



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 3, 2025 – 09:07 am GMT

PDB ID : 9IGL
Title : Crystal structure of P. syringae phosphinothricin acetyltransferase PSPTO_3321 in complex with L-phosphinothricin
Authors : Davies, A.M.; Trentham, D.; Sutton, B.J.; Brown, P.R.
Deposited on : 2025-02-19
Resolution : 2.50 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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.003 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.41

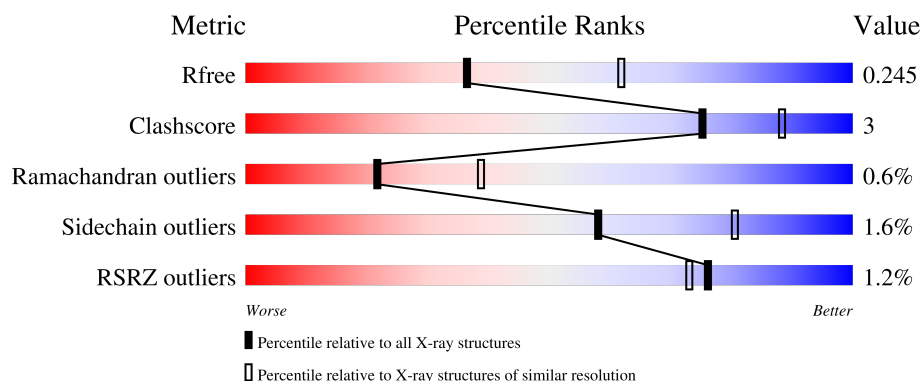
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	164625	5504 (2.50-2.50)
Clashscore	180529	6282 (2.50-2.50)
Ramachandran outliers	177936	6191 (2.50-2.50)
Sidechain outliers	177891	6193 (2.50-2.50)
RSRZ outliers	164620	5504 (2.50-2.50)

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	187	<div> <div>%</div> <div>86% 7% • 6%</div> </div>
1	B	187	<div> <div>%</div> <div>86% 6% 9%</div> </div>
1	C	187	<div> <div>%</div> <div>87% 6% 7%</div> </div>
1	D	187	<div> <div>82% 10% 8%</div> </div>
1	E	187	<div> <div>%</div> <div>83% 9% • 7%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	187	<div><div><div></div><div></div><div></div></div><div><div>2%</div><div>82%</div><div>10%</div><div>8%</div></div></div>
1	G	187	<div><div><div></div><div></div><div></div></div><div><div>2%</div><div>84%</div><div>9%</div><div>7%</div></div></div>
1	H	187	<div><div><div></div><div></div><div></div></div><div><div>2%</div><div>82%</div><div>9%</div><div>9%</div></div></div>

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 10802 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 Phosphinothricin N-acetyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	175	Total	C	N	O	S	0	0	0
			1331	845	236	245	5			
1	B	171	Total	C	N	O	S	0	0	0
			1294	827	233	229	5			
1	C	174	Total	C	N	O	S	0	0	0
			1314	837	233	239	5			
1	D	172	Total	C	N	O	S	0	0	0
			1320	834	238	243	5			
1	E	174	Total	C	N	O	S	0	0	0
			1316	839	228	244	5			
1	F	172	Total	C	N	O	S	0	0	0
			1311	833	238	235	5			
1	G	174	Total	C	N	O	S	0	0	0
			1317	839	234	239	5			
1	H	171	Total	C	N	O	S	0	0	0
			1306	829	238	234	5			

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	180	LEU	-	expression tag	UNP Q87ZV1
A	181	GLU	-	expression tag	UNP Q87ZV1
A	182	HIS	-	expression tag	UNP Q87ZV1
A	183	HIS	-	expression tag	UNP Q87ZV1
A	184	HIS	-	expression tag	UNP Q87ZV1
A	185	HIS	-	expression tag	UNP Q87ZV1
A	186	HIS	-	expression tag	UNP Q87ZV1
A	187	HIS	-	expression tag	UNP Q87ZV1
B	180	LEU	-	expression tag	UNP Q87ZV1
B	181	GLU	-	expression tag	UNP Q87ZV1
B	182	HIS	-	expression tag	UNP Q87ZV1
B	183	HIS	-	expression tag	UNP Q87ZV1
B	184	HIS	-	expression tag	UNP Q87ZV1

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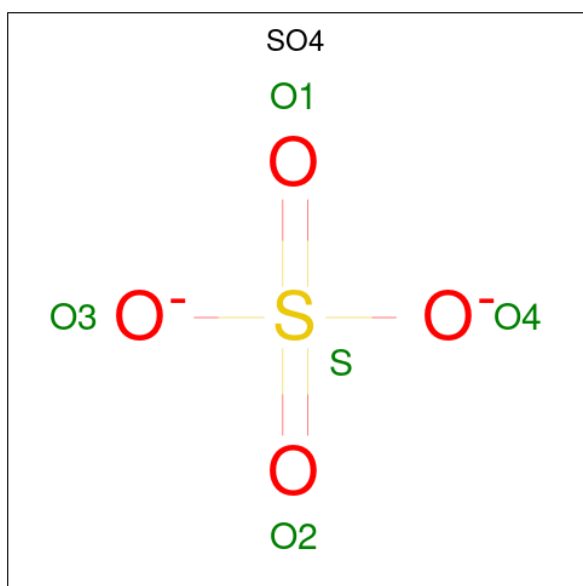
Chain	Residue	Modelled	Actual	Comment	Reference
B	185	HIS	-	expression tag	UNP Q87ZV1
B	186	HIS	-	expression tag	UNP Q87ZV1
B	187	HIS	-	expression tag	UNP Q87ZV1
C	180	LEU	-	expression tag	UNP Q87ZV1
C	181	GLU	-	expression tag	UNP Q87ZV1
C	182	HIS	-	expression tag	UNP Q87ZV1
C	183	HIS	-	expression tag	UNP Q87ZV1
C	184	HIS	-	expression tag	UNP Q87ZV1
C	185	HIS	-	expression tag	UNP Q87ZV1
C	186	HIS	-	expression tag	UNP Q87ZV1
C	187	HIS	-	expression tag	UNP Q87ZV1
D	180	LEU	-	expression tag	UNP Q87ZV1
D	181	GLU	-	expression tag	UNP Q87ZV1
D	182	HIS	-	expression tag	UNP Q87ZV1
D	183	HIS	-	expression tag	UNP Q87ZV1
D	184	HIS	-	expression tag	UNP Q87ZV1
D	185	HIS	-	expression tag	UNP Q87ZV1
D	186	HIS	-	expression tag	UNP Q87ZV1
D	187	HIS	-	expression tag	UNP Q87ZV1
E	180	LEU	-	expression tag	UNP Q87ZV1
E	181	GLU	-	expression tag	UNP Q87ZV1
E	182	HIS	-	expression tag	UNP Q87ZV1
E	183	HIS	-	expression tag	UNP Q87ZV1
E	184	HIS	-	expression tag	UNP Q87ZV1
E	185	HIS	-	expression tag	UNP Q87ZV1
E	186	HIS	-	expression tag	UNP Q87ZV1
E	187	HIS	-	expression tag	UNP Q87ZV1
F	180	LEU	-	expression tag	UNP Q87ZV1
F	181	GLU	-	expression tag	UNP Q87ZV1
F	182	HIS	-	expression tag	UNP Q87ZV1
F	183	HIS	-	expression tag	UNP Q87ZV1
F	184	HIS	-	expression tag	UNP Q87ZV1
F	185	HIS	-	expression tag	UNP Q87ZV1
F	186	HIS	-	expression tag	UNP Q87ZV1
F	187	HIS	-	expression tag	UNP Q87ZV1
G	180	LEU	-	expression tag	UNP Q87ZV1
G	181	GLU	-	expression tag	UNP Q87ZV1
G	182	HIS	-	expression tag	UNP Q87ZV1
G	183	HIS	-	expression tag	UNP Q87ZV1
G	184	HIS	-	expression tag	UNP Q87ZV1
G	185	HIS	-	expression tag	UNP Q87ZV1
G	186	HIS	-	expression tag	UNP Q87ZV1

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Chain	Residue	Modelled	Actual	Comment	Reference
G	187	HIS	-	expression tag	UNP Q87ZV1
H	180	LEU	-	expression tag	UNP Q87ZV1
H	181	GLU	-	expression tag	UNP Q87ZV1
H	182	HIS	-	expression tag	UNP Q87ZV1
H	183	HIS	-	expression tag	UNP Q87ZV1
H	184	HIS	-	expression tag	UNP Q87ZV1
H	185	HIS	-	expression tag	UNP Q87ZV1
H	186	HIS	-	expression tag	UNP Q87ZV1
H	187	HIS	-	expression tag	UNP Q87ZV1

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



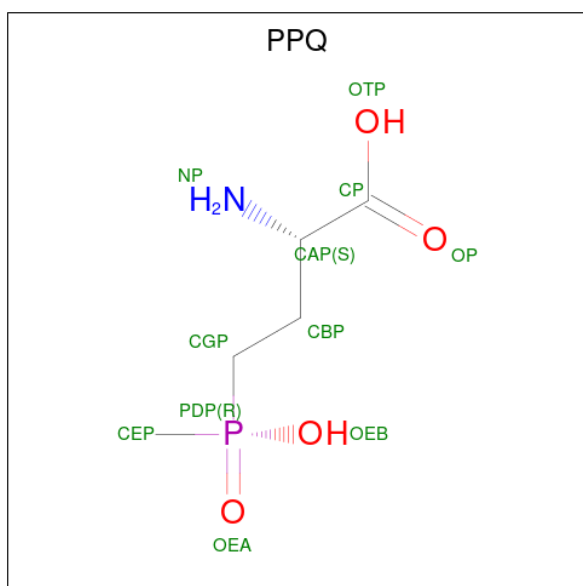
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		

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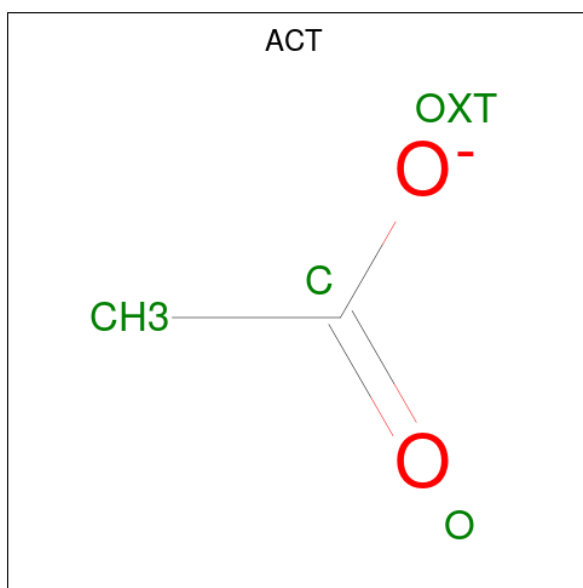
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	F	1	Total	O	S	0	0
			5	4	1		
2	G	1	Total	O	S	0	0
			5	4	1		
2	H	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is PHOSPHINOTHRICIN (three-letter code: PPQ) (formula: $C_5H_{12}NO_4P$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			11	5	1	4	1		
3	B	1	Total	C	N	O	P	0	0
			11	5	1	4	1		
3	C	1	Total	C	N	O	P	0	0
			11	5	1	4	1		
3	D	1	Total	C	N	O	P	0	0
			11	5	1	4	1		
3	E	1	Total	C	N	O	P	0	0
			11	5	1	4	1		
3	F	1	Total	C	N	O	P	0	0
			11	5	1	4	1		
3	H	1	Total	C	N	O	P	0	0
			11	5	1	4	1		
3	H	1	Total	C	N	O	P	0	0
			11	5	1	4	1		

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



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

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

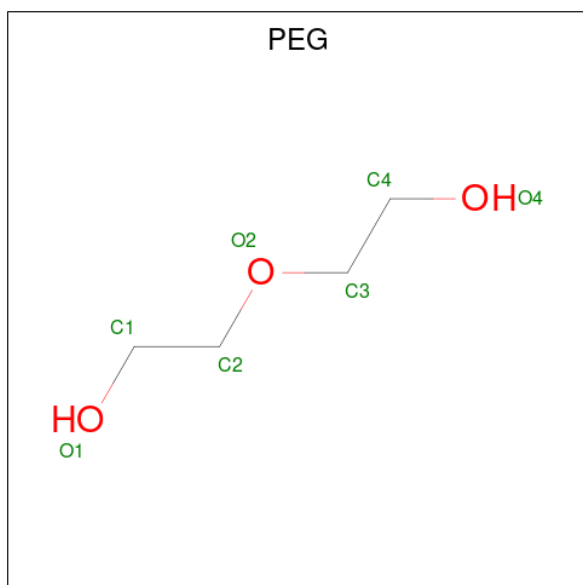
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	1	Total	Na	0	0
			1	1		

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	D	1	Total	C	O	0	0
			4	2	2		
6	E	1	Total	C	O	0	0
			4	2	2		
6	G	1	Total	C	O	0	0
			4	2	2		
6	H	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	G	1	Total	C	O	0	0
			7	4	3		

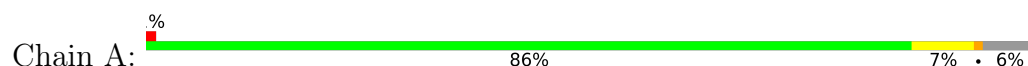
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	13	Total	O	0	0
			13	13		
8	B	8	Total	O	0	0
			8	8		
8	C	21	Total	O	0	0
			21	21		
8	D	19	Total	O	0	0
			19	19		
8	E	19	Total	O	0	0
			19	19		
8	F	16	Total	O	0	0
			16	16		
8	G	7	Total	O	0	0
			7	7		
8	H	12	Total	O	0	0
			12	12		

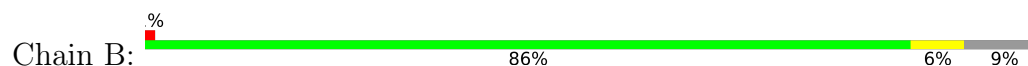
3 Residue-property plots [i](#)

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.

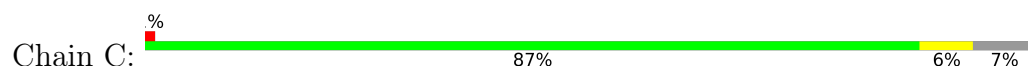
- Molecule 1: Phosphinothricin N-acetyltransferase



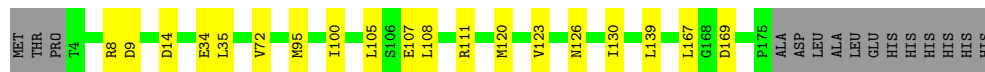
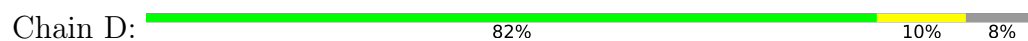
- Molecule 1: Phosphinothricin N-acetyltransferase



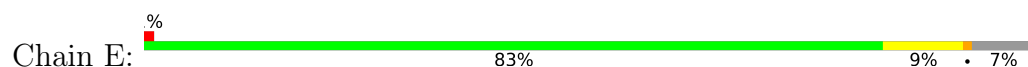
- Molecule 1: Phosphinothricin N-acetyltransferase



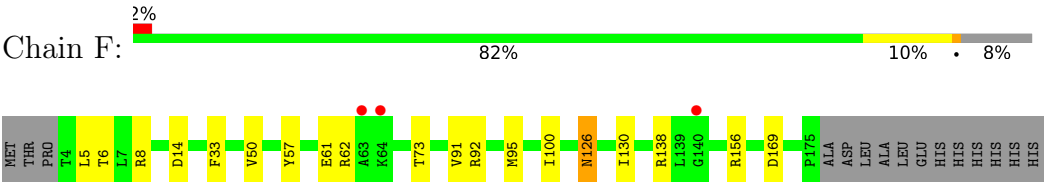
- Molecule 1: Phosphinothricin N-acetyltransferase



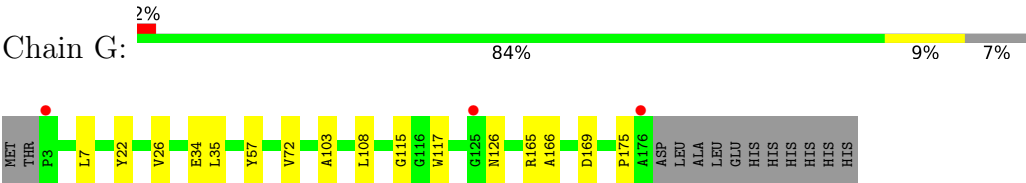
- Molecule 1: Phosphinothricin N-acetyltransferase



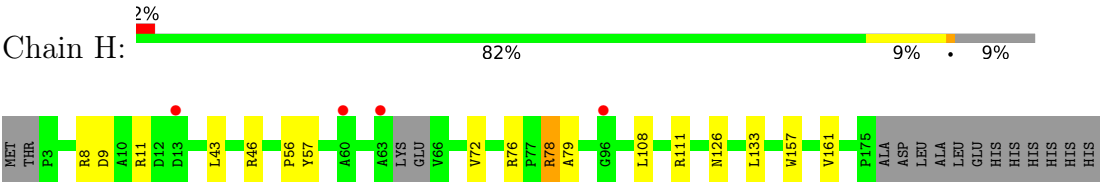
- Molecule 1: Phosphinothricin N-acetyltransferase



● Molecule 1: Phosphinothricin N-acetyltransferase



● Molecule 1: Phosphinothricin N-acetyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	138.58Å 97.60Å 117.59Å 90.00° 111.19° 90.00°	Depositor
Resolution (Å)	77.88 – 2.50 77.88 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.6 (77.88-2.50) 90.7 (77.88-2.50)	Depositor EDS
R_{merge}	0.31	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.78 (at 2.48Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, R_{free}	0.205 , 0.249 0.204 , 0.245	Depositor DCC
R_{free} test set	48027 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	30.1	Xtriage
Anisotropy	0.649	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 37.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	10802	wwPDB-VP
Average B, all atoms (Å ²)	41.0	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 21.65 % 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 6.7058e-03.*

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: SO4, NA, ACT, PEG, EDO, PPQ

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	0.23	0/1358	0.49	0/1841
1	B	0.23	0/1320	0.50	0/1787
1	C	0.23	0/1340	0.50	0/1814
1	D	0.24	0/1346	0.52	0/1824
1	E	0.24	0/1343	0.49	0/1820
1	F	0.24	0/1337	0.52	0/1810
1	G	0.23	0/1343	0.49	0/1817
1	H	0.23	0/1332	0.50	0/1803
All	All	0.23	0/10719	0.50	0/14516

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 [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	1331	0	1310	9	0
1	B	1294	0	1285	8	0
1	C	1314	0	1298	6	0
1	D	1320	0	1302	10	0
1	E	1316	0	1291	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	1311	0	1298	10	0
1	G	1317	0	1298	9	0
1	H	1306	0	1302	12	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
2	E	10	0	0	0	0
2	F	10	0	0	0	0
2	G	5	0	0	0	0
2	H	5	0	0	0	0
3	A	11	0	10	0	0
3	B	11	0	10	0	0
3	C	11	0	10	0	0
3	D	11	0	10	1	0
3	E	11	0	10	0	0
3	F	11	0	10	0	0
3	H	22	0	20	0	0
4	A	4	0	3	0	0
4	C	4	0	3	0	0
4	G	8	0	6	0	0
5	C	1	0	0	0	0
6	D	4	0	6	0	0
6	E	4	0	6	0	0
6	G	4	0	6	0	0
6	H	4	0	6	1	0
7	G	7	0	10	2	0
8	A	13	0	0	0	0
8	B	8	0	0	0	0
8	C	21	0	0	0	0
8	D	19	0	0	0	0
8	E	19	0	0	0	0
8	F	16	0	0	2	0
8	G	7	0	0	0	0
8	H	12	0	0	1	0
All	All	10802	0	10510	62	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 3.

All (62) 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:E:9:ASP:OD1	1:E:111:ARG:NH2	2.18	0.77
1:A:7:LEU:HD11	1:A:103:ALA:HB1	1.67	0.74
1:G:34:GLU:HG3	1:H:78:ARG:HG2	1.72	0.72
1:G:7:LEU:HD11	1:G:103:ALA:HB1	1.71	0.71
1:E:7:LEU:HD11	1:E:103:ALA:HB1	1.74	0.69
1:D:8:ARG:NH1	1:D:14:ASP:OD2	2.28	0.64
1:E:127:SER:HB2	1:E:159:ASP:HB2	1.79	0.63
1:A:134:ARG:HB3	1:A:138:ARG:HH21	1.62	0.62
1:H:9:ASP:OD1	1:H:111:ARG:NH1	2.32	0.62
1:A:126:ASN:HD21	1:A:128:GLU:HG2	1.63	0.61
1:C:118:ARG:NH1	1:C:170:GLY:O	2.29	0.61
1:F:8:ARG:NH1	1:F:14:ASP:OD2	2.29	0.60
1:H:56:PRO:HB3	1:H:111:ARG:HD2	1.83	0.60
1:D:95:MET:HB3	1:D:100:ILE:HD12	1.86	0.57
1:D:72:VAL:HG23	1:D:108:LEU:HD22	1.86	0.56
1:D:123:VAL:O	3:D:202:PPQ:NP	2.36	0.56
1:E:165:ARG:NH1	1:E:166:ALA:O	2.39	0.56
1:A:126:ASN:ND2	1:A:128:GLU:HG2	2.22	0.54
1:A:5:LEU:HD11	1:A:60:ALA:HB1	1.90	0.54
1:F:92:ARG:NH1	8:F:303:HOH:O	2.39	0.54
1:H:46:ARG:NH1	6:H:204:EDO:O2	2.38	0.53
1:A:9:ASP:OD1	1:A:111:ARG:NH2	2.33	0.52
1:H:8:ARG:HE	1:H:11:ARG:HD3	1.76	0.51
1:H:72:VAL:HG23	1:H:108:LEU:HD22	1.92	0.50
1:F:95:MET:HB3	1:F:100:ILE:HD12	1.94	0.50
1:D:9:ASP:OD1	1:D:111:ARG:NH2	2.45	0.49
7:G:205:PEG:H31	1:H:78:ARG:NH1	2.26	0.49
1:D:107:GLU:OE2	1:D:111:ARG:NH1	2.45	0.49
1:B:128:GLU:HB3	1:E:143:ARG:HD2	1.95	0.49
1:F:6:THR:HB	1:F:61:GLU:HB3	1.94	0.49
1:G:165:ARG:NH1	1:G:166:ALA:O	2.45	0.49
1:F:126:ASN:ND2	8:F:302:HOH:O	2.38	0.48
1:B:130:ILE:HD12	1:E:143:ARG:HB2	1.96	0.48
1:C:142:GLY:HA2	1:F:130:ILE:HD11	1.96	0.47
1:E:80:ALA:HB3	1:F:33:PHE:HB3	1.95	0.47
1:F:5:LEU:HD12	1:F:62:ARG:HG3	1.97	0.47
1:D:120:MET:HB2	1:D:167:LEU:HD11	1.97	0.46
1:E:72:VAL:HG23	1:E:108:LEU:HD22	1.98	0.45
1:H:76:ARG:NH1	8:H:301:HOH:O	2.44	0.45
7:G:205:PEG:H31	1:H:78:ARG:HH11	1.82	0.44
1:B:120:MET:HB2	1:B:167:LEU:HD11	2.00	0.44
1:A:102:GLN:HG3	1:A:139:LEU:HD11	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:130:ILE:HG21	1:E:137:GLU:HG2	1.98	0.43
1:H:133:LEU:HD21	1:H:161:VAL:HG11	2.00	0.43
1:B:105:LEU:HD23	1:B:139:LEU:HD12	2.00	0.43
1:D:105:LEU:HD23	1:D:139:LEU:HD12	1.99	0.43
1:A:35:LEU:HG	1:B:79:ALA:HB3	2.00	0.43
1:C:115:GLY:HA3	1:C:117:TRP:CZ3	2.54	0.43
1:G:115:GLY:HA3	1:G:117:TRP:CZ3	2.54	0.43
1:B:115:GLY:HA3	1:B:117:TRP:CZ3	2.55	0.42
1:E:79:ALA:O	1:E:82:ARG:HB2	2.19	0.42
1:G:72:VAL:HG23	1:G:108:LEU:HD22	2.02	0.42
1:G:175:PRO:HG3	1:H:157:TRP:CZ2	2.54	0.42
1:F:50:VAL:HG22	1:F:73:THR:HG22	2.02	0.42
1:C:79:ALA:HB3	1:D:35:LEU:HG	2.01	0.41
1:G:35:LEU:HG	1:H:79:ALA:HB3	2.03	0.41
1:F:91:VAL:HG12	1:F:95:MET:HB2	2.02	0.41
1:G:26:VAL:HG13	1:G:34:GLU:O	2.21	0.41
1:A:33:PHE:HB3	1:B:80:ALA:HB3	2.03	0.41
1:C:105:LEU:HD23	1:C:139:LEU:HD12	2.02	0.41
1:C:78:ARG:HD3	1:D:34:GLU:HG3	2.03	0.40
1:G:22:TYR:OH	1:G:34:GLU:OE1	2.31	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	173/187 (92%)	170 (98%)	2 (1%)	1 (1%)	22	39
1	B	169/187 (90%)	166 (98%)	2 (1%)	1 (1%)	22	39
1	C	172/187 (92%)	170 (99%)	1 (1%)	1 (1%)	22	39
1	D	170/187 (91%)	168 (99%)	1 (1%)	1 (1%)	22	39

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	172/187 (92%)	168 (98%)	3 (2%)	1 (1%)	22	39
1	F	170/187 (91%)	167 (98%)	2 (1%)	1 (1%)	22	39
1	G	172/187 (92%)	167 (97%)	4 (2%)	1 (1%)	22	39
1	H	167/187 (89%)	161 (96%)	5 (3%)	1 (1%)	22	39
All	All	1365/1496 (91%)	1337 (98%)	20 (2%)	8 (1%)	22	39

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	126	ASN
1	A	126	ASN
1	C	126	ASN
1	D	126	ASN
1	F	126	ASN
1	G	126	ASN
1	H	126	ASN
1	B	126	ASN

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	133/150 (89%)	131 (98%)	2 (2%)	60	82
1	B	126/150 (84%)	126 (100%)	0	100	100
1	C	129/150 (86%)	128 (99%)	1 (1%)	79	91
1	D	133/150 (89%)	131 (98%)	2 (2%)	60	82
1	E	131/150 (87%)	128 (98%)	3 (2%)	45	72
1	F	129/150 (86%)	125 (97%)	4 (3%)	35	62
1	G	130/150 (87%)	128 (98%)	2 (2%)	60	82
1	H	131/150 (87%)	128 (98%)	3 (2%)	45	72
All	All	1042/1200 (87%)	1025 (98%)	17 (2%)	58	80

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	127	SER
1	A	139	LEU
1	C	57	TYR
1	D	130	ILE
1	D	169	ASP
1	E	111	ARG
1	E	128	GLU
1	E	129	ASN
1	F	57	TYR
1	F	138	ARG
1	F	156	ARG
1	F	169	ASP
1	G	57	TYR
1	G	169	ASP
1	H	43	LEU
1	H	57	TYR
1	H	78	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 28 ligands modelled in this entry, 1 is monoatomic - leaving 27 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
6	EDO	E	204	-	3,3,3	0.45	0	2,2,2	0.35	0
3	PPQ	A	202	-	7,10,10	2.85	1 (14%)	7,14,14	1.51	1 (14%)
6	EDO	D	203	-	3,3,3	0.46	0	2,2,2	0.36	0
3	PPQ	H	203	-	7,10,10	2.86	1 (14%)	7,14,14	1.54	1 (14%)
3	PPQ	D	202	-	7,10,10	2.81	1 (14%)	7,14,14	1.50	1 (14%)
2	SO4	C	201	-	4,4,4	0.14	0	6,6,6	0.06	0
3	PPQ	C	202	-	7,10,10	2.83	1 (14%)	7,14,14	1.54	1 (14%)
2	SO4	A	201	-	4,4,4	0.15	0	6,6,6	0.05	0
2	SO4	F	201	-	4,4,4	0.14	0	6,6,6	0.05	0
4	ACT	C	203	-	3,3,3	1.30	0	3,3,3	1.36	0
6	EDO	H	204	-	3,3,3	0.46	0	2,2,2	0.33	0
3	PPQ	H	202	-	7,10,10	2.89	1 (14%)	7,14,14	1.50	1 (14%)
2	SO4	B	201	-	4,4,4	0.14	0	6,6,6	0.05	0
4	ACT	G	203	-	3,3,3	1.29	0	3,3,3	1.39	0
6	EDO	G	204	-	3,3,3	0.47	0	2,2,2	0.28	0
2	SO4	F	202	-	4,4,4	0.15	0	6,6,6	0.05	0
2	SO4	E	201	-	4,4,4	0.13	0	6,6,6	0.06	0
2	SO4	E	202	-	4,4,4	0.15	0	6,6,6	0.06	0
3	PPQ	F	203	-	7,10,10	2.82	1 (14%)	7,14,14	1.55	1 (14%)
2	SO4	D	201	-	4,4,4	0.14	0	6,6,6	0.06	0
4	ACT	A	203	-	3,3,3	1.28	0	3,3,3	1.39	0
4	ACT	G	202	-	3,3,3	1.31	0	3,3,3	1.37	0
2	SO4	G	201	-	4,4,4	0.14	0	6,6,6	0.06	0
2	SO4	H	201	-	4,4,4	0.14	0	6,6,6	0.05	0
7	PEG	G	205	-	6,6,6	0.11	0	5,5,5	0.07	0
3	PPQ	E	203	-	7,10,10	2.78	1 (14%)	7,14,14	1.52	2 (28%)
3	PPQ	B	202	-	7,10,10	2.87	1 (14%)	7,14,14	1.52	1 (14%)

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
6	EDO	G	204	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	EDO	E	204	-	-	1/1/1/1	-
3	PPQ	H	203	-	-	0/10/10/10	-
6	EDO	H	204	-	-	0/1/1/1	-
3	PPQ	A	202	-	-	0/10/10/10	-
3	PPQ	H	202	-	-	0/10/10/10	-
3	PPQ	F	203	-	-	0/10/10/10	-
7	PEG	G	205	-	-	2/4/4/4	-
6	EDO	D	203	-	-	0/1/1/1	-
3	PPQ	E	203	-	-	0/10/10/10	-
3	PPQ	D	202	-	-	0/10/10/10	-
3	PPQ	C	202	-	-	0/10/10/10	-
3	PPQ	B	202	-	-	0/10/10/10	-

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	202	PPQ	PDP-CGP	7.32	1.86	1.79
3	B	202	PPQ	PDP-CGP	7.29	1.86	1.79
3	H	203	PPQ	PDP-CGP	7.25	1.86	1.79
3	A	202	PPQ	PDP-CGP	7.25	1.86	1.79
3	C	202	PPQ	PDP-CGP	7.19	1.86	1.79
3	F	203	PPQ	PDP-CGP	7.13	1.86	1.79
3	D	202	PPQ	PDP-CGP	7.12	1.86	1.79
3	E	203	PPQ	PDP-CGP	7.04	1.86	1.79

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	203	PPQ	PDP-CGP-CBP	-2.91	109.21	114.53
3	D	202	PPQ	PDP-CGP-CBP	-2.86	109.31	114.53
3	H	203	PPQ	PDP-CGP-CBP	-2.78	109.44	114.53
3	C	202	PPQ	PDP-CGP-CBP	-2.78	109.44	114.53
3	A	202	PPQ	PDP-CGP-CBP	-2.76	109.47	114.53
3	H	202	PPQ	PDP-CGP-CBP	-2.73	109.53	114.53
3	E	203	PPQ	PDP-CGP-CBP	-2.69	109.61	114.53
3	B	202	PPQ	PDP-CGP-CBP	-2.67	109.65	114.53
3	E	203	PPQ	OTP-CP-CAP	2.04	120.34	113.38

There are no chirality outliers.

All (4) torsion outliers are listed below:

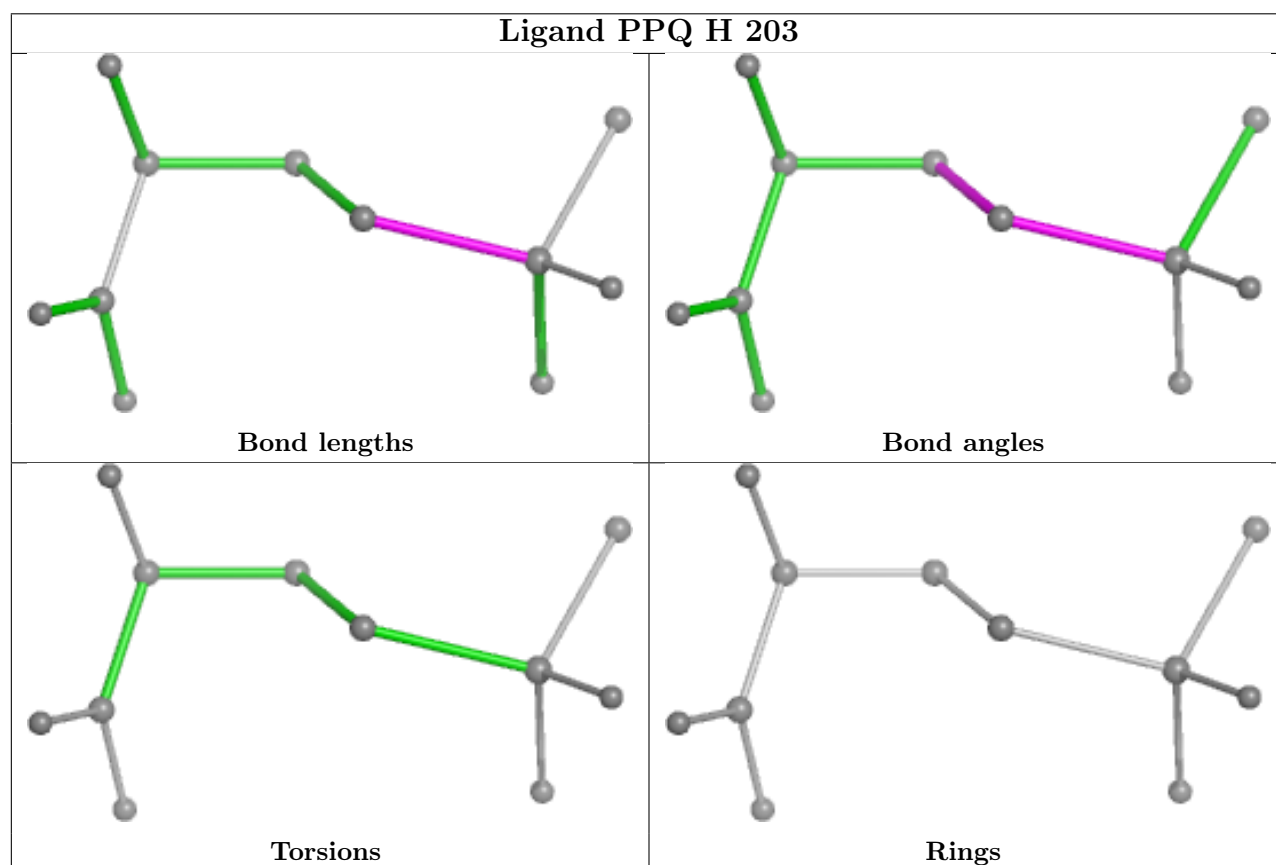
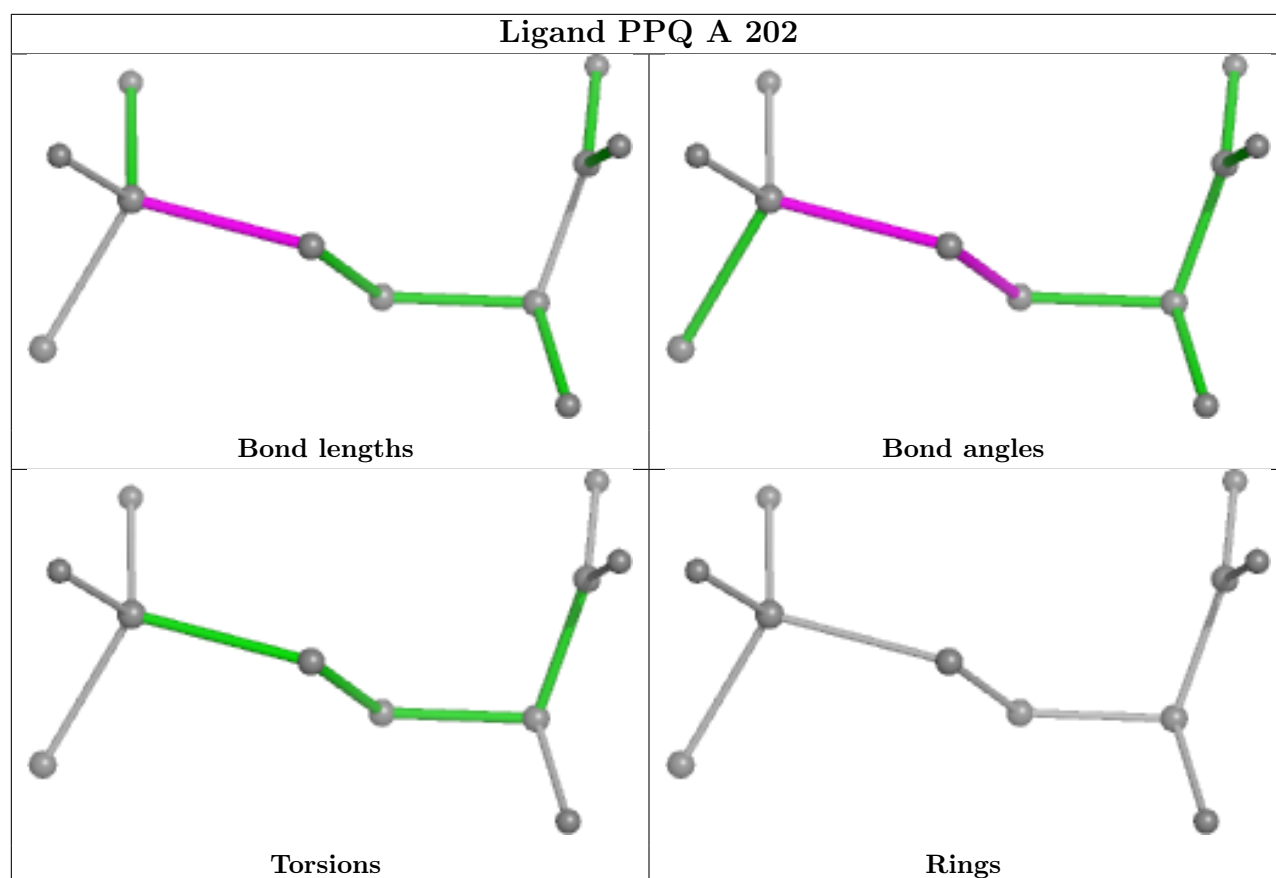
Mol	Chain	Res	Type	Atoms
7	G	205	PEG	O2-C3-C4-O4
6	E	204	EDO	O1-C1-C2-O2
7	G	205	PEG	C4-C3-O2-C2
6	G	204	EDO	O1-C1-C2-O2

There are no ring outliers.

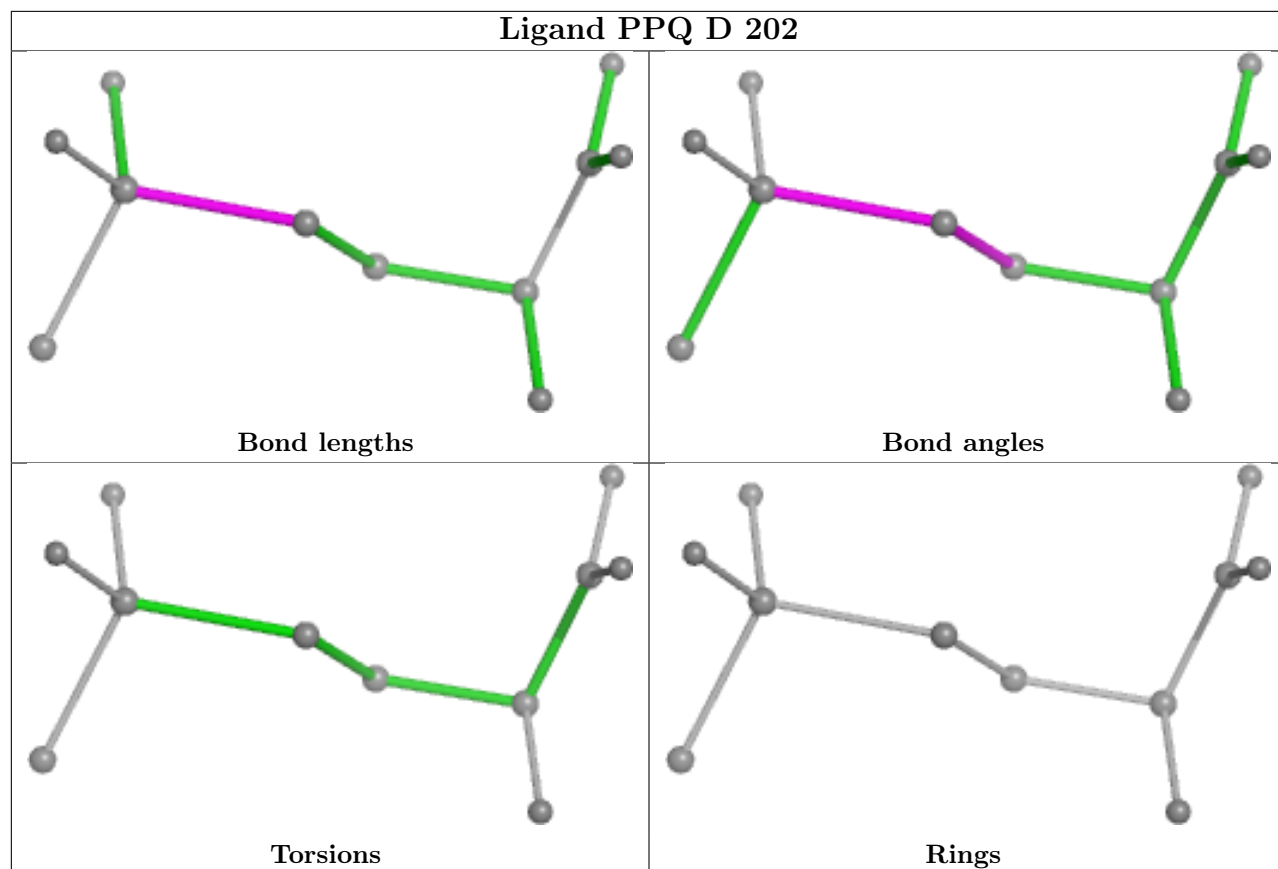
3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	202	PPQ	1	0
6	H	204	EDO	1	0
7	G	205	PEG	2	0

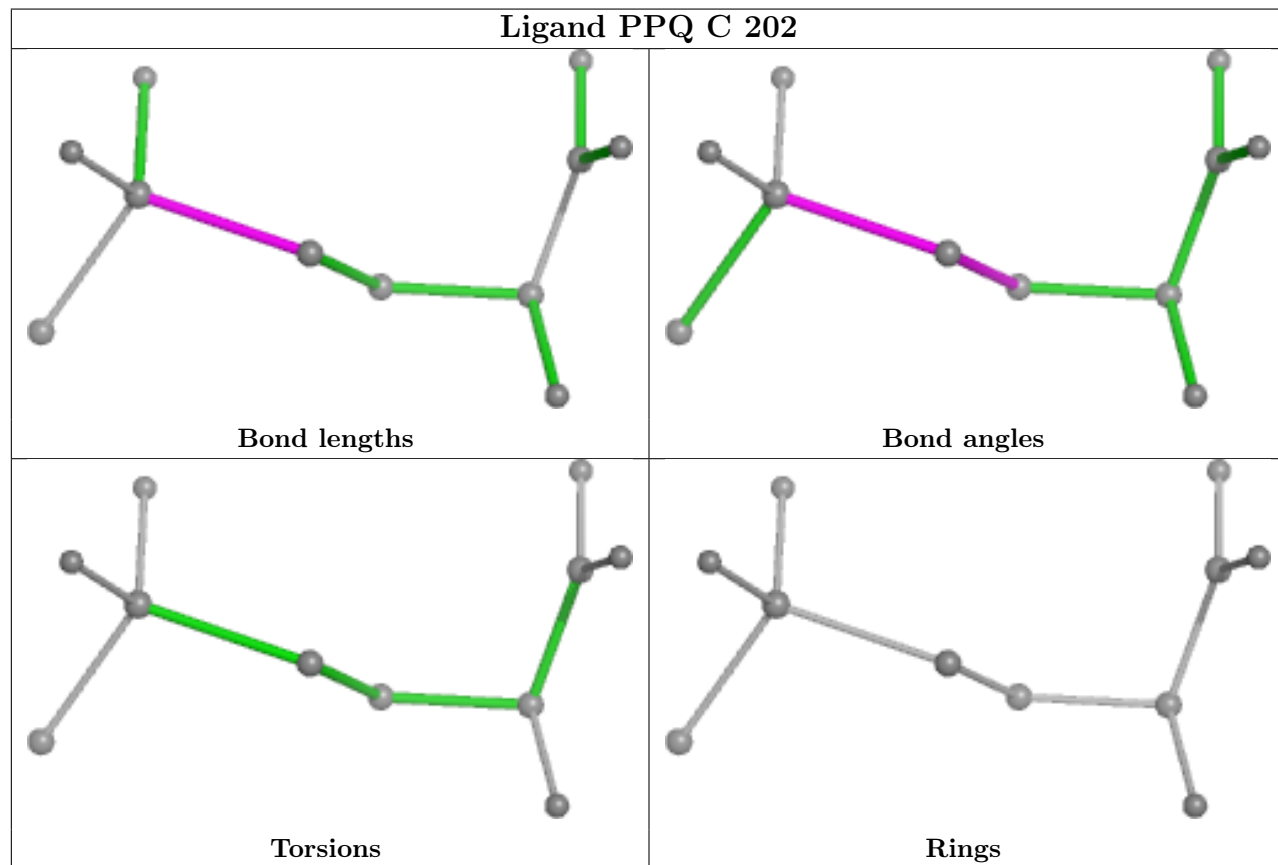
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

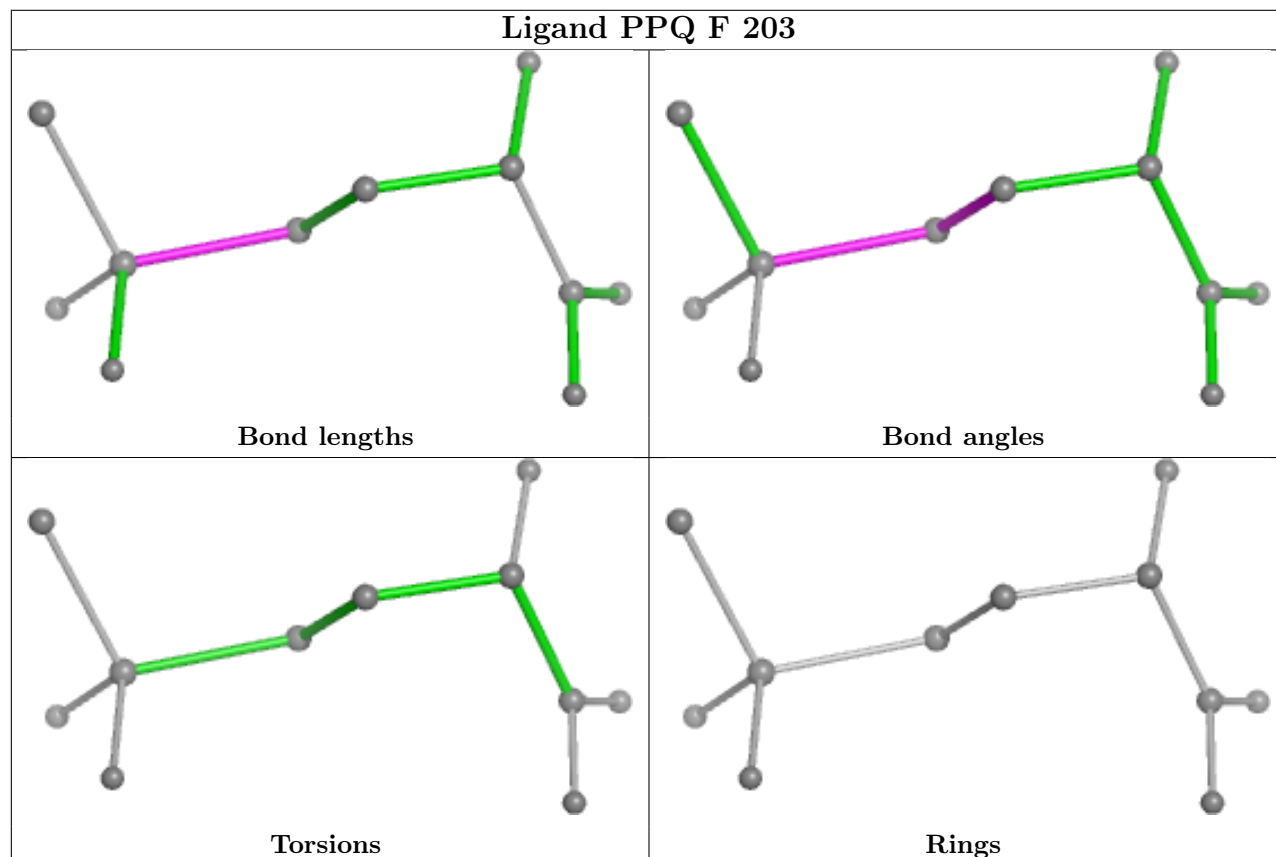
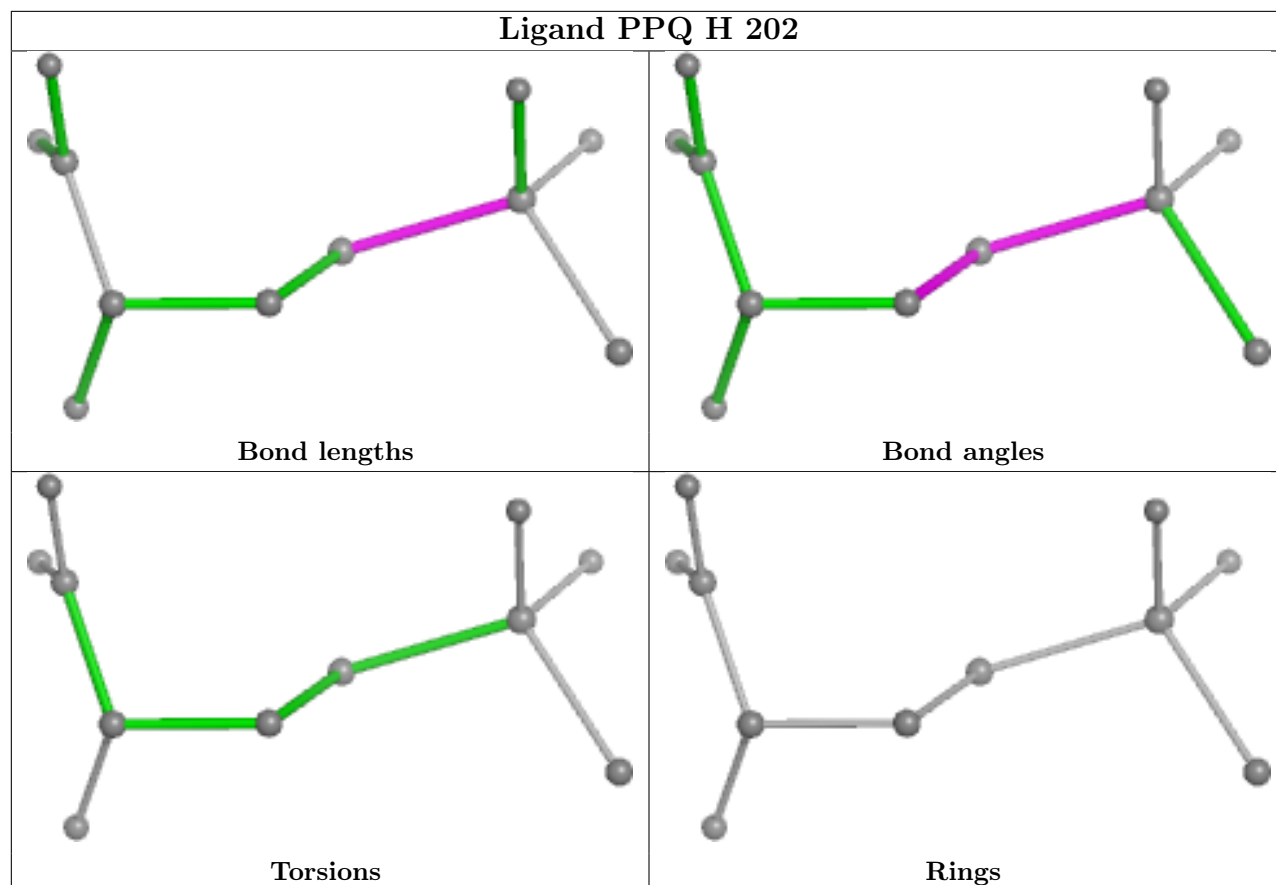


Ligand PPQ D 202

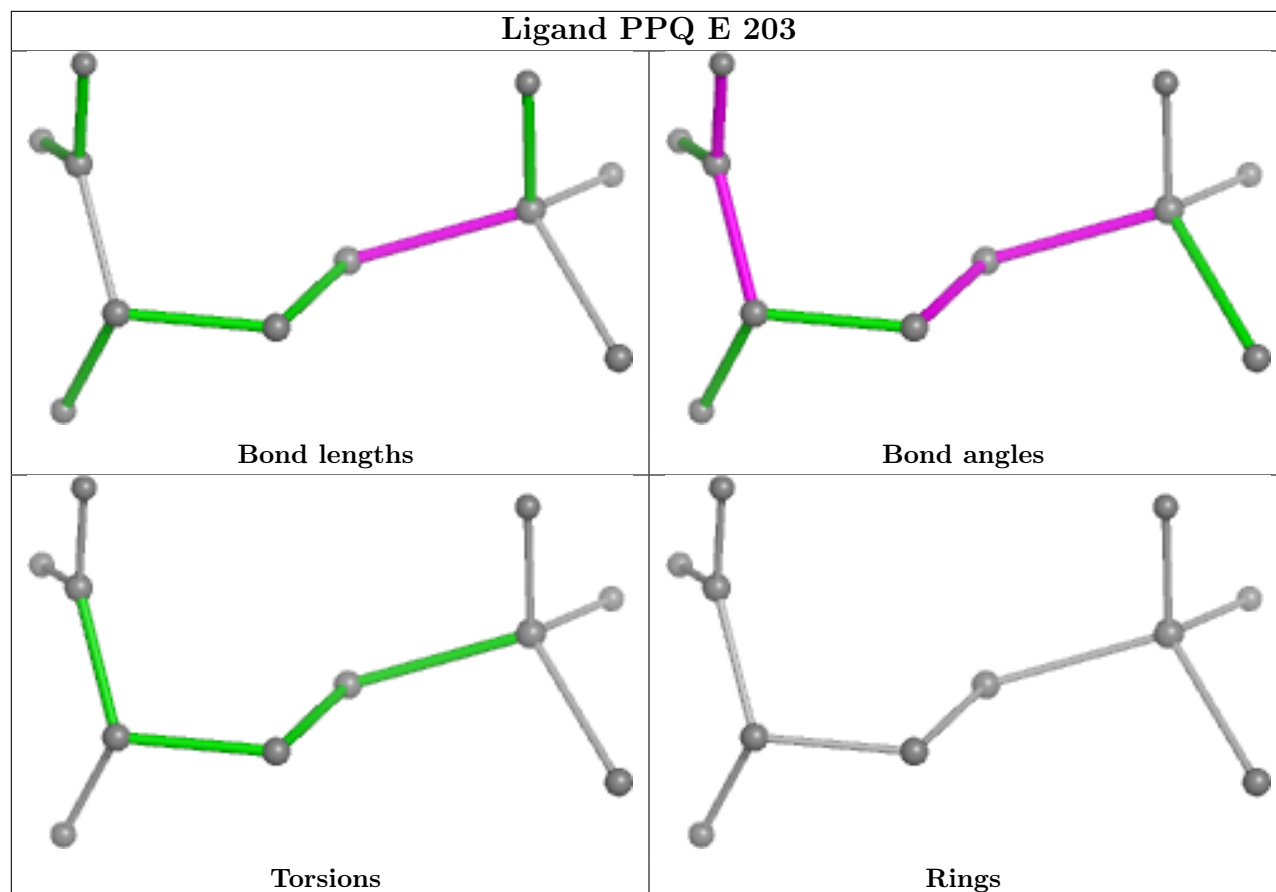


Ligand PPQ C 202

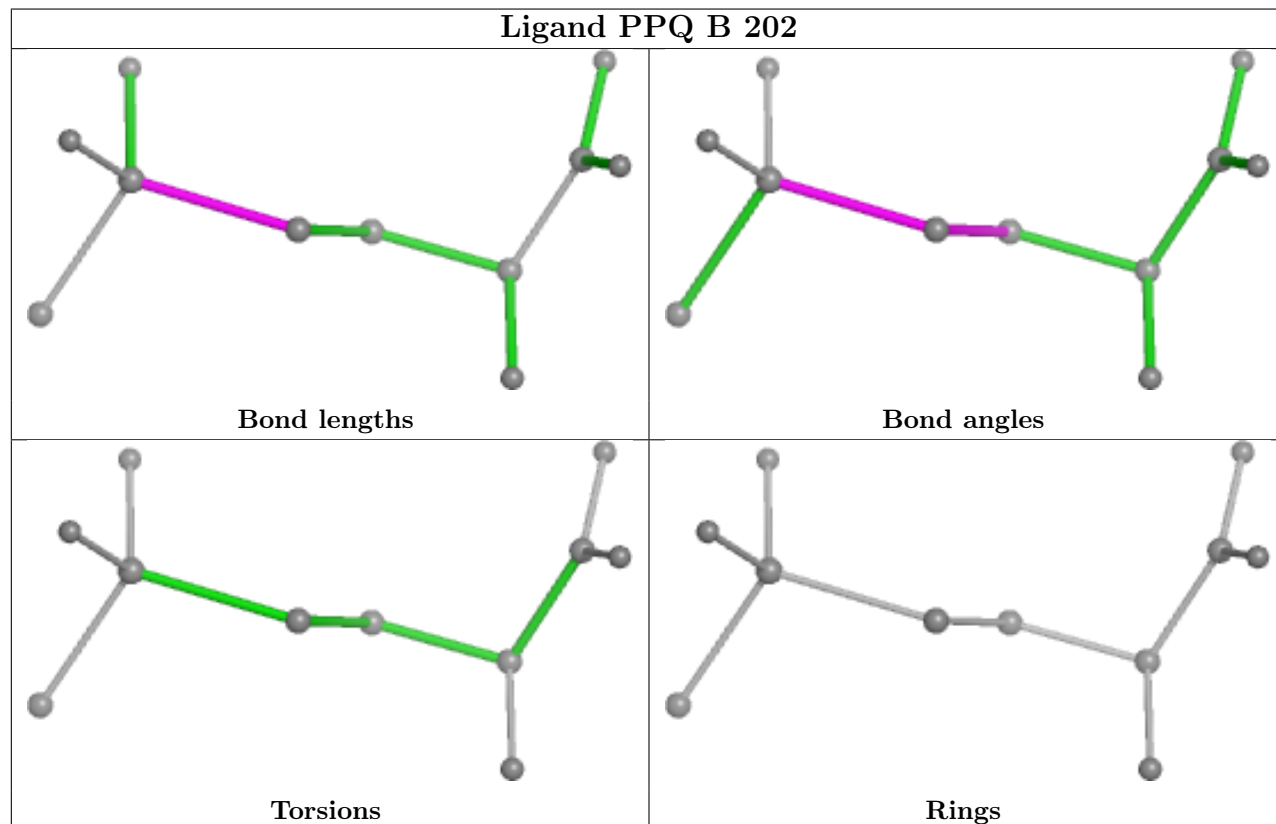




Ligand PPQ E 203



Ligand PPQ B 202



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	175/187 (93%)	0.17	2 (1%) 77 74	33, 42, 58, 81	0
1	B	171/187 (91%)	0.13	1 (0%) 85 83	29, 41, 63, 90	0
1	C	174/187 (93%)	0.01	2 (1%) 77 74	26, 38, 58, 76	0
1	D	172/187 (91%)	-0.07	0 100 100	26, 35, 50, 65	0
1	E	174/187 (93%)	-0.07	2 (1%) 77 74	27, 34, 48, 60	0
1	F	172/187 (91%)	0.05	3 (1%) 69 65	26, 39, 55, 73	0
1	G	174/187 (93%)	0.06	3 (1%) 69 65	27, 38, 55, 68	0
1	H	171/187 (91%)	0.43	4 (2%) 61 58	28, 48, 69, 80	0
All	All	1383/1496 (92%)	0.09	17 (1%) 76 73	26, 39, 59, 90	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	63	ALA	4.0
1	H	13	ASP	3.7
1	B	63	ALA	3.5
1	C	176	ALA	3.3
1	C	3	PRO	2.9
1	G	176	ALA	2.9
1	H	96	GLY	2.8
1	G	3	PRO	2.8
1	F	63	ALA	2.8
1	F	140	GLY	2.5
1	E	3	PRO	2.4
1	F	64	LYS	2.3
1	H	60	ALA	2.3
1	A	2	THR	2.3
1	E	30	ILE	2.2
1	A	29	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	G	125	GLY	2.1

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 monosaccharides 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.

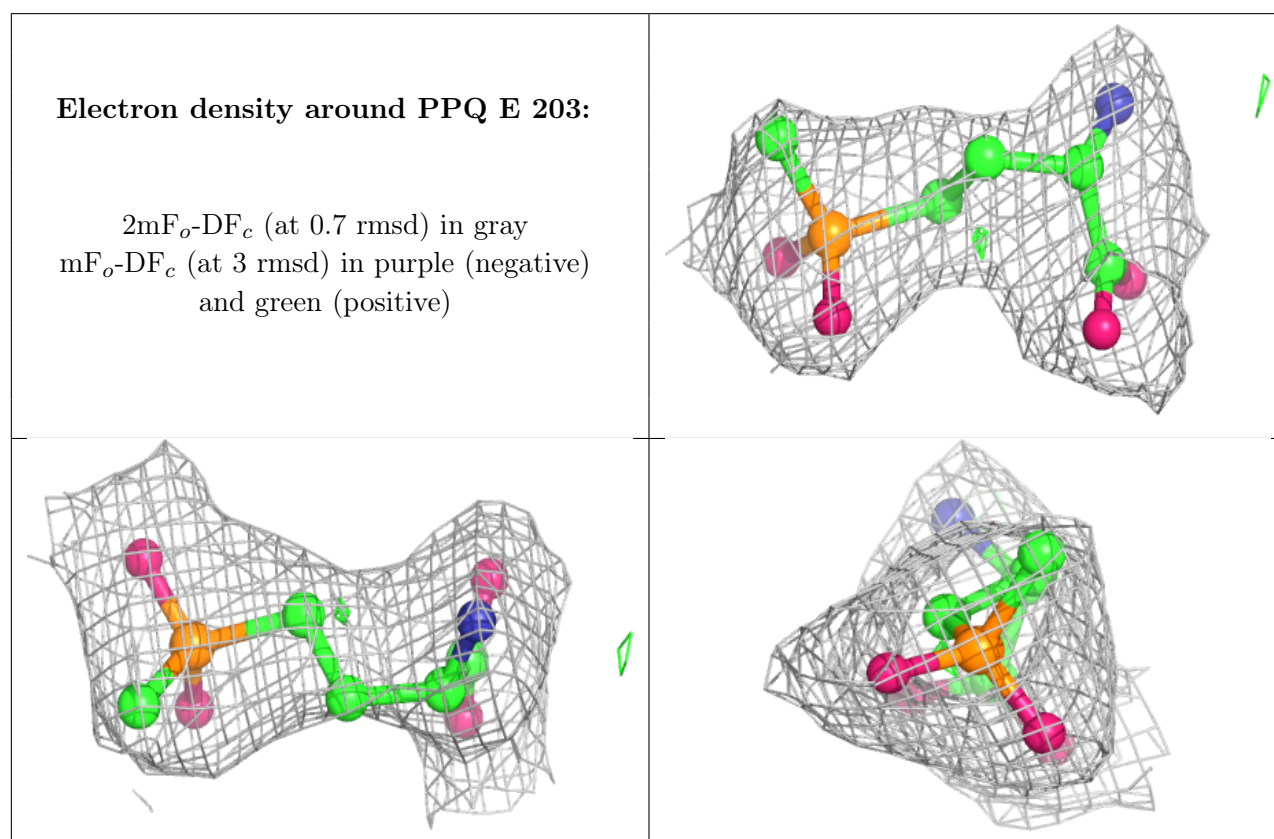
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	ACT	G	202	4/4	0.71	0.17	45,51,52,55	0
4	ACT	C	203	4/4	0.80	0.15	47,49,52,54	0
4	ACT	A	203	4/4	0.81	0.20	50,53,53,55	0
4	ACT	G	203	4/4	0.82	0.15	41,42,47,47	0
7	PEG	G	205	7/7	0.84	0.17	47,48,52,55	0
6	EDO	H	204	4/4	0.85	0.12	44,45,46,50	0
2	SO4	F	202	5/5	0.89	0.13	53,54,58,69	0
6	EDO	D	203	4/4	0.89	0.16	31,32,34,35	0
6	EDO	G	204	4/4	0.91	0.15	36,37,43,45	0
2	SO4	H	201	5/5	0.91	0.10	59,61,67,72	0
2	SO4	E	202	5/5	0.91	0.16	36,38,43,47	5
2	SO4	C	201	5/5	0.92	0.10	48,50,52,57	0
3	PPQ	E	203	11/11	0.92	0.10	31,38,39,41	0
6	EDO	E	204	4/4	0.93	0.10	33,35,36,37	0
3	PPQ	H	203	11/11	0.94	0.09	29,39,47,50	0
3	PPQ	C	202	11/11	0.94	0.10	29,35,43,45	0
3	PPQ	D	202	11/11	0.95	0.09	26,33,38,39	0
2	SO4	A	201	5/5	0.95	0.07	41,42,49,49	0
3	PPQ	H	202	11/11	0.95	0.09	32,36,43,45	0
2	SO4	E	201	5/5	0.95	0.08	39,39,44,48	0
5	NA	C	204	1/1	0.95	0.12	30,30,30,30	0
3	PPQ	B	202	11/11	0.96	0.09	29,33,40,42	0

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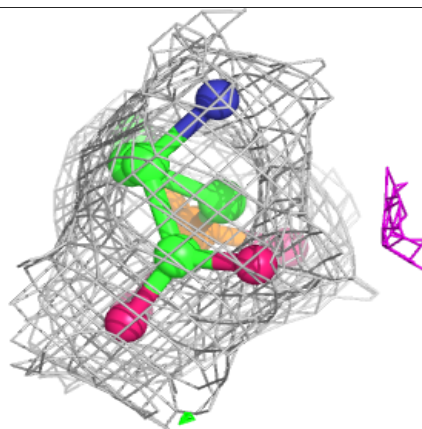
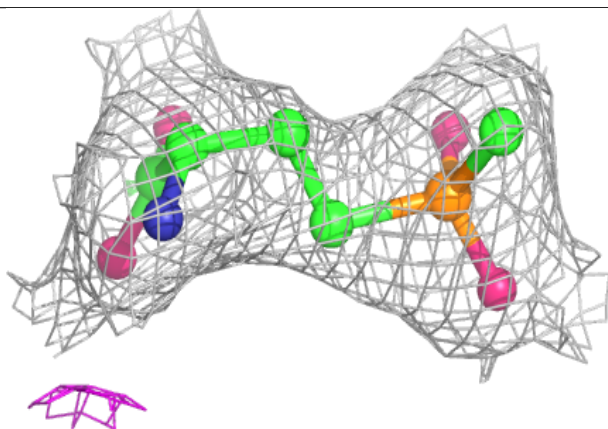
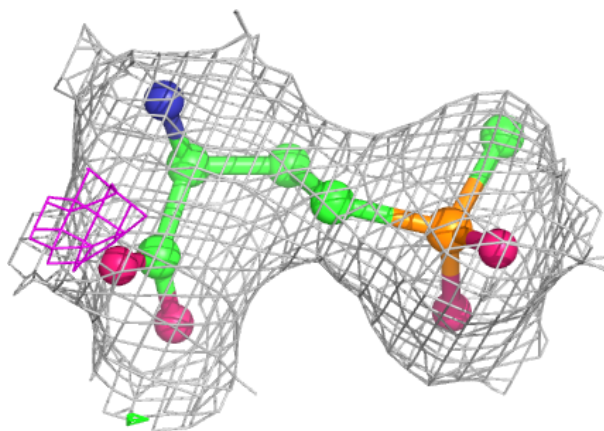
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	PPQ	A	202	11/11	0.96	0.10	34,39,43,43	0
3	PPQ	F	203	11/11	0.96	0.08	25,32,37,40	0
2	SO4	B	201	5/5	0.97	0.07	38,40,44,45	0
2	SO4	G	201	5/5	0.97	0.08	41,43,45,45	0
2	SO4	D	201	5/5	0.97	0.07	28,38,40,40	0
2	SO4	F	201	5/5	0.98	0.06	32,36,38,40	0

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.

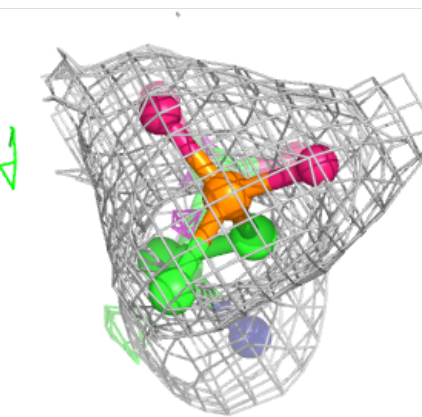
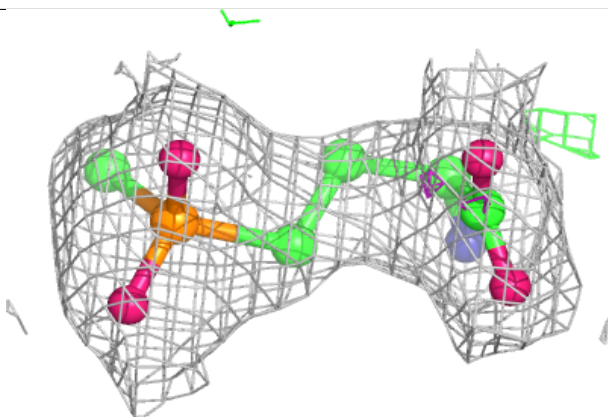
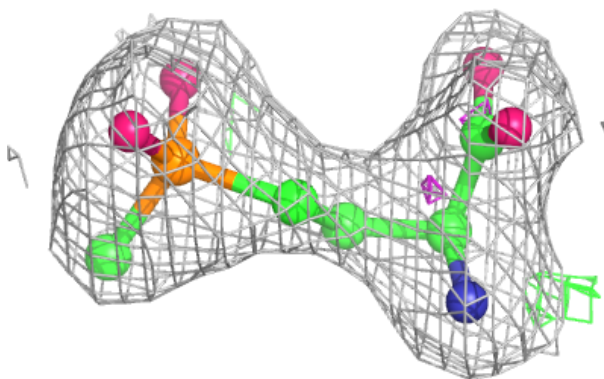


Electron density around PPQ H 203:

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

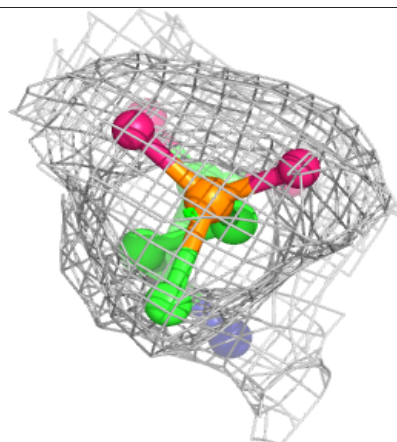
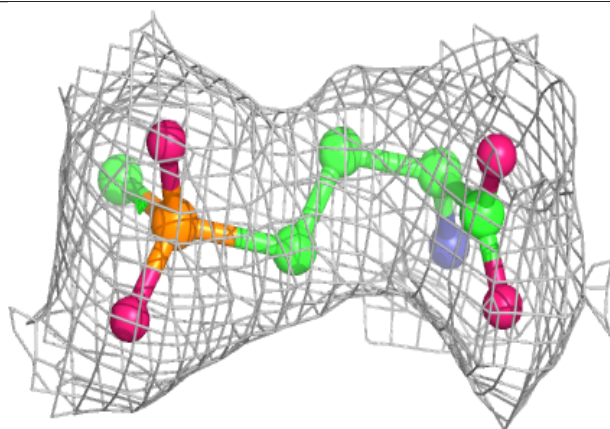
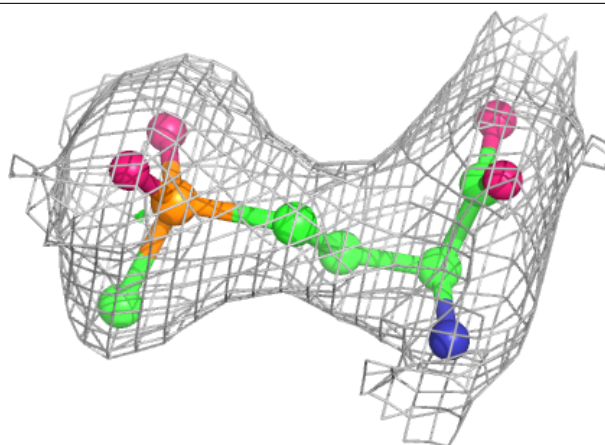
**Electron density around PPQ C 202:**

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

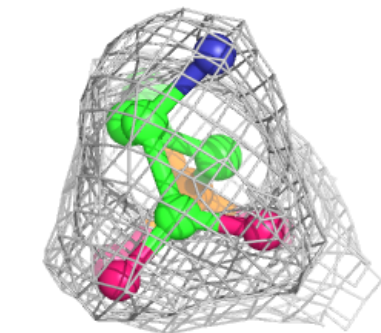
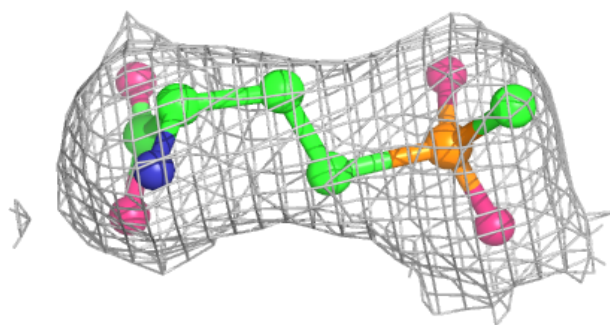
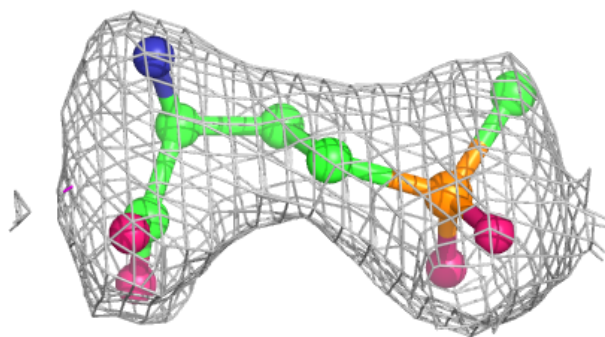


Electron density around PPQ D 202:

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

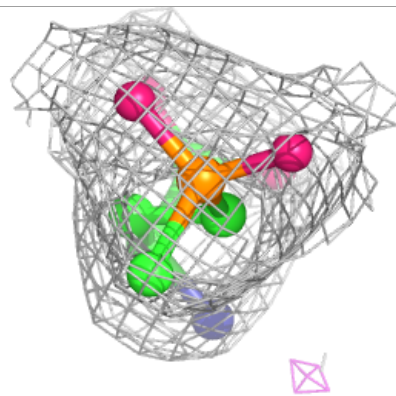
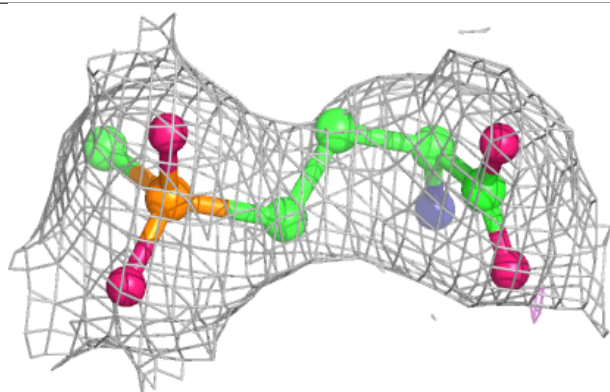
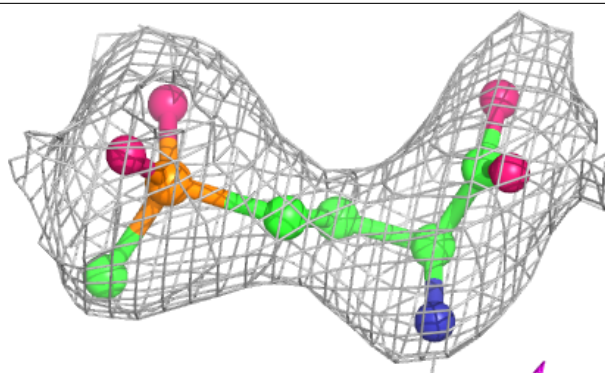
**Electron density around PPQ H 202:**

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

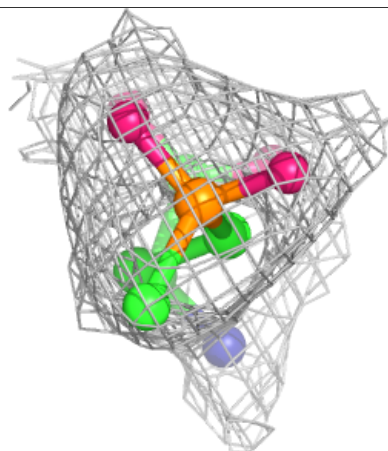
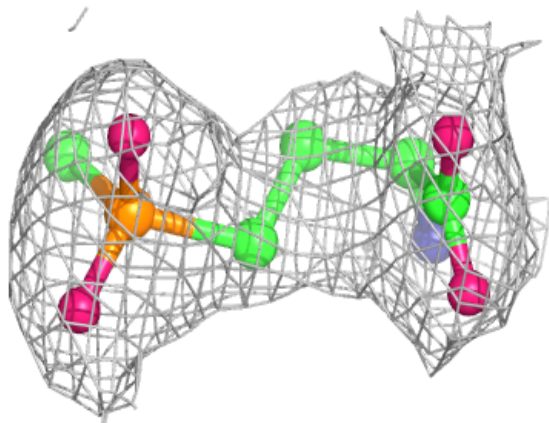
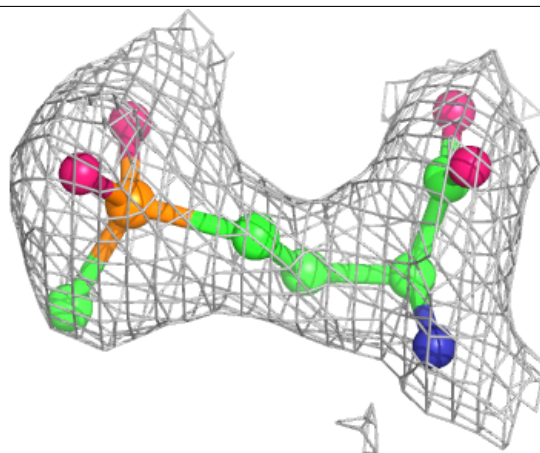


Electron density around PPQ B 202:

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

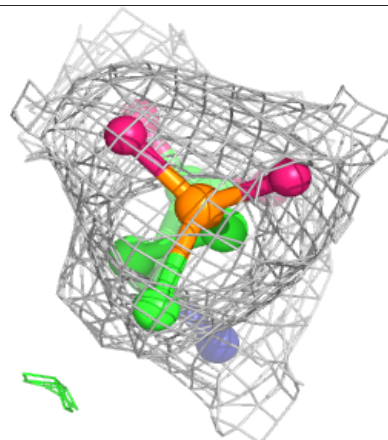
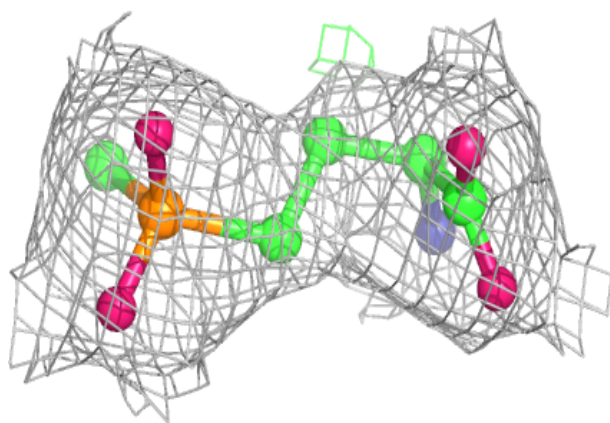
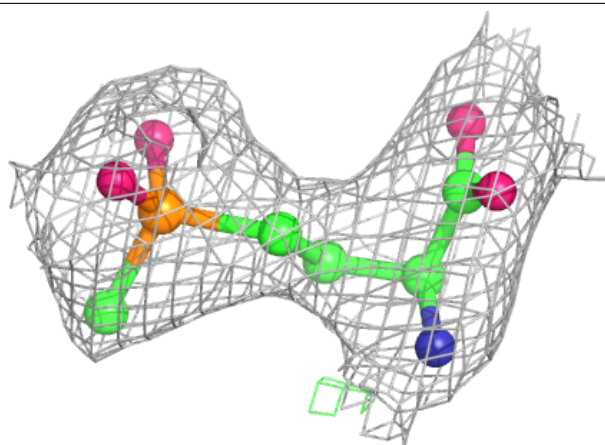
**Electron density around PPQ A 202:**

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



Electron density around PPQ F 203:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.