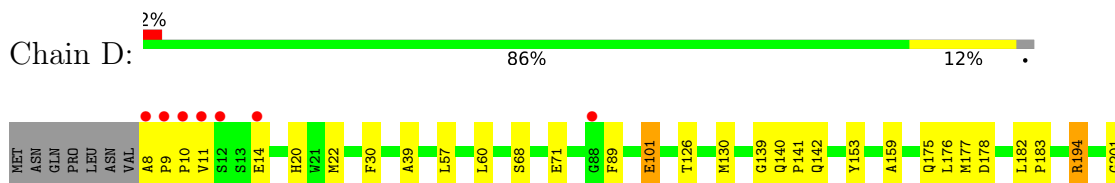
• Molecule 1: BETA-ALANINE--PYRUVATE TRANSAMINASE



• Molecule 1: BETA-ALANINE--PYRUVATE TRANSAMINASE



• Molecule 1: BETA-ALANINE--PYRUVATE TRANSAMINASE





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	119.23Å 192.47Å 77.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	71.72 – 1.65 71.72 – 1.65	Depositor EDS
% Data completeness (in resolution range)	98.8 (71.72-1.65) 98.8 (71.72-1.65)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.79 (at 1.65Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.220 , 0.260 (Not available) , 0.244	Depositor DCC
R_{free} test set	10593 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	17.1	Xtriage
Anisotropy	0.698	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 37.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	15751	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 82.44 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.7898e-07. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: CL, PLP, CA, PXG

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	0.58	0/3641	0.80	1/4927 (0.0%)
1	B	0.58	0/3662	0.81	0/4952
1	C	0.57	0/3651	0.80	0/4940
1	D	0.56	0/3664	0.82	0/4956
All	All	0.57	0/14618	0.81	1/19775 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	129	LYS	N-CA-C	-5.95	104.87	111.36

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3497	0	3502	25	0
1	B	3503	0	3523	38	0
1	C	3504	0	3518	38	0
1	D	3511	0	3524	41	0
2	A	50	0	26	10	0
2	B	50	0	26	10	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	50	0	26	8	0
2	D	50	0	26	7	0
3	A	16	0	7	1	0
3	B	16	0	7	1	0
3	C	16	0	7	1	0
3	D	16	0	7	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
6	A	410	0	0	5	0
6	B	367	0	0	4	0
6	C	390	0	0	5	0
6	D	299	0	0	5	0
All	All	15751	0	14199	149	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 5.

All (149) 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:C:470[B]:PXG:H12	1:D:89:PHE:CE2	1.77	1.19
1:C:363[B]:LYS:NZ	1:C:363[B]:LYS:HB2	1.53	1.15
2:C:470[B]:PXG:H12	1:D:89:PHE:HE2	0.94	1.05
1:B:210[B]:LYS:HB2	1:B:210[B]:LYS:HZ2	1.18	1.04
1:B:210[B]:LYS:CB	1:B:210[B]:LYS:NZ	2.19	1.04
1:B:210[B]:LYS:HB2	1:B:210[B]:LYS:NZ	1.76	0.95
1:C:363[B]:LYS:HB2	1:C:363[B]:LYS:HZ2	1.18	0.91
1:B:210[B]:LYS:HB3	1:B:210[B]:LYS:HZ3	1.33	0.90
1:C:363[B]:LYS:NZ	1:C:363[B]:LYS:CB	2.34	0.90
1:B:210[B]:LYS:CB	1:B:210[B]:LYS:HZ3	1.85	0.87
1:C:347[A]:ARG:HG2	1:C:347[A]:ARG:HH11	1.43	0.84
1:A:89:PHE:CE2	2:B:470[B]:PXG:H12	2.13	0.83
1:C:140[B]:GLN:HG2	1:C:142[B]:GLN:HE22	1.41	0.83
2:C:470[B]:PXG:C12	1:D:89:PHE:HE2	1.86	0.83
1:C:363[B]:LYS:HB2	1:C:363[B]:LYS:HZ3	1.41	0.81
1:A:402:ALA:HB2	1:A:447[A]:ILE:HD11	1.64	0.79
2:A:470[B]:PXG:C12	1:B:89:PHE:HE2	1.95	0.79

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:402:ALA:HB2	1:D:447[B]:ILE:HD11	1.64	0.79
1:C:177[B]:MET:HB3	1:D:176[B]:LEU:O	1.83	0.78
1:A:110[B]:GLU:HG3	6:A:2316:HOH:O	1.84	0.76
1:A:140:GLN:HB3	1:A:142[B]:GLN:HE22	1.51	0.73
1:C:14[B]:GLU:HA	1:C:14[B]:GLU:OE1	1.89	0.72
1:A:142[B]:GLN:NE2	6:A:2155:HOH:O	2.23	0.71
1:C:352[B]:GLN:HE21	1:C:352[B]:GLN:H	1.39	0.69
1:A:317[A]:GLU:H	1:A:317[A]:GLU:CD	2.01	0.68
1:C:140[B]:GLN:HA	1:C:142[B]:GLN:NE2	2.08	0.68
2:C:470[A]:PXG:H12	6:C:2062:HOH:O	1.95	0.66
1:C:363[B]:LYS:CB	1:C:363[B]:LYS:HZ3	2.05	0.66
1:B:78[A]:ARG:HG2	1:B:78[A]:ARG:HH11	1.60	0.66
1:B:402:ALA:HB2	1:B:447[A]:ILE:HD11	1.79	0.64
2:D:470[A]:PXG:H12	6:D:2122:HOH:O	1.95	0.64
2:A:470[A]:PXG:O3	2:A:470[A]:PXG:N9	2.30	0.64
1:C:347[A]:ARG:HG2	1:C:347[A]:ARG:NH1	2.14	0.63
1:D:251[A]:GLN:HG3	6:D:2198:HOH:O	1.98	0.63
2:A:470[B]:PXG:H12	1:B:89:PHE:HE2	1.64	0.62
1:B:101[B]:GLU:HA	1:B:101[B]:GLU:OE1	2.00	0.61
1:C:182:LEU:HD22	6:C:2234:HOH:O	1.99	0.61
1:C:176[B]:LEU:O	1:D:177[B]:MET:HG2	2.01	0.61
2:A:470[A]:PXG:H12	1:B:89:PHE:CE2	2.36	0.60
2:B:470[A]:PXG:H12	6:B:2041:HOH:O	2.02	0.59
3:B:501:PLP:H2A2	6:B:2366:HOH:O	2.02	0.59
1:A:435:ARG:NH2	6:A:2396:HOH:O	2.36	0.58
2:C:470[B]:PXG:O3	2:C:470[B]:PXG:N9	2.36	0.58
1:C:140[B]:GLN:HA	1:C:142[B]:GLN:HE22	1.68	0.58
2:B:470[B]:PXG:O3	2:B:470[B]:PXG:N9	2.36	0.57
1:A:89:PHE:HE2	2:B:470[B]:PXG:H12	1.69	0.57
2:D:470[B]:PXG:O3	2:D:470[B]:PXG:N9	2.35	0.57
1:D:201:GLY:HA2	1:D:238:PRO:HG2	1.88	0.56
1:A:402:ALA:HB2	1:A:447[A]:ILE:CD1	2.35	0.56
1:B:200:GLY:O	1:B:203[A]:GLU:HG3	2.06	0.55
1:D:60:LEU:HD13	2:D:470[B]:PXG:H12	1.89	0.54
1:D:126:THR:O	1:D:130[A]:MET:HG3	2.08	0.54
1:A:71:GLU:HB2	1:A:344:ILE:HD11	1.90	0.54
1:D:10:PRO:HB2	1:D:14[A]:GLU:HB3	1.90	0.54
1:A:89:PHE:HE2	2:B:470[B]:PXG:C12	2.21	0.54
1:D:359:PRO:O	1:D:363[B]:LYS:HG2	2.08	0.53
1:B:247:GLU:O	1:B:251[A]:GLN:HG2	2.08	0.53
1:D:71:GLU:HB2	1:D:344:ILE:HD11	1.90	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:470[B]:PXG:H12	1:B:89:PHE:CE2	2.42	0.53
1:A:60:LEU:HD13	2:A:470[A]:PXG:H12	1.89	0.53
1:B:402:ALA:HB2	1:B:447[A]:ILE:CD1	2.38	0.53
1:C:260:GLU:HG3	1:C:284:MET:HG3	1.91	0.53
2:D:470[A]:PXG:O3	2:D:470[A]:PXG:N9	2.43	0.52
1:C:71:GLU:HB2	1:C:344:ILE:HD11	1.91	0.52
1:C:11:VAL:HG12	1:C:14[A]:GLU:HG2	1.90	0.51
1:C:89:PHE:CE2	2:D:470[B]:PXG:H12	2.45	0.51
1:C:16:ASN:HD22	1:D:101[A]:GLU:CD	2.19	0.51
1:A:89:PHE:CE2	2:B:470[B]:PXG:C12	2.89	0.50
1:D:297:MET:HE3	1:D:334:ALA:HB1	1.93	0.49
1:A:444:LEU:HA	1:A:447[A]:ILE:HD12	1.94	0.49
1:D:159:ALA:HA	1:D:177[A]:MET:SD	2.52	0.49
1:D:260:GLU:HG3	1:D:284:MET:HG3	1.94	0.49
1:A:21:TRP:CZ3	1:B:130[A]:MET:HE3	2.47	0.49
1:B:210[B]:LYS:HE3	6:B:2210:HOH:O	2.11	0.49
2:B:470[A]:PXG:O3	2:B:470[A]:PXG:N9	2.46	0.49
2:A:470[B]:PXG:N9	2:A:470[B]:PXG:O3	2.46	0.48
1:B:183:PRO:HG3	1:B:207:GLU:HG3	1.94	0.48
1:D:11:VAL:HG22	1:D:14[B]:GLU:HG2	1.96	0.48
1:D:405[A]:LYS:HG2	6:D:2281:HOH:O	2.14	0.48
1:B:78[A]:ARG:HG2	1:B:78[A]:ARG:NH1	2.27	0.48
1:D:183:PRO:HG3	1:D:207:GLU:HG3	1.94	0.48
1:D:182:LEU:HD22	6:D:2172:HOH:O	2.14	0.48
1:D:11:VAL:CG2	1:D:14[B]:GLU:HG2	2.44	0.47
1:B:444:LEU:HA	1:B:447[A]:ILE:HD12	1.96	0.47
2:C:470[A]:PXG:N9	2:C:470[A]:PXG:O3	2.46	0.47
1:C:153:TYR:HE2	2:C:470[B]:PXG:H4A1	1.79	0.47
1:B:251[A]:GLN:NE2	1:B:251[A]:GLN:HA	2.30	0.47
1:D:194[A]:ARG:HD3	6:D:2152:HOH:O	2.14	0.47
1:B:61:TRP:HE1	2:B:470[B]:PXG:C7	2.28	0.46
1:A:153:TYR:HE2	2:A:470[A]:PXG:H4A1	1.79	0.46
3:C:501:PLP:H4A	6:C:2389:HOH:O	2.16	0.45
6:C:2089:HOH:O	1:D:68[A]:SER:HB2	2.17	0.45
1:D:283:LEU:HD23	1:D:302:ALA:HA	1.99	0.45
1:B:130[A]:MET:HE2	1:B:130[A]:MET:HB3	1.84	0.45
1:C:11:VAL:CG1	1:C:14[A]:GLU:HG2	2.46	0.45
1:D:140:GLN:N	1:D:141:PRO:HD3	2.31	0.45
1:D:139:GLY:C	1:D:141:PRO:HD3	2.42	0.44
1:B:283:LEU:HD23	1:B:302:ALA:HA	1.99	0.44
1:A:76:VAL:HG13	1:A:333:VAL:HG13	1.99	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:57:LEU:HD23	1:D:60:LEU:HA	1.98	0.44
2:A:470[A]:PXG:C12	1:B:89:PHE:CE2	3.00	0.44
1:B:201:GLY:HA2	1:B:238:PRO:HG2	2.00	0.44
1:A:283:LEU:HD23	1:A:302:ALA:HA	2.00	0.44
1:B:153:TYR:HE2	2:B:470[B]:PXG:H4A1	1.82	0.44
1:C:283:LEU:HD23	1:C:302:ALA:HA	1.99	0.43
1:B:130[A]:MET:HE1	1:B:302:ALA:HB2	2.00	0.43
1:C:60:LEU:HD11	2:C:470[B]:PXG:C13	2.48	0.43
1:A:14[A]:GLU:HA	1:A:14[A]:GLU:OE1	2.18	0.43
1:B:210[B]:LYS:CE	6:B:2210:HOH:O	2.66	0.43
1:A:141:PRO:CG	1:C:142[B]:GLN:HG3	2.49	0.43
1:D:243:GLN:HE21	1:D:279:VAL:HG22	1.84	0.43
1:D:345:LEU:HA	1:D:350:LEU:HD12	1.99	0.43
1:B:260:GLU:HG3	1:B:284:MET:HG3	2.01	0.43
1:B:32:LYS:HE3	1:B:32:LYS:HB3	1.71	0.43
1:C:22:MET:HE1	1:C:30:PHE:CD1	2.54	0.42
1:C:162:SER:OG	1:C:177[B]:MET:HG3	2.19	0.42
1:B:10:PRO:HB2	1:B:14:GLU:HB2	2.01	0.42
1:C:139:GLY:C	1:C:141:PRO:HD3	2.44	0.42
1:C:140[B]:GLN:HG2	1:C:142[B]:GLN:NE2	2.22	0.42
1:A:416:GLY:HA3	6:A:2273:HOH:O	2.19	0.42
1:C:185:THR:HB	1:C:238:PRO:HD3	2.01	0.42
3:A:501:PLP:H4A	6:A:2278:HOH:O	2.19	0.42
1:B:57:LEU:HD23	1:B:60:LEU:HA	2.01	0.42
1:D:226:GLU:HG2	2:D:470[B]:PXG:H2A3	2.02	0.42
1:D:22:MET:HE1	1:D:30:PHE:CD1	2.55	0.42
1:A:212:ILE:HG23	1:A:217:ALA:HB2	2.02	0.42
1:B:402:ALA:CB	1:B:447[A]:ILE:HD11	2.49	0.41
1:C:253[A]:ASN:HD22	1:C:253[A]:ASN:HA	1.66	0.41
1:D:153:TYR:HE2	2:D:470[B]:PXG:H4A1	1.85	0.41
1:C:97:PHE:CD1	1:D:20:HIS:HB3	2.55	0.41
1:D:352[B]:GLN:HE21	1:D:352[B]:GLN:HB2	1.65	0.41
1:B:53:VAL:HG11	1:B:407:TRP:CZ3	2.55	0.41
1:D:142[B]:GLN:HE21	1:D:142[B]:GLN:HB2	1.68	0.41
1:A:142[B]:GLN:HB3	1:C:141:PRO:HB3	2.02	0.41
1:B:391[A]:ARG:NH2	1:B:401:GLU:OE1	2.52	0.41
1:C:11:VAL:HG12	1:C:14[A]:GLU:CG	2.50	0.41
1:C:83:LEU:HB2	1:D:39:ALA:HA	2.03	0.41
1:B:297:MET:HE3	1:B:334:ALA:HB1	2.03	0.41
2:A:470[B]:PXG:H4A1	2:A:470[B]:PXG:H11	1.78	0.40
1:D:8:ALA:HA	1:D:9:PRO:HD3	1.95	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:142[B]:GLN:H	1:A:142[B]:GLN:CD	2.28	0.40
1:B:352[A]:GLN:NE2	1:B:352[A]:GLN:HA	2.37	0.40
1:A:89:PHE:HE2	2:B:470[A]:PXE:C12	2.34	0.40
1:C:251[A]:GLN:HG3	6:C:2262:HOH:O	2.22	0.40
1:C:347[A]:ARG:NH1	1:C:347[A]:ARG:CG	2.84	0.40
1:D:402:ALA:HB2	1:D:447[B]:ILE:CD1	2.44	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	463/448 (103%)	448 (97%)	12 (3%)	3 (1%)	21	8
1	B	465/448 (104%)	447 (96%)	17 (4%)	1 (0%)	43	27
1	C	464/448 (104%)	445 (96%)	17 (4%)	2 (0%)	30	15
1	D	466/448 (104%)	449 (96%)	16 (3%)	1 (0%)	43	27
All	All	1858/1792 (104%)	1789 (96%)	62 (3%)	7 (0%)	30	15

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	288	LYS
1	C	216	ASP
1	D	216	ASP
1	A	216	ASP
1	B	288	LYS
1	C	234	VAL
1	A	234	VAL

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	367/350 (105%)	359 (98%)	8 (2%)	45	23
1	B	370/350 (106%)	366 (99%)	4 (1%)	65	48
1	C	368/350 (105%)	359 (98%)	9 (2%)	43	20
1	D	370/350 (106%)	362 (98%)	8 (2%)	45	23
All	All	1475/1400 (105%)	1446 (98%)	29 (2%)	61	26

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

Mol	Chain	Res	Type
1	A	102	LYS
1	A	175[A]	GLN
1	A	175[B]	GLN
1	A	317[A]	GLU
1	A	317[B]	GLU
1	A	352[A]	GLN
1	A	352[B]	GLN
1	A	408	GLN
1	B	11	VAL
1	B	13	SER
1	B	253[A]	ASN
1	B	253[B]	ASN
1	C	14[A]	GLU
1	C	14[B]	GLU
1	C	60	LEU
1	C	140[A]	GLN
1	C	140[B]	GLN
1	C	175[A]	GLN
1	C	175[B]	GLN
1	C	253[A]	ASN
1	C	253[B]	ASN
1	D	101[A]	GLU
1	D	101[B]	GLU
1	D	175	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	194[A]	ARG
1	D	194[B]	ARG
1	D	429	ARG
1	D	431[A]	GLU
1	D	431[B]	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	73	GLN
1	A	373	ASN
1	B	31	GLN
1	B	73	GLN
1	B	353	GLN
1	B	373	ASN
1	C	16	ASN
1	C	29	ASN
1	C	79	GLN
1	C	409	GLN
1	D	73	GLN
1	D	79	GLN
1	D	98	GLN
1	D	243	GLN
1	D	313	GLN
1	D	349	ASN
1	D	353	GLN
1	D	373	ASN
1	D	409	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 18 ligands modelled in this entry, 6 are monoatomic - leaving 12 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	PLP	C	501	-	16,16,16	2.74	3 (18%)	20,23,23	1.67	5 (25%)
2	PXG	D	470[B]	-	26,26,26	0.74	0	36,37,37	0.96	2 (5%)
2	PXG	A	470[B]	-	26,26,26	0.70	0	36,37,37	0.95	2 (5%)
2	PXG	D	470[A]	-	26,26,26	0.75	0	36,37,37	0.91	2 (5%)
2	PXG	B	470[B]	-	26,26,26	0.76	0	36,37,37	0.93	2 (5%)
2	PXG	A	470[A]	-	26,26,26	0.73	0	36,37,37	0.92	1 (2%)
2	PXG	C	470[B]	-	26,26,26	0.72	0	36,37,37	0.89	2 (5%)
2	PXG	B	470[A]	-	26,26,26	0.75	0	36,37,37	1.05	4 (11%)
3	PLP	D	501	-	16,16,16	2.79	3 (18%)	20,23,23	1.72	4 (20%)
2	PXG	C	470[A]	-	26,26,26	0.69	0	36,37,37	0.98	3 (8%)
3	PLP	A	501	-	16,16,16	2.74	3 (18%)	20,23,23	1.83	4 (20%)
3	PLP	B	501	-	16,16,16	2.70	3 (18%)	20,23,23	1.71	4 (20%)

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	PLP	C	501	-	-	2/8/8/8	0/1/1/1
2	PXG	D	470[B]	-	-	6/15/15/15	0/2/2/2
2	PXG	A	470[B]	-	-	7/15/15/15	0/2/2/2
2	PXG	D	470[A]	-	-	3/15/15/15	0/2/2/2
2	PXG	B	470[B]	-	-	4/15/15/15	0/2/2/2
2	PXG	A	470[A]	-	-	6/15/15/15	0/2/2/2
2	PXG	C	470[B]	-	-	3/15/15/15	0/2/2/2
2	PXG	B	470[A]	-	-	7/15/15/15	0/2/2/2

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PLP	D	501	-	-	2/8/8/8	0/1/1/1
2	PXG	C	470[A]	-	-	7/15/15/15	0/2/2/2
3	PLP	A	501	-	-	2/8/8/8	0/1/1/1
3	PLP	B	501	-	-	2/8/8/8	0/1/1/1

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	501	PLP	C3-C2	8.02	1.49	1.41
3	B	501	PLP	C3-C2	7.70	1.49	1.41
3	A	501	PLP	C3-C2	7.65	1.48	1.41
3	C	501	PLP	C3-C2	7.38	1.48	1.41
3	C	501	PLP	C4-C5	5.56	1.49	1.42
3	A	501	PLP	C4-C5	5.51	1.49	1.42
3	D	501	PLP	C4-C5	5.39	1.49	1.42
3	B	501	PLP	C4-C5	5.24	1.49	1.42
3	C	501	PLP	C4-C3	4.88	1.49	1.41
3	D	501	PLP	C4-C3	4.78	1.49	1.41
3	B	501	PLP	C4-C3	4.56	1.48	1.41
3	A	501	PLP	C4-C3	4.53	1.48	1.41

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	501	PLP	C4-C3-C2	-4.67	117.51	120.14
3	D	501	PLP	C4-C3-C2	-4.46	117.63	120.14
3	A	501	PLP	C4-C3-C2	-4.41	117.66	120.14
3	C	501	PLP	C4-C3-C2	-4.14	117.81	120.14
3	A	501	PLP	O4P-C5A-C5	3.29	115.52	109.36
2	D	470[B]	PXG	C6-C5-C4	3.04	120.36	118.06
2	C	470[A]	PXG	C6-C5-C4	2.95	120.29	118.06
2	B	470[A]	PXG	C6-C5-C4	2.90	120.25	118.06
3	C	501	PLP	O4P-C5A-C5	2.73	114.47	109.36
3	D	501	PLP	O4P-C5A-C5	2.73	114.47	109.36
3	A	501	PLP	C6-N1-C2	2.57	123.86	119.20
3	D	501	PLP	C6-N1-C2	2.53	123.79	119.20
3	C	501	PLP	C6-N1-C2	2.50	123.72	119.20
3	B	501	PLP	C6-N1-C2	2.50	123.72	119.20
2	D	470[B]	PXG	C5-C6-N1	-2.45	119.85	123.83
2	B	470[A]	PXG	C5-C6-N1	-2.43	119.88	123.83
3	B	501	PLP	O4A-C4A-C4	-2.38	119.16	124.80

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	470[B]	PXG	C5-C6-N1	-2.32	120.05	123.83
2	C	470[B]	PXG	C6-C5-C4	2.32	119.82	118.06
2	C	470[A]	PXG	C5-C6-N1	-2.30	120.09	123.83
3	D	501	PLP	O4P-P-O1P	-2.27	100.31	106.44
3	C	501	PLP	O3P-P-O2P	2.24	116.19	107.80
2	D	470[A]	PXG	C5-C6-N1	-2.22	120.22	123.83
2	A	470[B]	PXG	O2-C7-C8	2.19	120.45	114.84
2	C	470[A]	PXG	C4A-C4-C3	2.18	122.88	119.98
3	B	501	PLP	O3P-P-O2P	2.17	115.95	107.80
3	C	501	PLP	O2P-P-O4P	-2.17	101.02	106.67
2	B	470[B]	PXG	C5-C6-N1	-2.14	120.36	123.83
2	D	470[A]	PXG	OP2-P-OP4	-2.12	101.13	106.67
3	A	501	PLP	O4A-C4A-C4	-2.06	119.91	124.80
2	B	470[A]	PXG	O2-C7-C8	2.06	120.13	114.84
2	B	470[B]	PXG	O2-C7-C8	2.05	120.11	114.84
2	B	470[A]	PXG	C4A-C4-C3	2.03	122.68	119.98
2	A	470[A]	PXG	C5-C6-N1	-2.02	120.55	123.83
2	A	470[B]	PXG	OP1-P-OP4	-2.02	101.41	106.67

There are no chirality outliers.

All (51) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	470[A]	PXG	C5-C4-C4A-N9
2	A	470[B]	PXG	C5-C4-C4A-N9
2	B	470[A]	PXG	C5-C4-C4A-N9
2	B	470[B]	PXG	C5-C4-C4A-N9
2	C	470[A]	PXG	C5-C4-C4A-N9
2	C	470[B]	PXG	C5-C4-C4A-N9
2	D	470[A]	PXG	C5-C4-C4A-N9
2	D	470[B]	PXG	C5-C4-C4A-N9
3	B	501	PLP	C3-C4-C4A-O4A
3	D	501	PLP	C3-C4-C4A-O4A
2	A	470[A]	PXG	O8-C7-C8-C9
2	A	470[A]	PXG	O8-C7-C8-C13
2	A	470[A]	PXG	O2-C7-C8-C13
2	A	470[A]	PXG	O2-C7-C8-C9
3	B	501	PLP	C5-C4-C4A-O4A
2	A	470[B]	PXG	C4-C4A-N9-C10
2	B	470[A]	PXG	C4-C4A-N9-C10
3	A	501	PLP	C3-C4-C4A-O4A
3	C	501	PLP	C3-C4-C4A-O4A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
3	A	501	PLP	C5-C4-C4A-O4A
2	D	470[B]	PXG	O2-C7-C8-C13
2	D	470[A]	PXG	C4-C4A-N9-C10
2	D	470[B]	PXG	O8-C7-C8-C13
2	C	470[A]	PXG	C4-C4A-N9-C10
2	D	470[B]	PXG	O2-C7-C8-C9
2	D	470[B]	PXG	O8-C7-C8-C9
2	B	470[B]	PXG	C9-C10-N9-C4A
2	A	470[A]	PXG	C3-C4-C4A-N9
2	A	470[B]	PXG	C3-C4-C4A-N9
2	B	470[A]	PXG	C3-C4-C4A-N9
2	B	470[B]	PXG	C3-C4-C4A-N9
2	C	470[A]	PXG	C3-C4-C4A-N9
2	C	470[B]	PXG	C3-C4-C4A-N9
2	D	470[A]	PXG	C3-C4-C4A-N9
2	D	470[B]	PXG	C3-C4-C4A-N9
2	B	470[B]	PXG	C11-C10-N9-C4A
2	C	470[A]	PXG	O2-C7-C8-C13
2	C	470[A]	PXG	O8-C7-C8-C13
3	D	501	PLP	C5-C4-C4A-O4A
2	C	470[A]	PXG	O2-C7-C8-C9
2	A	470[B]	PXG	O2-C7-C8-C13
2	A	470[B]	PXG	O2-C7-C8-C9
2	C	470[A]	PXG	O8-C7-C8-C9
2	A	470[B]	PXG	O8-C7-C8-C13
2	A	470[B]	PXG	O8-C7-C8-C9
2	C	470[B]	PXG	C4-C4A-N9-C10
2	B	470[A]	PXG	O8-C7-C8-C9
3	C	501	PLP	C5-C4-C4A-O4A
2	B	470[A]	PXG	O2-C7-C8-C9
2	B	470[A]	PXG	O2-C7-C8-C13
2	B	470[A]	PXG	O8-C7-C8-C13

There are no ring outliers.

11 monomers are involved in 38 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	501	PLP	1	0
2	D	470[B]	PXG	5	0
2	A	470[B]	PXG	5	0
2	D	470[A]	PXG	2	0
2	B	470[B]	PXG	7	0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	470[A]	PXG	5	0
2	C	470[B]	PXG	6	0
2	B	470[A]	PXG	3	0
2	C	470[A]	PXG	2	0
3	A	501	PLP	1	0
3	B	501	PLP	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.

Ligand PXG D 470 (B)

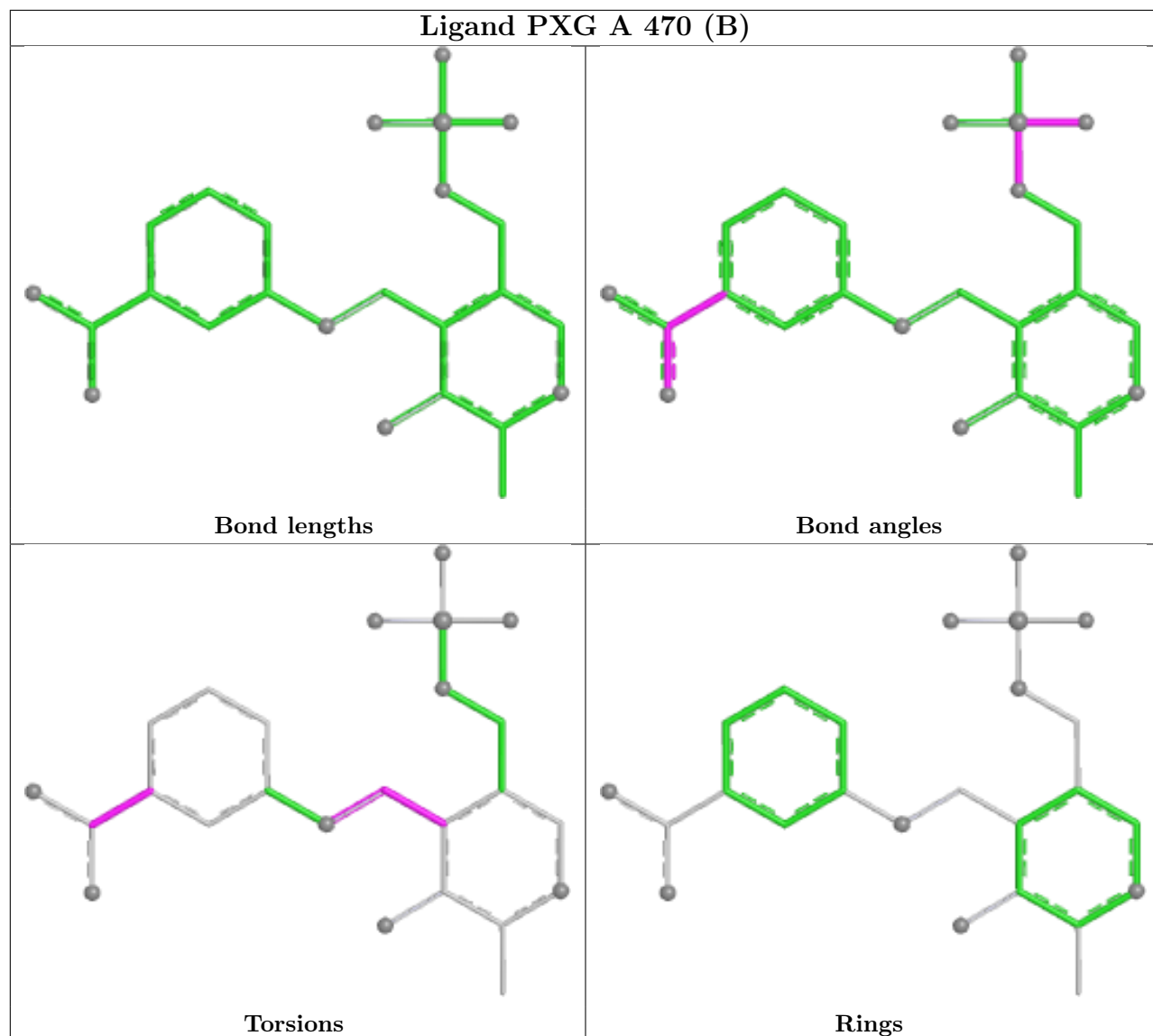
Bond lengths

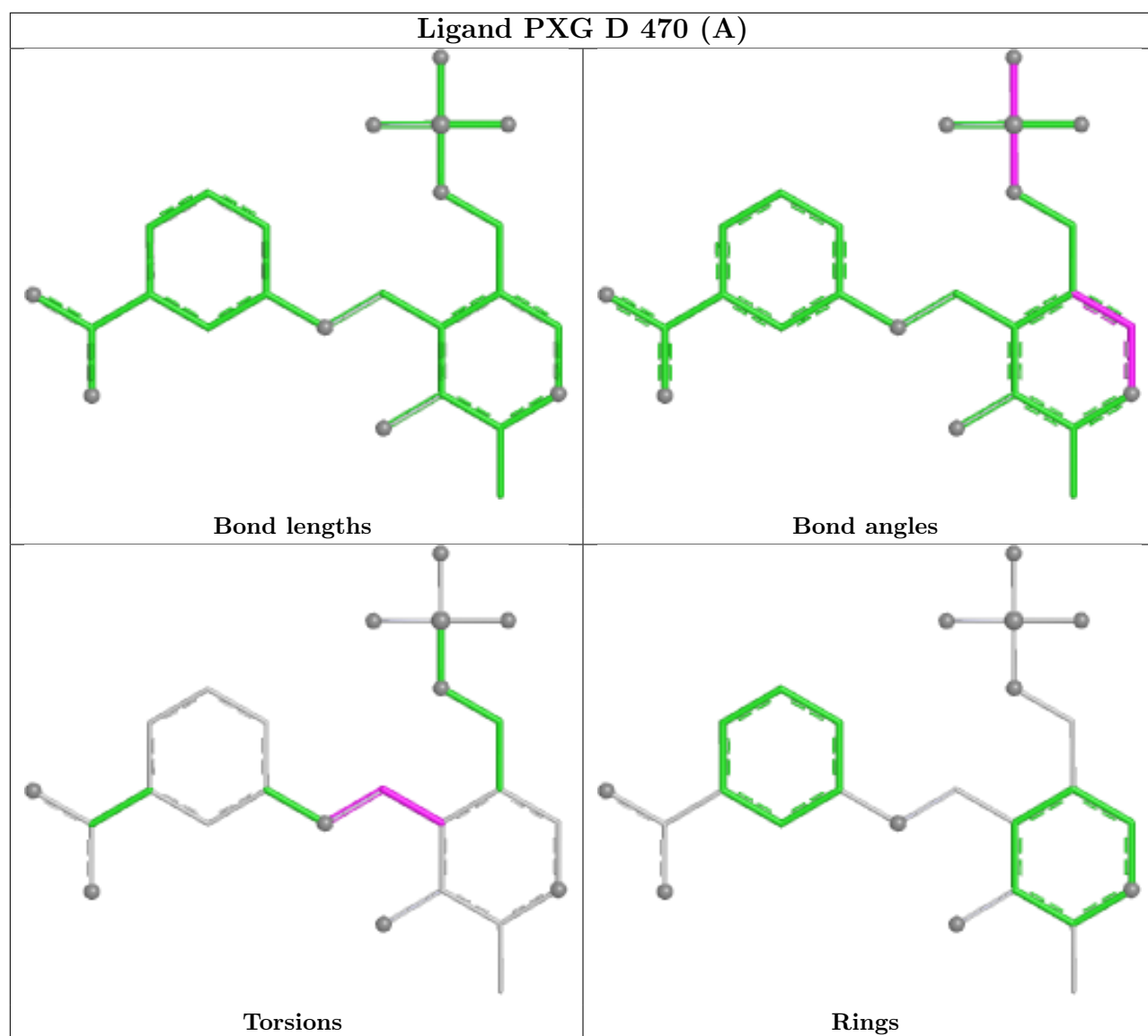
Bond angles

Torsions

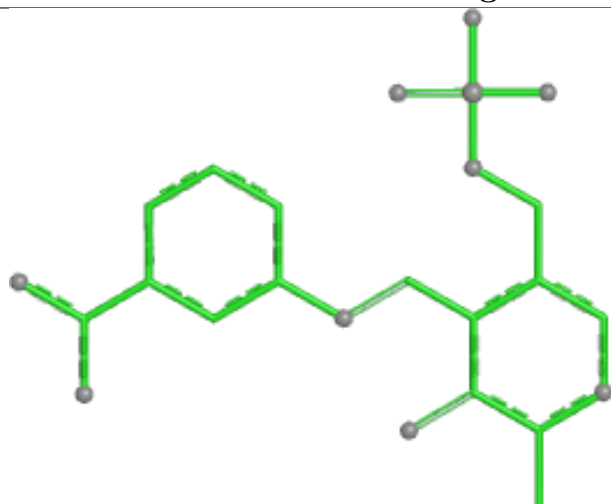
Rings

Ligand PXG A 470 (B)

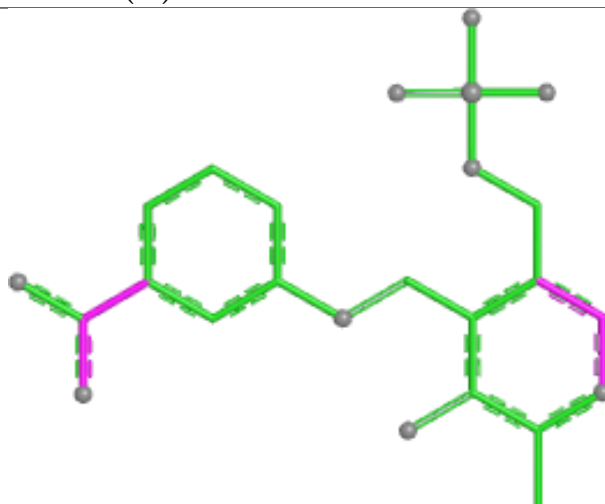




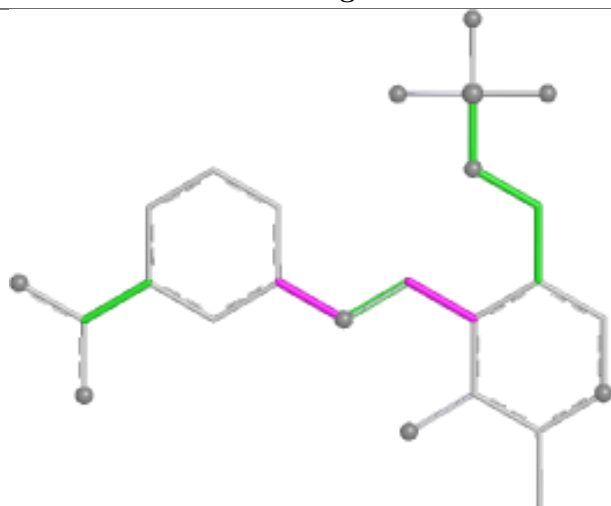
Ligand PXG B 470 (B)



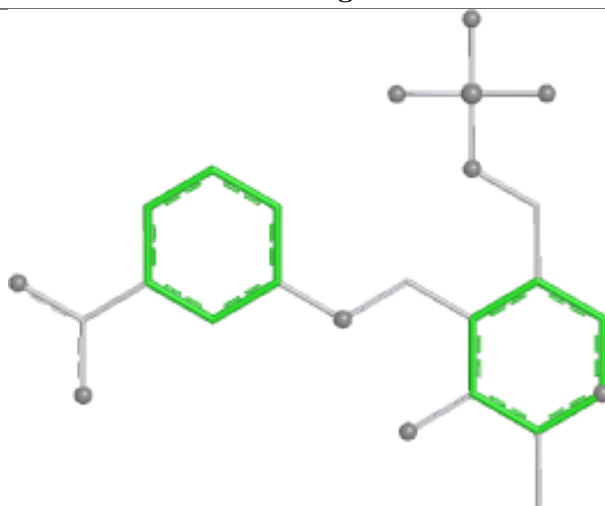
Bond lengths



Bond angles

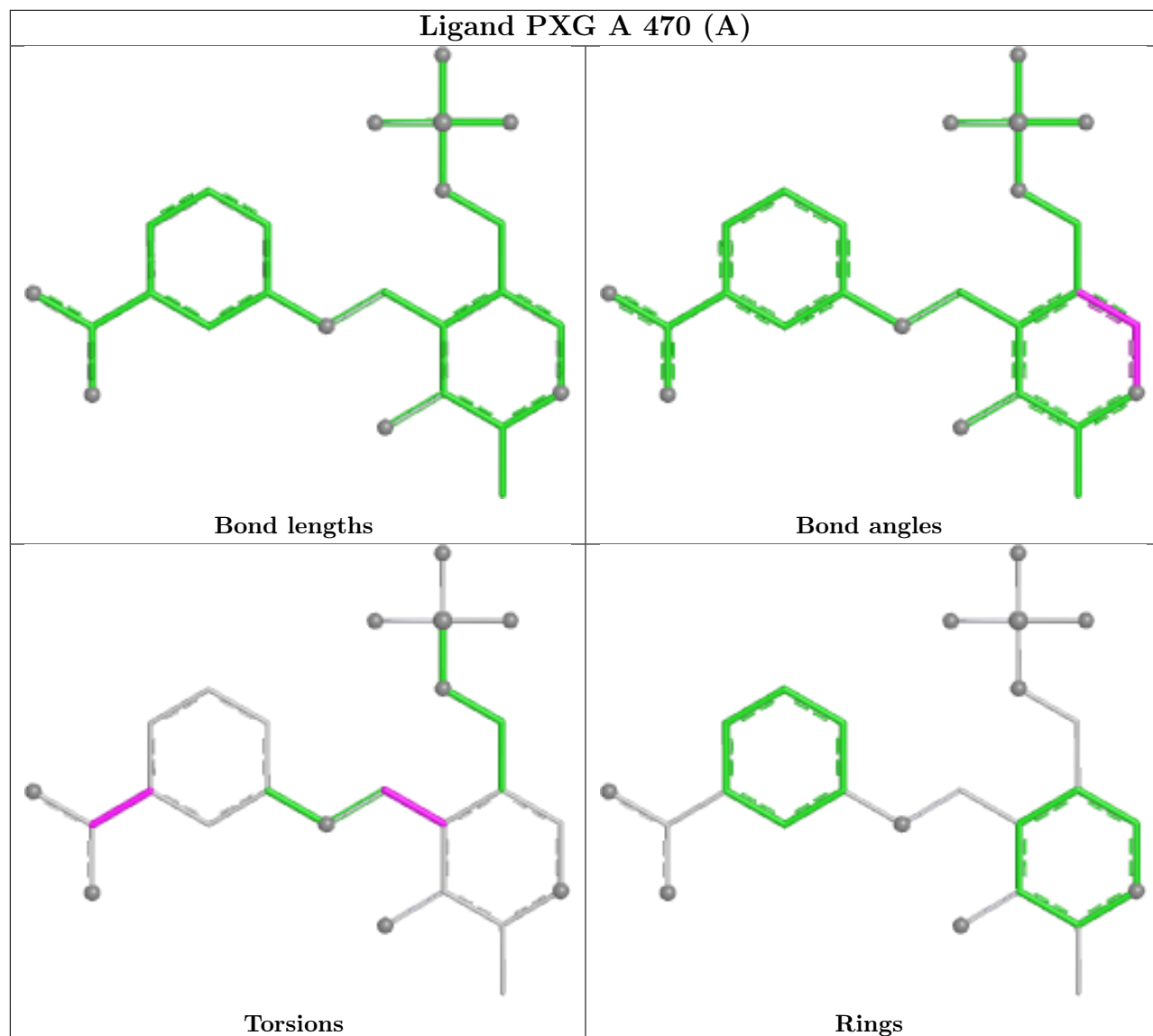


Torsions

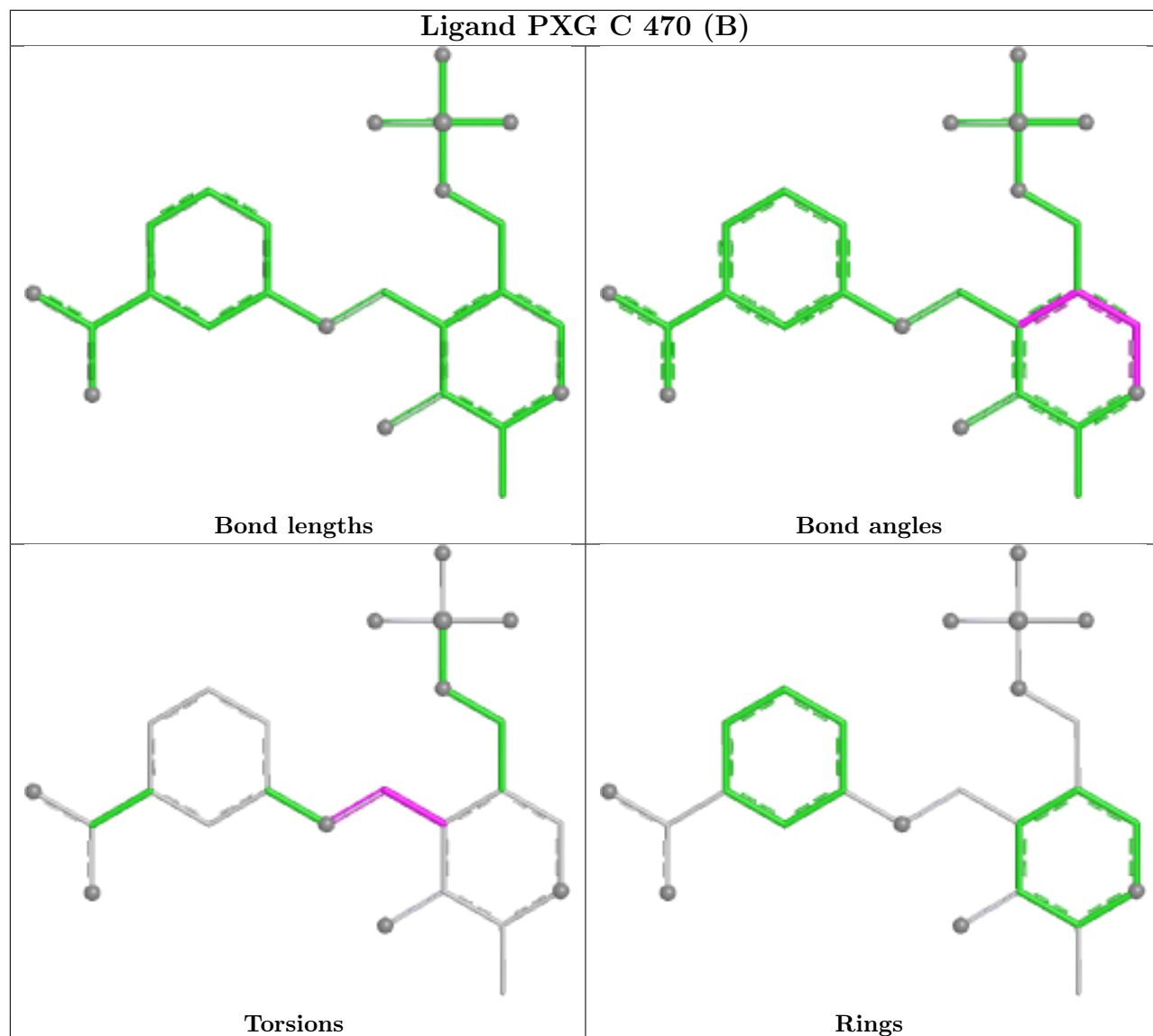


Rings

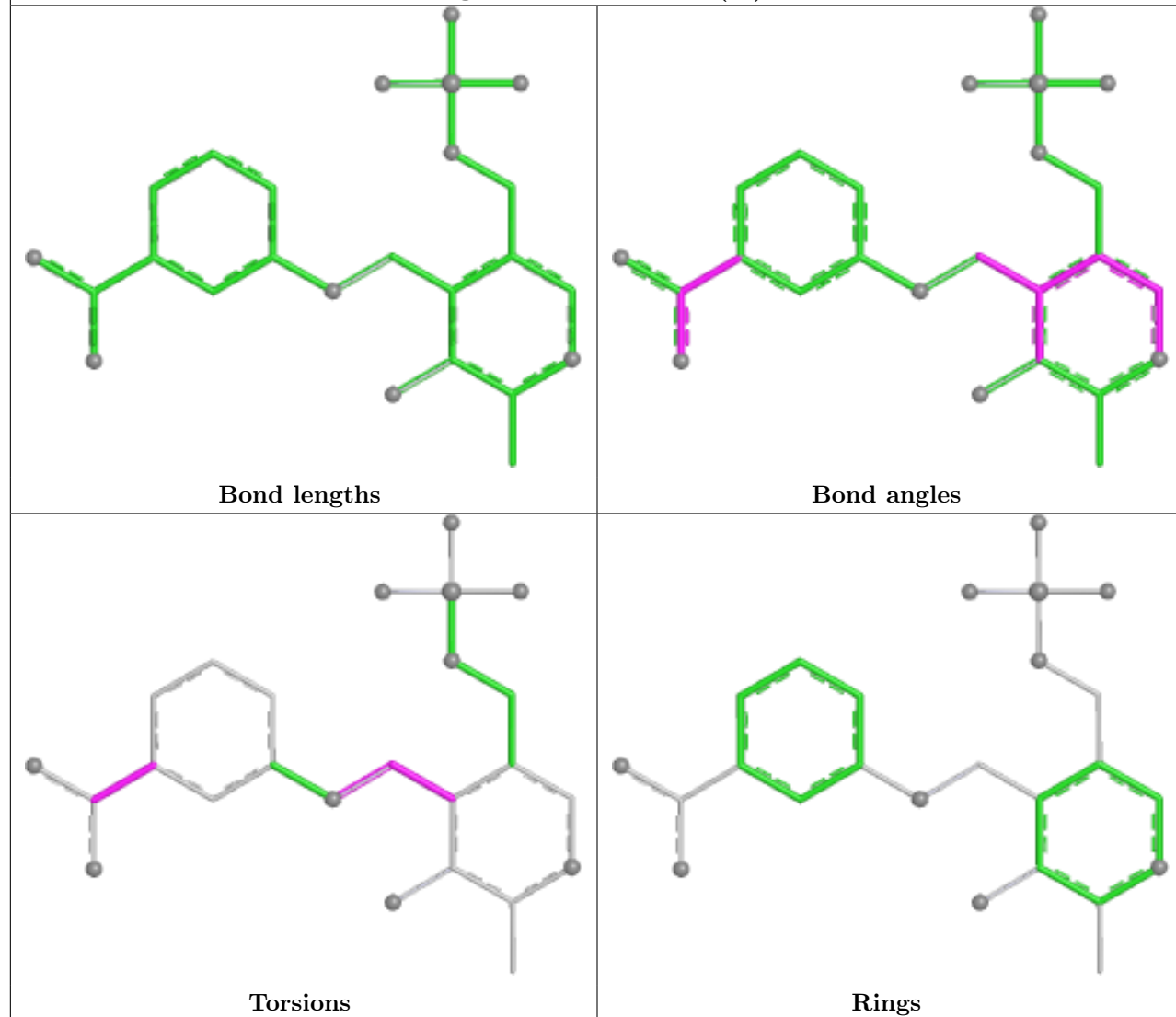
Ligand PXG A 470 (A)

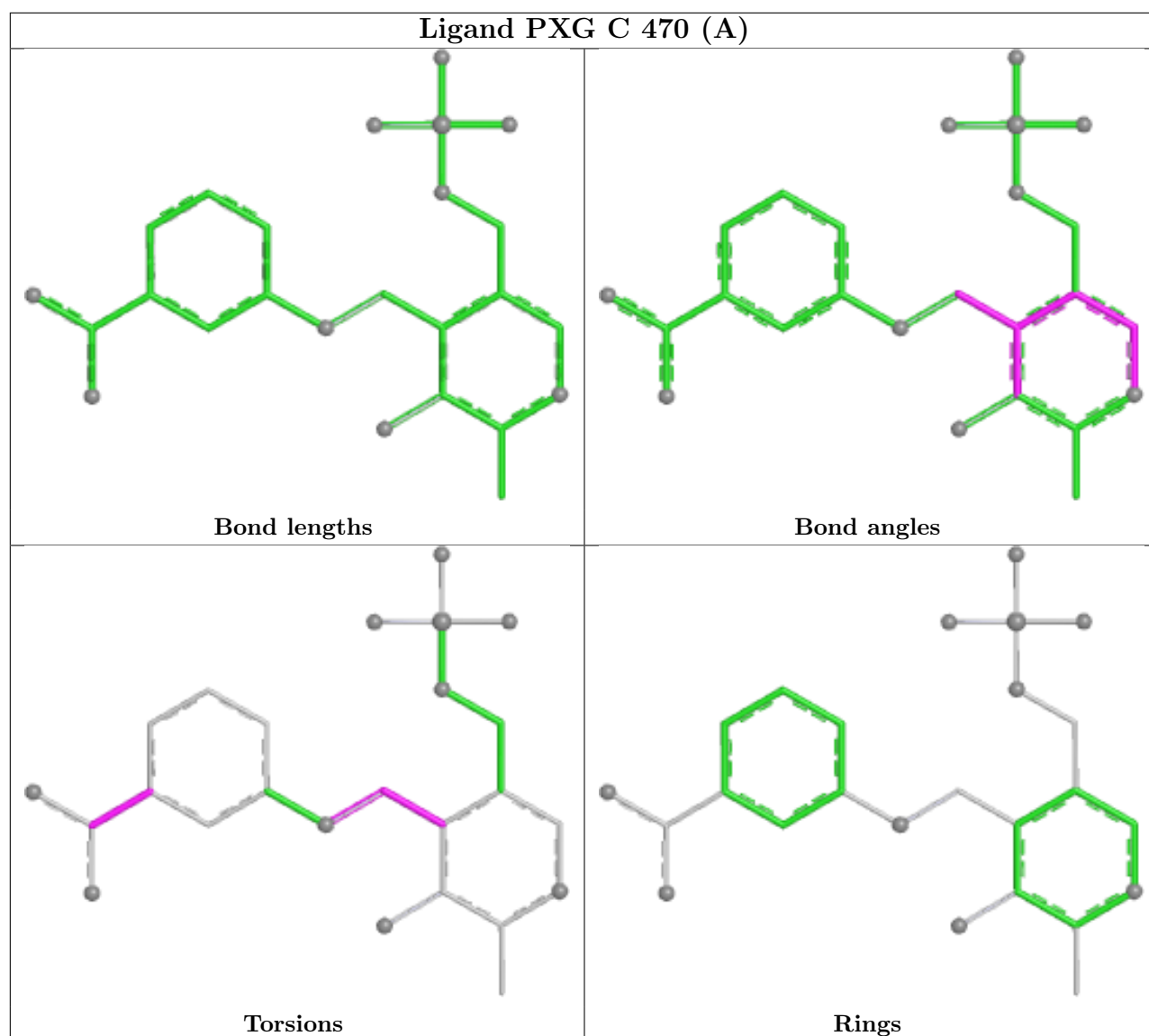


Ligand PXG C 470 (B)



Ligand PXG B 470 (A)





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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	441/448 (98%)	0.30	8 (1%) 67 73	8, 19, 32, 109	24 (5%)
1	B	440/448 (98%)	0.29	6 (1%) 73 78	8, 19, 31, 106	27 (6%)
1	C	441/448 (98%)	0.24	7 (1%) 70 75	9, 19, 31, 66	25 (5%)
1	D	441/448 (98%)	0.30	8 (1%) 67 73	10, 19, 32, 62	27 (6%)
All	All	1763/1792 (98%)	0.28	29 (1%) 70 75	8, 19, 32, 109	103 (5%)

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	10	PRO	7.6
1	A	11	VAL	6.8
1	A	8	ALA	6.6
1	A	9	PRO	6.3
1	B	11	VAL	5.9
1	B	10	PRO	5.6
1	D	11	VAL	5.5
1	B	9	PRO	4.7
1	C	9	PRO	4.7
1	D	8	ALA	4.7
1	C	8	ALA	4.2
1	D	448	ALA	4.1
1	D	9	PRO	3.7
1	C	10	PRO	3.6
1	B	13	SER	3.6
1	D	10	PRO	3.5
1	C	11	VAL	3.4
1	B	12	SER	3.3
1	C	448	ALA	3.2
1	B	314	ALA	3.0
1	C	32	LYS	2.9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	12	SER	2.8
1	A	12	SER	2.8
1	A	13	SER	2.8
1	A	81	GLY	2.6
1	A	448	ALA	2.5
1	D	14[A]	GLU	2.4
1	C	12	SER	2.3
1	D	88	GLY	2.3

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides 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	PLP	B	501	16/16	0.91	0.17	16,40,75,87	0
3	PLP	A	501	16/16	0.92	0.14	19,37,73,80	0
3	PLP	C	501	16/16	0.92	0.15	15,39,71,83	0
2	PXG	B	470[B]	25/25	0.93	0.11	15,24,33,36	25
2	PXG	D	470[A]	25/25	0.93	0.12	9,19,38,44	25
2	PXG	D	470[B]	25/25	0.93	0.12	10,20,34,38	25
2	PXG	A	470[A]	25/25	0.93	0.12	13,19,42,45	25
2	PXG	A	470[B]	25/25	0.93	0.12	12,21,41,42	25
2	PXG	B	470[A]	25/25	0.93	0.11	13,20,35,36	25
3	PLP	D	501	16/16	0.94	0.12	16,41,64,74	0
5	CL	A	503	1/1	0.95	0.06	18,18,18,18	1
5	CL	C	503	1/1	0.95	0.05	16,16,16,16	1
2	PXG	C	470[A]	25/25	0.96	0.10	11,21,40,41	25
2	PXG	C	470[B]	25/25	0.96	0.10	18,23,38,39	25
5	CL	D	503	1/1	0.96	0.06	18,18,18,18	1

Continued on next page...

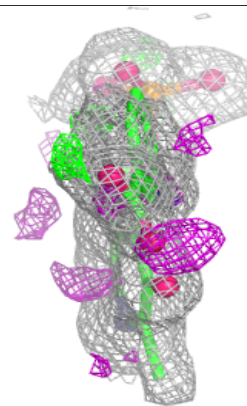
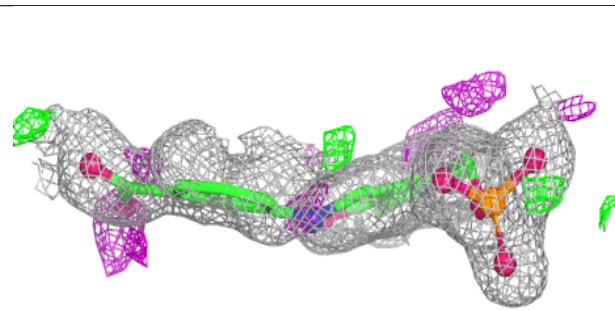
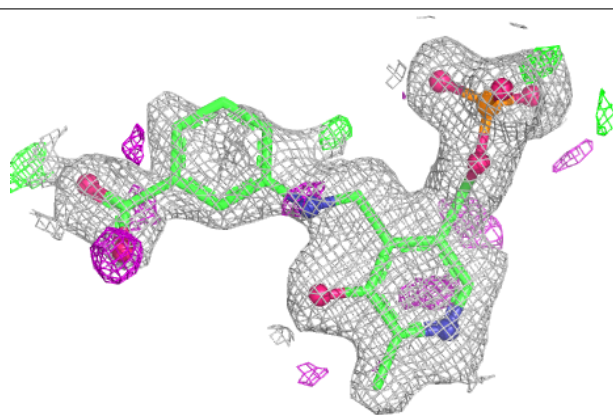
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	CL	B	503	1/1	0.97	0.05	17,17,17,17	1
4	CA	A	502	1/1	0.99	0.07	24,24,24,24	0
4	CA	B	502	1/1	0.99	0.08	26,26,26,26	0

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

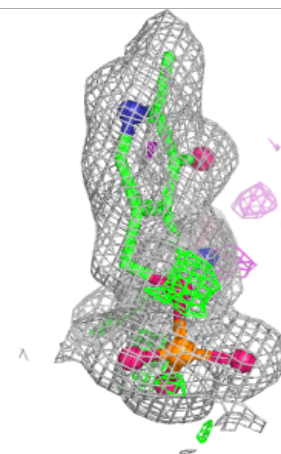
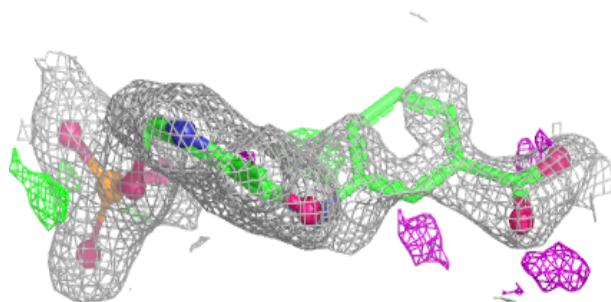
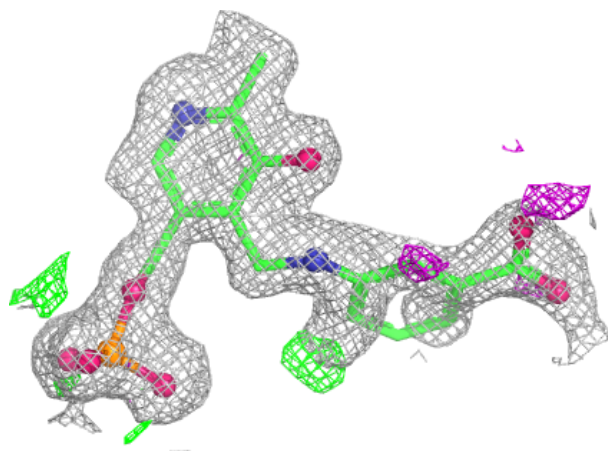
Electron density around PXG B 470 (B):

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



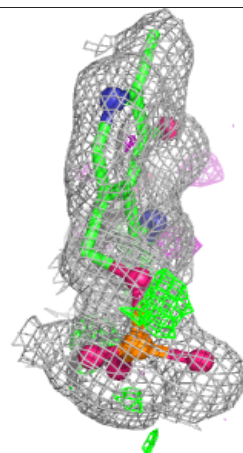
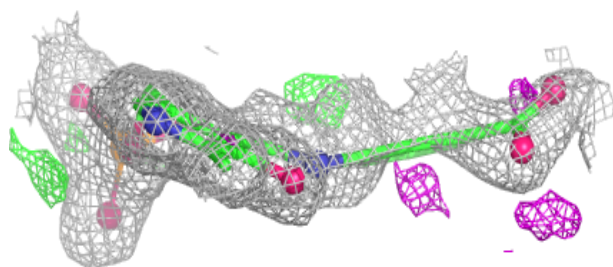
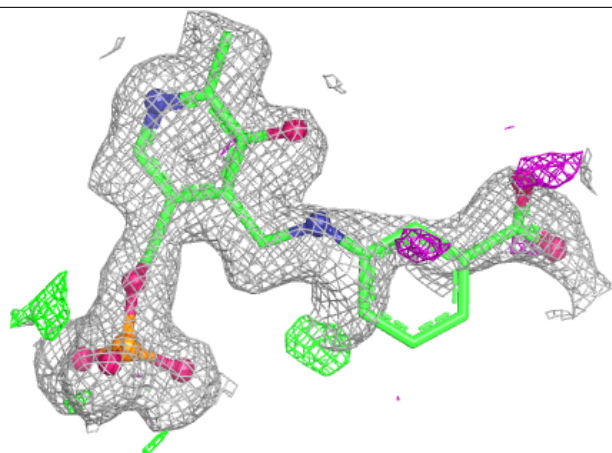
Electron density around PXG D 470 (A):

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



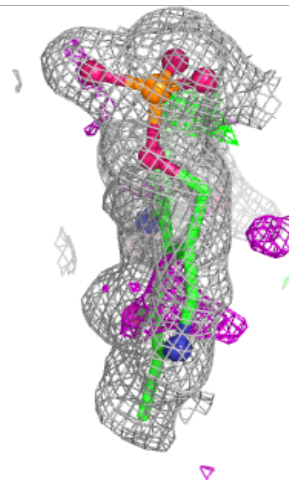
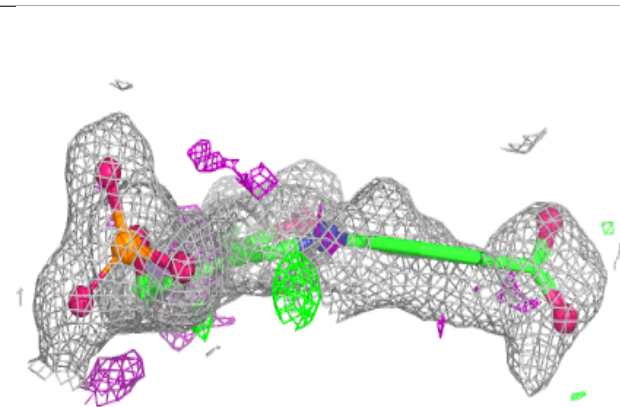
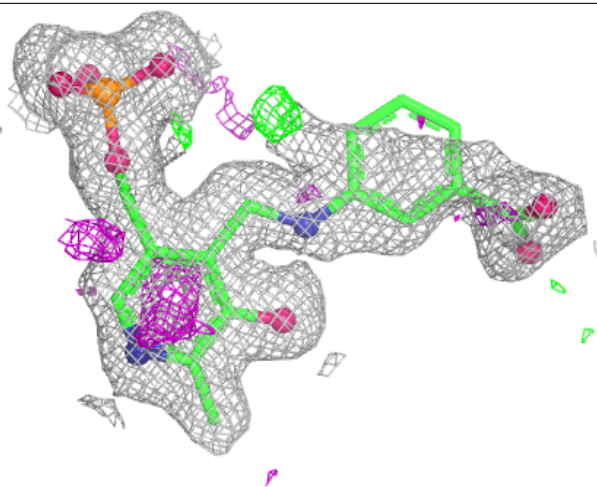
Electron density around PXG D 470 (B):

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



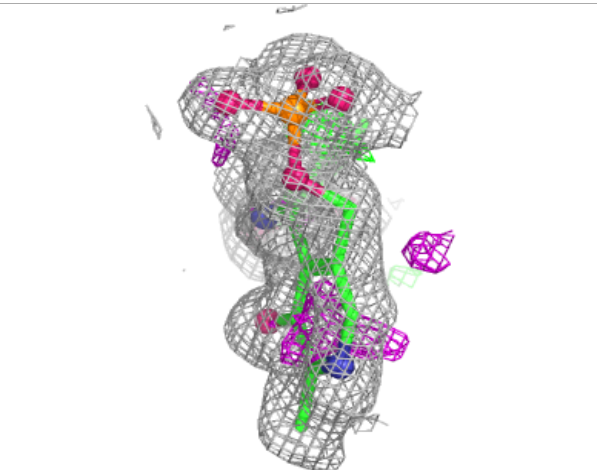
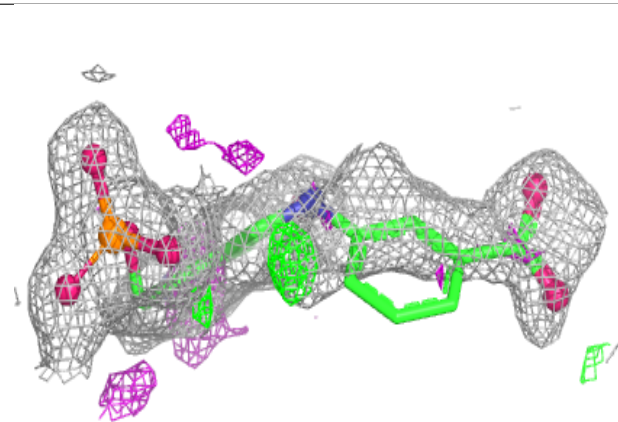
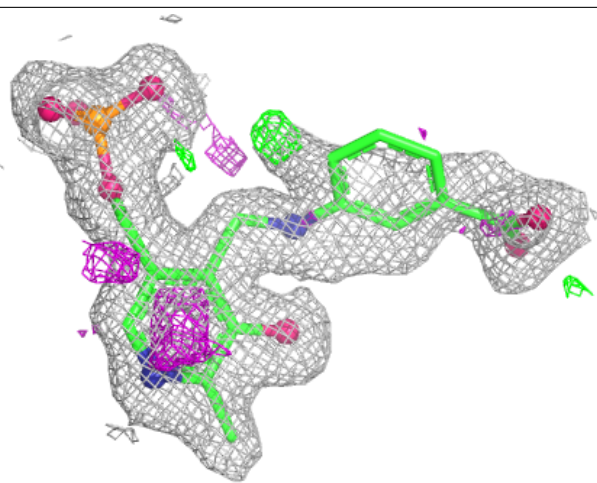
Electron density around PXG A 470 (A):

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



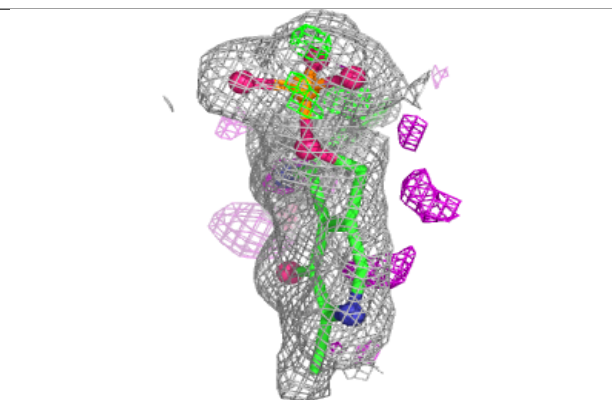
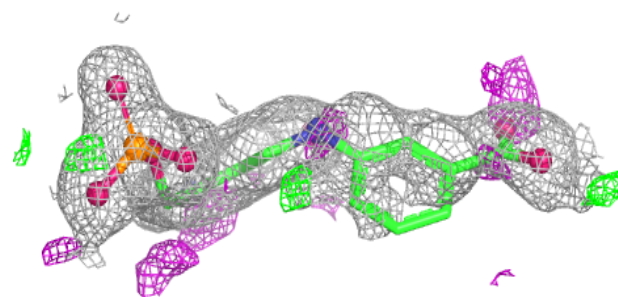
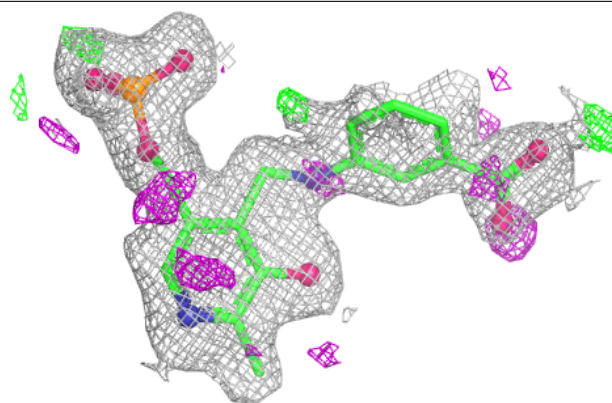
Electron density around PXG A 470 (B):

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

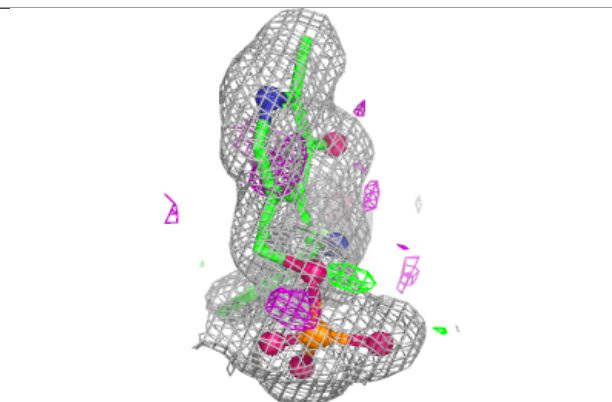
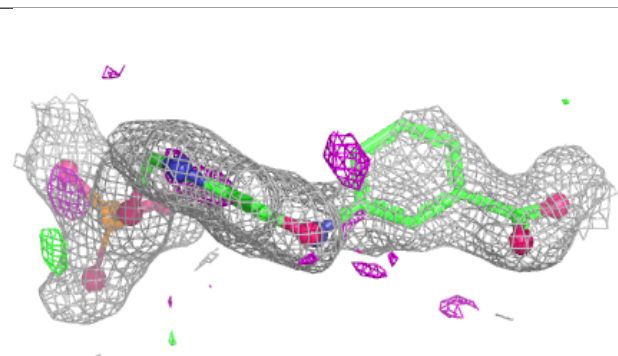
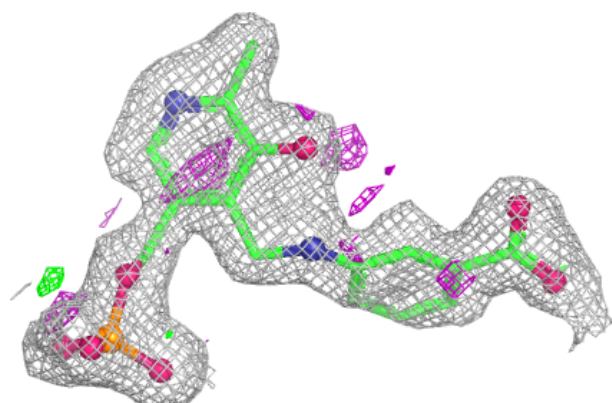


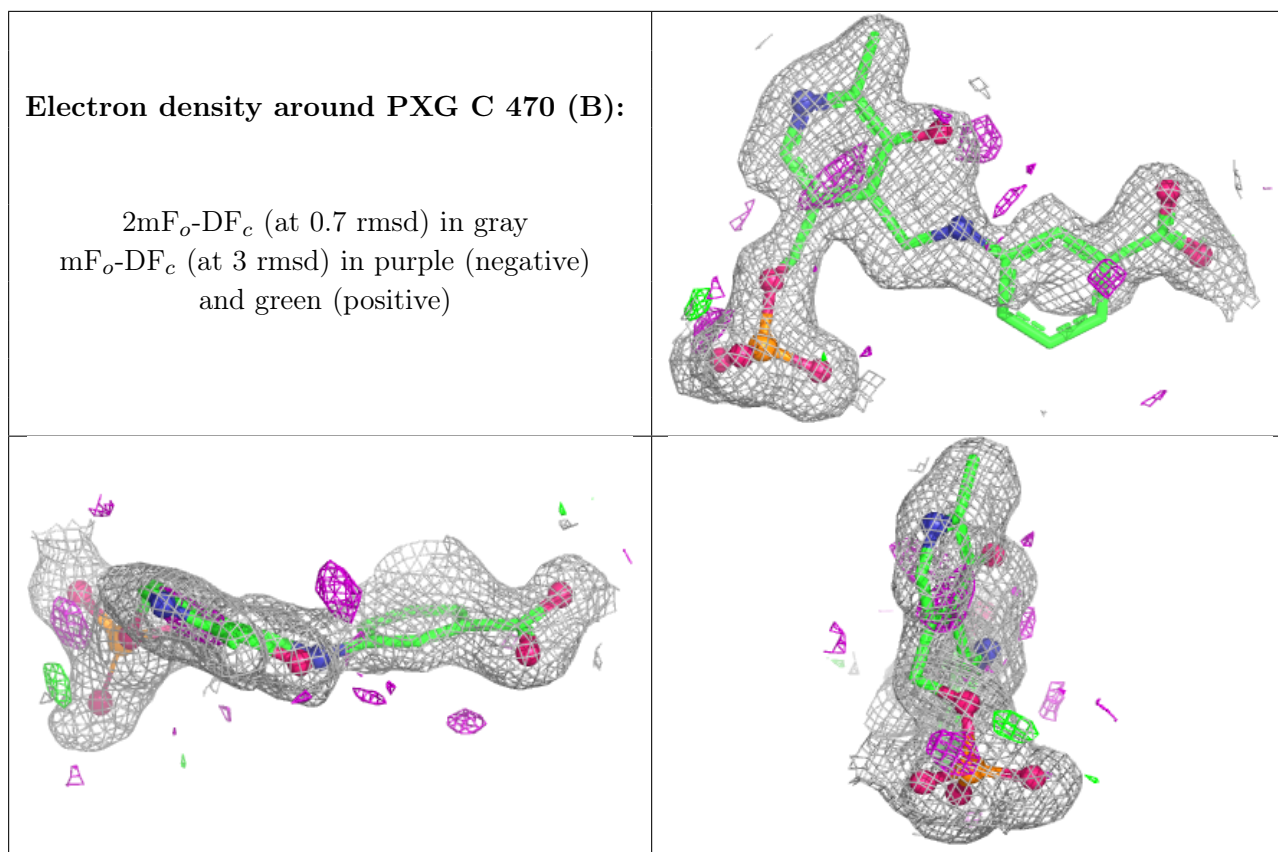
Electron density around PXG B 470 (A):

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

**Electron density around PXG C 470 (A):**

$2mF_o-DF_c$ (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.