



Full wwPDB X-ray Structure Validation Report ⓘ

May 24, 2020 – 01:37 pm BST

PDB ID : 6U49
Title : Structure-based discovery of a novel small-molecule inhibitor of methicillin-resistant *S. aureus*
Authors : Liu, J.; Kozhaya, L.; Torres, V.J.; Unutmaz, D.; Lu, M.
Deposited on : 2019-08-23
Resolution : 2.35 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 following versions of software and data (see [references ⓘ](#)) 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 : 2.11
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) : 2.11

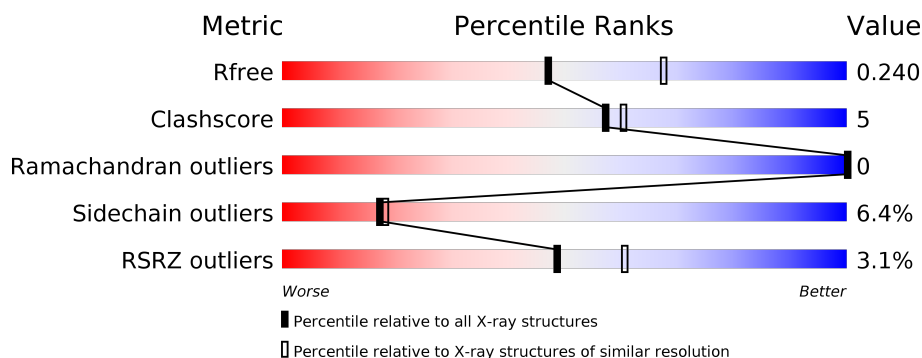
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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.



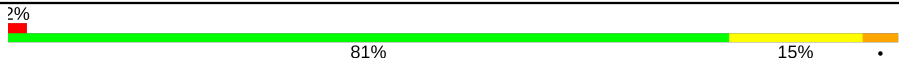
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1164 (2.36-2.36)
Clashscore	141614	1232 (2.36-2.36)
Ramachandran outliers	138981	1211 (2.36-2.36)
Sidechain outliers	138945	1212 (2.36-2.36)
RSRZ outliers	127900	1150 (2.36-2.36)

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 on 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	293	<div> <div>2%</div> <div> <div></div> <div>81%</div> <div>15%</div> <div>• •</div> </div> </div>
1	B	293	<div> <div>2%</div> <div> <div></div> <div>82%</div> <div>14%</div> <div>•</div> </div> </div>
1	C	293	<div> <div>5%</div> <div> <div></div> <div>84%</div> <div>13%</div> <div>•</div> </div> </div>
1	D	293	<div> <div>5%</div> <div> <div></div> <div>84%</div> <div>13%</div> <div>•</div> </div> </div>
1	E	293	<div> <div>3%</div> <div> <div></div> <div>80%</div> <div>15%</div> <div>5%</div> <div>•</div> </div> </div>
1	F	293	<div> <div>3%</div> <div> <div></div> <div>80%</div> <div>14%</div> <div>5%</div> <div>•</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	G	293	 A horizontal bar chart showing the quality of chain G. The bar is divided into four segments: a small red segment at the beginning labeled '2%', followed by a large green segment labeled '81%', then a yellow segment labeled '15%', and a small orange segment at the end. A small black dot is located at the far right end of the bar.

2 Entry composition [i](#)

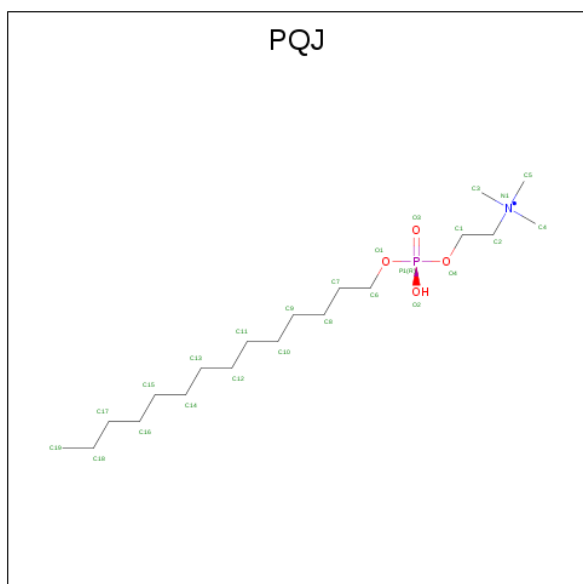
There are 4 unique types of molecules in this entry. The entry contains 17541 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Alpha-hemolysin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	293	Total	C	N	O	S	0	0	0
			2345	1472	401	465	7			
1	B	293	Total	C	N	O	S	0	0	0
			2345	1472	401	465	7			
1	C	293	Total	C	N	O	S	0	0	0
			2345	1472	401	465	7			
1	D	293	Total	C	N	O	S	0	0	0
			2345	1472	401	465	7			
1	E	293	Total	C	N	O	S	0	0	0
			2345	1472	401	465	7			
1	F	293	Total	C	N	O	S	0	0	0
			2345	1472	401	465	7			
1	G	293	Total	C	N	O	S	0	0	0
			2345	1472	401	465	7			

- Molecule 2 is fos-choline-14 (three-letter code: PQJ) (formula: $C_{19}H_{43}NO_4P$) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			12	6	1	4	1		
2	A	1	Total	C	N	O	P	0	0
			12	6	1	4	1		
2	A	1	Total	C	N	O	P	0	0
			11	5	1	4	1		
2	B	1	Total	C	N	O	P	0	0
			11	5	1	4	1		
2	B	1	Total	C	N	O	P	0	0
			12	6	1	4	1		
2	B	1	Total	C	N	O	P	0	0
			12	6	1	4	1		
2	C	1	Total	C	N	O	P	0	0
			12	6	1	4	1		
2	C	1	Total	C	N	O	P	0	0
			11	5	1	4	1		
2	D	1	Total	C	N	O	P	0	0
			11	5	1	4	1		
2	D	1	Total	C	N	O	P	0	0
			12	6	1	4	1		
2	D	1	Total	C	N	O	P	0	0
			12	6	1	4	1		
2	E	1	Total	C	N	O	P	0	0
			12	6	1	4	1		
2	E	1	Total	C	N	O	P	0	0
			12	6	1	4	1		
2	E	1	Total	C	N	O	P	0	0
			11	5	1	4	1		
2	E	1	Total	C	N	O	P	0	0
			11	5	1	4	1		
2	F	1	Total	C	N	O	P	0	0
			12	6	1	4	1		
2	F	1	Total	C	N	O	P	0	0
			12	6	1	4	1		
2	F	1	Total	C	N	O	P	0	0
			11	5	1	4	1		
2	F	1	Total	C	N	O	P	0	0
			11	5	1	4	1		
2	G	1	Total	C	N	O	P	0	0
			12	6	1	4	1		
2	G	1	Total	C	N	O	P	0	0
			12	6	1	4	1		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		
3	D	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	G	1	Total	O	S	0	0
			5	4	1		

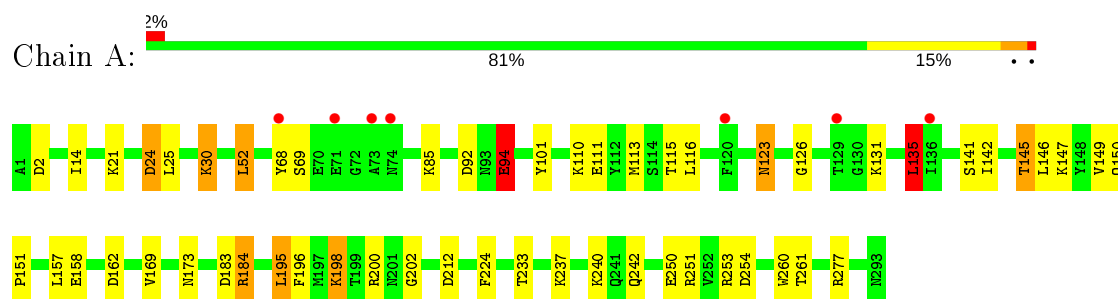
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	121	Total	O	0	0
			121	121		
4	B	133	Total	O	0	0
			133	133		
4	C	95	Total	O	0	0
			95	95		
4	D	114	Total	O	0	0
			114	114		
4	E	123	Total	O	0	0
			123	123		
4	F	141	Total	O	0	0
			141	141		
4	G	130	Total	O	0	0
			130	130		

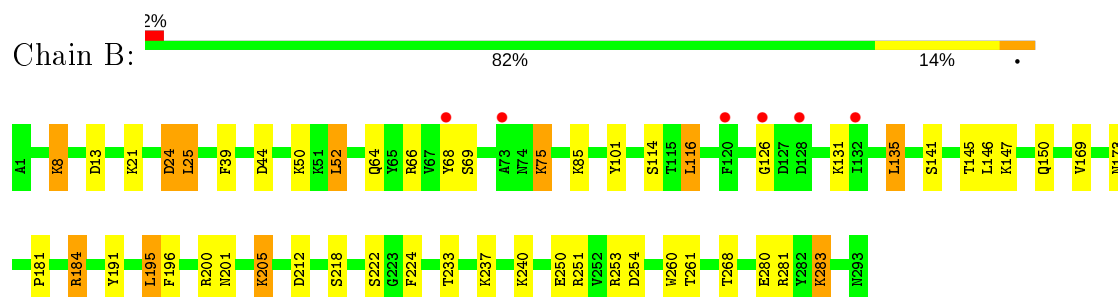
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

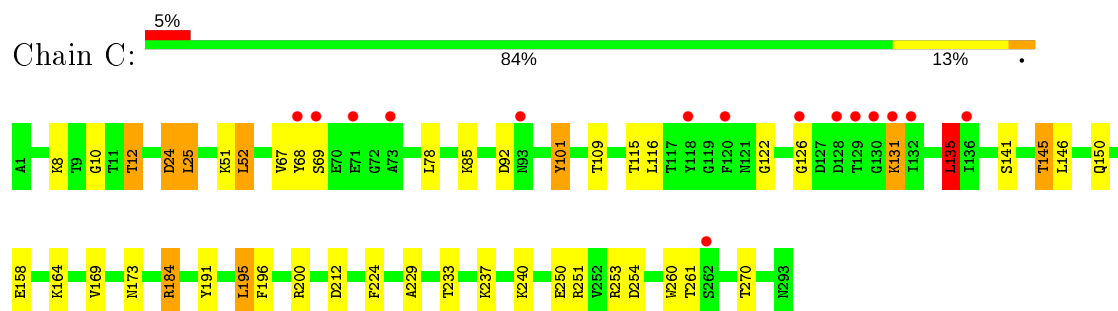
• Molecule 1: Alpha-hemolysin



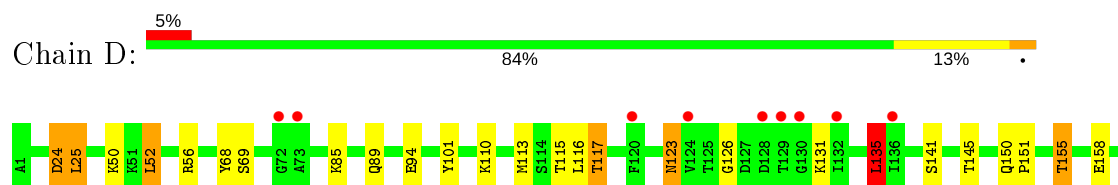
• Molecule 1: Alpha-hemolysin



• Molecule 1: Alpha-hemolysin

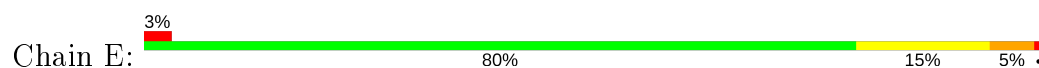


• Molecule 1: Alpha-hemolysin

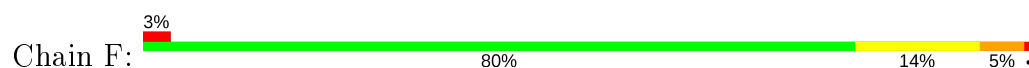




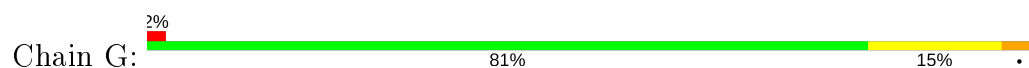
• Molecule 1: Alpha-hemolysin



• Molecule 1: Alpha-hemolysin



• Molecule 1: Alpha-hemolysin



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	150.37Å 135.04Å 132.45Å 90.00° 91.53° 90.00°	Depositor
Resolution (Å)	132.40 – 2.35 47.27 – 2.35	Depositor EDS
% Data completeness (in resolution range)	94.3 (132.40-2.35) 94.3 (47.27-2.35)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.93 (at 2.34Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.194 , 0.239 0.195 , 0.240	Depositor DCC
R_{free} test set	5010 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	28.7	Xtriage
Anisotropy	0.616	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 34.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.005 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	17541	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.53% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: PQJ, 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	0.98	1/2397 (0.0%)	1.21	27/3243 (0.8%)
1	B	0.96	0/2397	1.16	20/3243 (0.6%)
1	C	0.95	1/2397 (0.0%)	1.12	13/3243 (0.4%)
1	D	1.00	3/2397 (0.1%)	1.15	16/3243 (0.5%)
1	E	0.98	1/2397 (0.0%)	1.19	20/3243 (0.6%)
1	F	1.05	7/2397 (0.3%)	1.19	26/3243 (0.8%)
1	G	0.99	1/2397 (0.0%)	1.17	24/3243 (0.7%)
All	All	0.99	14/16779 (0.1%)	1.17	146/22701 (0.6%)

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	24	ASP	CB-CG	-8.42	1.34	1.51
1	F	158	GLU	CD-OE1	8.41	1.34	1.25
1	F	250	GLU	CD-OE1	-8.03	1.16	1.25
1	D	94	GLU	CD-OE1	7.16	1.33	1.25
1	D	158	GLU	CD-OE2	6.28	1.32	1.25
1	F	148	TYR	CE1-CZ	6.06	1.46	1.38
1	G	250	GLU	CD-OE1	-6.01	1.19	1.25
1	E	106	SER	CB-OG	-5.66	1.34	1.42
1	C	158	GLU	CD-OE2	5.51	1.31	1.25
1	A	158	GLU	CD-OE1	5.40	1.31	1.25
1	F	74	ASN	CB-CG	5.33	1.63	1.51
1	F	94	GLU	CD-OE2	5.19	1.31	1.25
1	F	240	LYS	CD-CE	5.14	1.64	1.51
1	D	289	GLU	CD-OE2	-5.13	1.20	1.25

All (146) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	251	ARG	NE-CZ-NH2	-17.00	111.80	120.30
1	E	251	ARG	NE-CZ-NH2	-16.56	112.02	120.30
1	C	251	ARG	NE-CZ-NH2	-16.24	112.18	120.30
1	A	251	ARG	NE-CZ-NH2	-16.16	112.22	120.30
1	G	251	ARG	NE-CZ-NH2	-15.97	112.31	120.30
1	D	251	ARG	NE-CZ-NH2	-14.85	112.88	120.30
1	F	251	ARG	NE-CZ-NH2	-14.36	113.12	120.30
1	F	251	ARG	NE-CZ-NH1	13.30	126.95	120.30
1	A	251	ARG	NE-CZ-NH1	13.19	126.90	120.30
1	E	251	ARG	NE-CZ-NH1	13.11	126.85	120.30
1	B	251	ARG	NE-CZ-NH1	13.01	126.81	120.30
1	D	251	ARG	NE-CZ-NH1	12.66	126.63	120.30
1	G	251	ARG	NE-CZ-NH1	12.51	126.56	120.30
1	C	251	ARG	NE-CZ-NH1	11.94	126.27	120.30
1	E	123	ASN	CB-CA-C	-10.98	88.44	110.40
1	C	184	ARG	NE-CZ-NH2	-10.96	114.82	120.30
1	A	123	ASN	CB-CA-C	-10.85	88.70	110.40
1	G	123	ASN	CB-CA-C	-10.80	88.81	110.40
1	D	123	ASN	CB-CA-C	-10.44	89.53	110.40
1	F	24	ASP	CB-CG-OD2	-10.07	109.23	118.30
1	D	89	GLN	CA-CB-CG	10.03	135.46	113.40
1	E	169	VAL	CG1-CB-CG2	9.64	126.33	110.90
1	A	202	GLY	N-CA-C	-9.44	89.50	113.10
1	B	135	LEU	CA-CB-CG	9.37	136.85	115.30
1	F	169	VAL	CG1-CB-CG2	9.11	125.47	110.90
1	E	135	LEU	CA-CB-CG	9.04	136.10	115.30
1	C	135	LEU	CA-CB-CG	8.63	135.14	115.30
1	A	52	LEU	CA-CB-CG	8.56	135.00	115.30
1	F	240	LYS	CD-CE-NZ	8.52	131.30	111.70
1	B	75	LYS	CD-CE-NZ	8.49	131.22	111.70
1	D	135	LEU	CA-CB-CG	8.29	134.37	115.30
1	G	135	LEU	CB-CG-CD2	8.28	125.08	111.00
1	A	184	ARG	NE-CZ-NH2	-8.27	116.16	120.30
1	A	135	LEU	CA-CB-CG	8.23	134.22	115.30
1	A	94	GLU	CA-CB-CG	-8.12	95.55	113.40
1	E	25	LEU	CB-CG-CD1	8.08	124.73	111.00
1	C	52	LEU	CA-CB-CG	8.07	133.86	115.30
1	E	52	LEU	CA-CB-CG	8.05	133.82	115.30
1	B	25	LEU	CB-CG-CD1	7.99	124.58	111.00
1	G	25	LEU	CB-CG-CD1	7.99	124.58	111.00
1	F	52	LEU	CA-CB-CG	7.95	133.58	115.30
1	G	201	ASN	N-CA-CB	-7.87	96.44	110.60
1	A	94	GLU	OE1-CD-OE2	-7.76	113.99	123.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	52	LEU	CA-CB-CG	7.70	133.01	115.30
1	E	184	ARG	NE-CZ-NH2	-7.68	116.46	120.30
1	F	280	GLU	CA-CB-CG	7.61	130.13	113.40
1	F	135	LEU	CA-CB-CG	7.53	132.62	115.30
1	B	184	ARG	NE-CZ-NH2	-7.49	116.56	120.30
1	C	25	LEU	CB-CG-CD1	7.41	123.59	111.00
1	B	52	LEU	CA-CB-CG	7.40	132.33	115.30
1	F	200	ARG	CG-CD-NE	7.39	127.32	111.80
1	G	52	LEU	CA-CB-CG	7.09	131.62	115.30
1	E	50	LYS	CD-CE-NZ	-7.07	95.45	111.70
1	D	184	ARG	NE-CZ-NH2	-7.06	116.77	120.30
1	F	201	ASN	N-CA-CB	-6.97	98.05	110.60
1	A	25	LEU	CB-CG-CD2	6.96	122.84	111.00
1	G	201	ASN	CB-CA-C	-6.95	96.50	110.40
1	F	25	LEU	CB-CG-CD1	6.83	122.62	111.00
1	G	190	VAL	CG1-CB-CG2	6.79	121.77	110.90
1	F	66	ARG	CB-CG-CD	6.72	129.08	111.60
1	F	111	GLU	CA-CB-CG	6.71	128.16	113.40
1	B	253	ARG	NE-CZ-NH1	-6.67	116.97	120.30
1	E	212	ASP	CB-CG-OD1	6.65	124.28	118.30
1	D	24	ASP	CB-CG-OD2	6.63	124.26	118.30
1	A	25	LEU	CA-CB-CG	6.60	130.48	115.30
1	C	212	ASP	CB-CG-OD1	6.51	124.16	118.30
1	F	201	ASN	CB-CA-C	-6.47	97.46	110.40
1	E	204	MET	CG-SD-CE	-6.37	90.02	100.20
1	F	212	ASP	CB-CG-OD1	6.34	124.01	118.30
1	D	25	LEU	CB-CG-CD1	6.32	121.74	111.00
1	A	212	ASP	CB-CG-OD1	6.31	123.98	118.30
1	B	212	ASP	CB-CG-OD1	6.30	123.97	118.30
1	A	24	ASP	CB-CG-OD2	6.24	123.91	118.30
1	C	24	ASP	CB-CG-OD2	6.22	123.90	118.30
1	G	212	ASP	CB-CG-OD1	6.21	123.89	118.30
1	E	289	GLU	OE1-CD-OE2	-6.18	115.89	123.30
1	D	212	ASP	CB-CG-OD1	6.17	123.85	118.30
1	G	212	ASP	CB-CG-OD2	-6.14	112.78	118.30
1	A	123	ASN	N-CA-CB	-6.10	99.62	110.60
1	A	242	GLN	CA-CB-CG	6.09	126.79	113.40
1	G	123	ASN	N-CA-CB	-6.04	99.73	110.60
1	B	24	ASP	CB-CG-OD2	5.92	123.63	118.30
1	E	24	ASP	CB-CG-OD1	-5.91	112.98	118.30
1	G	135	LEU	CA-CB-CG	5.91	128.89	115.30
1	A	253	ARG	NE-CZ-NH1	-5.90	117.35	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	283	LYS	CD-CE-NZ	5.89	125.25	111.70
1	B	205	LYS	CA-CB-CG	5.86	126.29	113.40
1	F	251	ARG	CD-NE-CZ	5.86	131.80	123.60
1	A	198	LYS	CD-CE-NZ	5.83	125.11	111.70
1	A	116	LEU	CB-CG-CD1	5.82	120.89	111.00
1	G	281	ARG	NE-CZ-NH2	5.81	123.20	120.30
1	B	50	LYS	CD-CE-NZ	-5.80	98.36	111.70
1	E	123	ASN	N-CA-CB	-5.76	100.23	110.60
1	F	281	ARG	NE-CZ-NH1	-5.72	117.44	120.30
1	E	104	ARG	NE-CZ-NH2	-5.71	117.44	120.30
1	A	30	LYS	CB-CG-CD	5.71	126.44	111.60
1	F	51	LYS	CD-CE-NZ	-5.68	98.65	111.70
1	B	146	LEU	CB-CG-CD2	-5.67	101.36	111.00
1	D	158	GLU	CG-CD-OE2	5.65	129.59	118.30
1	A	24	ASP	CB-CG-OD1	-5.57	113.28	118.30
1	D	251	ARG	CD-NE-CZ	5.57	131.40	123.60
1	D	116	LEU	CB-CG-CD1	5.55	120.43	111.00
1	C	251	ARG	CD-NE-CZ	5.53	131.34	123.60
1	F	290	GLU	N-CA-CB	5.51	120.52	110.60
1	G	24	ASP	CB-CG-OD1	-5.49	113.36	118.30
1	C	253	ARG	NE-CZ-NH1	-5.49	117.56	120.30
1	C	24	ASP	CB-CG-OD1	-5.47	113.38	118.30
1	A	94	GLU	CG-CD-OE2	5.46	129.22	118.30
1	D	116	LEU	CA-CB-CG	5.45	127.82	115.30
1	G	131	LYS	CD-CE-NZ	5.39	124.10	111.70
1	F	201	ASN	N-CA-C	5.38	125.53	111.00
1	G	50	LYS	CD-CE-NZ	-5.37	99.35	111.70
1	B	280	GLU	OE1-CD-OE2	-5.37	116.86	123.30
1	E	281	ARG	NE-CZ-NH1	-5.36	117.62	120.30
1	G	273	LYS	CD-CE-NZ	5.34	123.98	111.70
1	G	116	LEU	CB-CG-CD2	5.33	120.07	111.00
1	F	24	ASP	CB-CG-OD1	5.32	123.09	118.30
1	C	146	LEU	CB-CG-CD2	-5.32	101.95	111.00
1	A	251	ARG	CD-NE-CZ	5.31	131.03	123.60
1	E	24	ASP	CB-CG-OD2	5.30	123.07	118.30
1	B	251	ARG	CD-NE-CZ	5.29	131.01	123.60
1	E	283	LYS	CB-CG-CD	5.28	125.33	111.60
1	E	163	LYS	CD-CE-NZ	-5.27	99.58	111.70
1	G	158	GLU	OE1-CD-OE2	5.27	129.62	123.30
1	G	158	GLU	CG-CD-OE2	-5.25	107.80	118.30
1	C	164	LYS	CD-CE-NZ	5.25	123.77	111.70
1	A	116	LEU	CA-CB-CG	5.24	127.36	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	212	ASP	CB-CG-OD2	-5.24	113.59	118.30
1	F	116	LEU	CB-CG-CD2	5.22	119.88	111.00
1	B	44	ASP	CB-CG-OD2	-5.21	113.61	118.30
1	G	201	ASN	N-CA-C	5.21	125.06	111.00
1	A	212	ASP	CB-CG-OD2	-5.19	113.62	118.30
1	G	251	ARG	CD-NE-CZ	5.19	130.87	123.60
1	D	24	ASP	CB-CG-OD1	-5.19	113.63	118.30
1	F	184	ARG	NE-CZ-NH2	-5.16	117.72	120.30
1	B	13	ASP	CB-CG-OD2	-5.14	113.67	118.30
1	E	251	ARG	CD-NE-CZ	5.14	130.79	123.60
1	A	158	GLU	CG-CD-OE2	-5.13	108.03	118.30
1	F	123	ASN	N-CA-CB	5.12	119.81	110.60
1	D	158	GLU	OE1-CD-OE2	-5.12	117.16	123.30
1	A	162	ASP	CB-CG-OD1	5.09	122.88	118.30
1	A	2	ASP	CB-CG-OD1	5.05	122.84	118.30
1	B	281	ARG	NE-CZ-NH1	-5.04	117.78	120.30
1	F	250	GLU	CG-CD-OE2	5.02	128.34	118.30
1	B	116	LEU	CB-CG-CD2	5.00	119.51	111.00
1	G	253	ARG	NE-CZ-NH1	-5.00	117.80	120.30

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	2345	0	2270	30	0
1	B	2345	0	2270	25	0
1	C	2345	0	2270	21	0
1	D	2345	0	2270	27	0
1	E	2345	0	2270	28	0
1	F	2345	0	2270	31	0
1	G	2345	0	2270	31	0
2	A	35	0	0	0	0
2	B	35	0	0	0	0
2	C	23	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	35	0	0	0	0
2	E	46	0	0	0	0
2	F	46	0	0	0	0
2	G	24	0	0	0	0
3	B	5	0	0	0	0
3	C	5	0	0	0	0
3	D	5	0	0	0	0
3	E	5	0	0	0	0
3	G	5	0	0	0	0
4	A	121	0	0	8	1
4	B	133	0	0	5	1
4	C	95	0	0	1	0
4	D	114	0	0	3	1
4	E	123	0	0	2	1
4	F	141	0	0	6	0
4	G	130	0	0	7	0
All	All	17541	0	15890	159	2

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 (159) 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:12:THR:HG21	1:F:56:ARG:HH12	1.34	0.93
1:C:12:THR:HG21	1:D:56:ARG:HH12	1.35	0.92
1:G:145:THR:HG22	4:G:560:HOH:O	1.67	0.91
1:F:12:THR:HG21	1:G:56:ARG:HH12	1.35	0.90
1:F:12:THR:HG21	1:G:56:ARG:NH1	1.87	0.89
1:B:268:THR:HG22	4:B:511:HOH:O	1.77	0.85
1:C:12:THR:HG21	1:D:56:ARG:NH1	1.91	0.84
1:E:12:THR:HG21	1:F:56:ARG:NH1	1.93	0.84
1:G:145:THR:CG2	4:G:560:HOH:O	2.22	0.82
1:E:230:THR:HG23	4:E:565:HOH:O	1.81	0.81
1:F:280:GLU:HG2	4:F:511:HOH:O	1.80	0.80
1:D:248:ILE:HD12	4:D:594:HOH:O	1.83	0.79
1:A:145:THR:HG22	4:A:527:HOH:O	1.82	0.78
1:E:115:THR:HG22	1:F:145:THR:HG22	1.65	0.78
1:F:268:THR:HG22	4:F:445:HOH:O	1.83	0.77
1:D:248:ILE:CD1	4:D:594:HOH:O	2.32	0.76
1:A:94:GLU:HG2	4:A:520:HOH:O	1.89	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:115:THR:HG22	1:B:145:THR:HG22	1.74	0.70
1:A:145:THR:CG2	4:A:527:HOH:O	2.39	0.69
1:G:270:THR:HG23	4:G:527:HOH:O	1.93	0.68
1:E:88:LEU:HD13	1:E:230:THR:HG21	1.75	0.66
1:G:268:THR:HG22	4:G:527:HOH:O	1.95	0.66
1:G:74:ASN:HB2	4:G:551:HOH:O	1.98	0.63
1:E:184:ARG:HD2	1:E:254:ASP:OD2	1.99	0.63
1:D:123:ASN:HB2	1:D:135:LEU:HB3	1.82	0.62
1:C:115:THR:HG22	1:D:145:THR:HG22	1.81	0.61
1:A:123:ASN:HB2	1:A:135:LEU:HB3	1.82	0.61
1:G:270:THR:CG2	4:G:527:HOH:O	2.49	0.61
1:G:74:ASN:ND2	4:G:501:HOH:O	2.22	0.60
1:B:218:SER:HB3	4:B:602:HOH:O	2.00	0.60
1:F:184:ARG:HD2	1:F:254:ASP:OD2	2.00	0.60
1:A:145:THR:HG21	4:A:611:HOH:O	2.02	0.60
1:D:184:ARG:HD2	1:D:254:ASP:OD2	2.02	0.60
1:D:113:MET:CE	1:E:147:LYS:HD3	2.31	0.59
1:E:123:ASN:HB2	1:E:135:LEU:HB3	1.85	0.59
1:G:184:ARG:HD2	1:G:254:ASP:OD2	2.02	0.59
1:A:184:ARG:HD2	1:A:254:ASP:OD2	2.02	0.58
1:G:68:TYR:CE2	1:G:69:SER:HB2	2.38	0.58
1:B:184:ARG:HD2	1:B:254:ASP:OD2	2.02	0.58
1:B:66:ARG:HD2	4:B:615:HOH:O	2.03	0.58
1:E:167:TRP:HH2	1:E:230:THR:HG22	1.69	0.58
1:C:184:ARG:HD2	1:C:254:ASP:OD2	2.03	0.57
1:D:113:MET:HE2	1:E:147:LYS:HD3	1.86	0.57
1:G:123:ASN:HB2	1:G:135:LEU:HB3	1.86	0.57
1:A:68:TYR:CE2	1:A:69:SER:HB2	2.40	0.57
1:D:155:THR:HB	1:D:169:VAL:HG22	1.85	0.57
1:D:68:TYR:CE2	1:D:69:SER:HB2	2.40	0.57
1:E:68:TYR:CE2	1:E:69:SER:HB2	2.39	0.57
1:E:30:LYS:HG3	4:E:515:HOH:O	2.03	0.57
1:E:52:LEU:HD22	1:E:233:THR:HG22	1.87	0.56
1:C:68:TYR:CE2	1:C:69:SER:HB2	2.40	0.56
1:F:168:LYS:NZ	4:F:401:HOH:O	2.29	0.56
1:F:68:TYR:CE2	1:F:69:SER:HB2	2.40	0.56
1:B:68:TYR:CE2	1:B:69:SER:HB2	2.40	0.55
1:A:21:LYS:HD2	4:A:533:HOH:O	2.05	0.55
1:E:111:GLU:OE2	1:F:147:LYS:HD2	2.07	0.55
1:D:52:LEU:HD22	1:D:233:THR:HG22	1.89	0.54
1:E:195:LEU:HD13	1:E:196:PHE:CE2	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:195:LEU:HD13	1:B:196:PHE:CE2	2.43	0.53
1:E:169:VAL:HG11	1:E:224:PHE:CZ	2.43	0.53
1:A:195:LEU:HD13	1:A:196:PHE:CE2	2.44	0.53
1:D:195:LEU:HD13	1:D:196:PHE:CE2	2.44	0.53
1:C:195:LEU:HD13	1:C:196:PHE:CE2	2.43	0.53
1:F:148:TYR:OH	1:G:178:ASN:ND2	2.32	0.53
1:G:195:LEU:HD13	1:G:196:PHE:CE2	2.44	0.53
1:F:195:LEU:HD13	1:F:196:PHE:CE2	2.44	0.53
1:F:52:LEU:HD22	1:F:233:THR:HG22	1.91	0.53
1:F:169:VAL:HG11	1:F:224:PHE:CZ	2.44	0.53
1:F:277:ARG:NH1	4:F:402:HOH:O	2.42	0.52
1:F:8:LYS:HD2	1:G:16:SER:HB3	1.92	0.51
1:A:52:LEU:HD22	1:A:233:THR:HG22	1.92	0.51
1:C:52:LEU:HD22	1:C:233:THR:HG22	1.93	0.51
1:B:52:LEU:HD22	1:B:233:THR:HG22	1.91	0.51
1:D:150:GLN:NE2	1:D:173:ASN:HD21	2.09	0.51
1:E:52:LEU:CD2	1:E:233:THR:HG22	2.40	0.51
1:A:113:MET:CE	1:B:147:LYS:HD3	2.41	0.50
1:G:52:LEU:HD22	1:G:233:THR:HG22	1.91	0.50
1:A:183:ASP:HB2	4:A:591:HOH:O	2.11	0.50
1:E:150:GLN:NE2	1:E:173:ASN:HD21	2.10	0.50
1:E:110:LYS:NZ	1:F:173:ASN:OD1	2.42	0.50
1:A:150:GLN:NE2	1:A:173:ASN:HD21	2.08	0.50
1:C:85:LYS:HB2	1:C:250:GLU:HB3	1.94	0.50
1:A:111:GLU:OE2	1:B:147:LYS:HD2	2.12	0.50
1:D:50:LYS:HE2	1:E:24:ASP:O	2.12	0.49
1:E:85:LYS:HB2	1:E:250:GLU:HB3	1.93	0.49
1:B:150:GLN:NE2	1:B:173:ASN:HD21	2.10	0.49
1:A:126:GLY:HA2	1:A:131:LYS:O	2.12	0.49
1:E:126:GLY:HA2	1:E:131:LYS:O	2.13	0.49
1:F:52:LEU:CD2	1:F:233:THR:HG22	2.43	0.49
1:G:126:GLY:HA2	1:G:131:LYS:O	2.13	0.49
1:A:113:MET:HE2	1:B:147:LYS:HD3	1.95	0.49
1:F:150:GLN:NE2	1:F:173:ASN:HD21	2.11	0.49
1:C:126:GLY:HA2	1:C:131:LYS:O	2.12	0.49
1:B:85:LYS:HB2	1:B:250:GLU:HB3	1.93	0.49
1:F:183:ASP:HB2	4:F:489:HOH:O	2.13	0.49
1:G:85:LYS:HB2	1:G:250:GLU:HB3	1.95	0.48
1:A:85:LYS:HB2	1:A:250:GLU:HB3	1.94	0.48
1:D:50:LYS:NZ	4:D:505:HOH:O	2.46	0.48
1:G:150:GLN:NE2	1:G:173:ASN:HD21	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:150:GLN:NE2	1:C:173:ASN:HD21	2.11	0.48
1:D:126:GLY:HA2	1:D:131:LYS:O	2.13	0.48
4:A:540:HOH:O	1:G:110:LYS:HE2	2.12	0.48
1:B:126:GLY:HA2	1:B:131:LYS:O	2.14	0.48
1:G:52:LEU:CD2	1:G:233:THR:HG22	2.43	0.48
1:D:52:LEU:CD2	1:D:233:THR:HG22	2.43	0.48
1:F:126:GLY:HA2	1:F:131:LYS:O	2.14	0.48
1:A:52:LEU:CD2	1:A:233:THR:HG22	2.44	0.48
1:C:52:LEU:CD2	1:C:233:THR:HG22	2.43	0.47
1:B:8:LYS:HE3	1:C:10:GLY:O	2.14	0.47
1:B:52:LEU:CD2	1:B:233:THR:HG22	2.45	0.47
1:B:64:GLN:NE2	4:B:509:HOH:O	2.48	0.47
1:D:117:THR:HG23	1:D:141:SER:HB2	1.97	0.47
1:E:117:THR:HG23	1:E:141:SER:HB2	1.97	0.46
1:G:188:ASN:OD1	1:G:190:VAL:HG13	2.15	0.46
1:B:114:SER:O	1:C:145:THR:HA	2.16	0.46
1:E:167:TRP:CH2	1:E:230:THR:HG22	2.48	0.46
1:F:8:LYS:HG2	1:G:13:ASP:HB2	1.97	0.46
1:A:151:PRO:HB3	1:G:109:THR:HG22	1.98	0.46
1:F:85:LYS:HB2	1:F:250:GLU:HB3	1.97	0.46
1:A:14:ILE:HD11	1:B:39:PHE:HE1	1.79	0.46
1:C:51:LYS:NZ	4:C:502:HOH:O	2.49	0.46
1:F:117:THR:HG23	1:F:141:SER:HB2	1.97	0.45
1:F:8:LYS:HE2	1:G:10:GLY:O	2.16	0.45
1:B:260:TRP:CD1	1:B:261:THR:O	2.70	0.45
1:A:169:VAL:HG21	1:A:224:PHE:CZ	2.52	0.45
1:A:260:TRP:CD1	1:A:261:THR:O	2.70	0.45
1:A:14:ILE:HD11	1:B:39:PHE:CE1	2.51	0.45
1:D:110:LYS:NZ	1:E:173:ASN:OD1	2.45	0.45
1:D:260:TRP:CD1	1:D:261:THR:O	2.70	0.45
1:G:169:VAL:HG21	1:G:224:PHE:CZ	2.52	0.45
1:D:85:LYS:HB2	1:D:250:GLU:HB3	1.98	0.44
1:F:282:TYR:CD1	1:F:293:ASN:HB3	2.52	0.44
1:F:260:TRP:CD1	1:F:261:THR:O	2.70	0.44
1:A:146:LEU:HD22	1:B:181:PRO:HD3	2.00	0.44
1:G:260:TRP:CD1	1:G:261:THR:O	2.71	0.44
1:F:198:LYS:HE3	4:F:474:HOH:O	2.17	0.44
1:C:260:TRP:CD1	1:C:261:THR:O	2.71	0.44
1:A:110:LYS:HE2	4:B:533:HOH:O	2.18	0.43
1:E:260:TRP:CD1	1:E:261:THR:O	2.71	0.43
1:C:169:VAL:HG21	1:C:224:PHE:CZ	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:149:VAL:HG11	4:A:619:HOH:O	2.18	0.43
1:B:191:TYR:CZ	1:B:200:ARG:HD3	2.54	0.43
1:D:169:VAL:HG21	1:D:224:PHE:CZ	2.53	0.43
1:C:109:THR:HG22	1:D:151:PRO:HB3	2.01	0.43
1:D:191:TYR:CZ	1:D:200:ARG:HD3	2.54	0.43
1:G:191:TYR:CZ	1:G:200:ARG:HD3	2.54	0.42
1:E:191:TYR:CZ	1:E:200:ARG:HD3	2.53	0.42
1:C:191:TYR:CZ	1:C:200:ARG:HD3	2.54	0.42
1:B:169:VAL:HG21	1:B:224:PHE:CZ	2.55	0.42
1:A:145:THR:HA	1:G:114:SER:O	2.19	0.42
1:A:157:LEU:O	1:B:222:SER:HB3	2.20	0.41
1:F:114:SER:O	1:G:145:THR:HA	2.19	0.41
1:C:109:THR:HA	1:D:151:PRO:HA	2.03	0.41
1:A:147:LYS:HD2	1:G:111:GLU:OE2	2.21	0.41
1:E:101:TYR:HA	1:E:229:ALA:O	2.21	0.41
1:C:122:GLY:HA2	1:C:135:LEU:O	2.21	0.40
1:F:253:ARG:HD2	1:F:253:ARG:HH11	1.72	0.40
1:C:101:TYR:HA	1:C:229:ALA:O	2.22	0.40
1:D:282:TYR:CD1	1:D:293:ASN:HB3	2.56	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:604:HOH:O	4:E:607:HOH:O 2_556]	2.08	0.12
4:B:616:HOH:O	4:D:601:HOH:O 2_556]	2.12	0.08

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	291/293 (99%)	281 (97%)	10 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	291/293 (99%)	278 (96%)	13 (4%)	0	100	100
1	C	291/293 (99%)	280 (96%)	11 (4%)	0	100	100
1	D	291/293 (99%)	279 (96%)	12 (4%)	0	100	100
1	E	291/293 (99%)	278 (96%)	13 (4%)	0	100	100
1	F	291/293 (99%)	278 (96%)	13 (4%)	0	100	100
1	G	291/293 (99%)	279 (96%)	12 (4%)	0	100	100
All	All	2037/2051 (99%)	1953 (96%)	84 (4%)	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	259/259 (100%)	244 (94%)	15 (6%)	20	22
1	B	259/259 (100%)	244 (94%)	15 (6%)	20	22
1	C	259/259 (100%)	242 (93%)	17 (7%)	16	17
1	D	259/259 (100%)	248 (96%)	11 (4%)	30	36
1	E	259/259 (100%)	235 (91%)	24 (9%)	9	8
1	F	259/259 (100%)	241 (93%)	18 (7%)	15	15
1	G	259/259 (100%)	243 (94%)	16 (6%)	18	19
All	All	1813/1813 (100%)	1697 (94%)	116 (6%)	17	18

All (116) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	ASP
1	A	30	LYS
1	A	92	ASP
1	A	94	GLU
1	A	101	TYR

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Mol	Chain	Res	Type
1	A	135	LEU
1	A	141	SER
1	A	142	ILE
1	A	145	THR
1	A	195	LEU
1	A	198	LYS
1	A	200	ARG
1	A	237	LYS
1	A	240	LYS
1	A	277	ARG
1	B	8	LYS
1	B	21	LYS
1	B	24	ASP
1	B	25	LEU
1	B	75	LYS
1	B	101	TYR
1	B	116	LEU
1	B	135	LEU
1	B	141	SER
1	B	195	LEU
1	B	201	ASN
1	B	205	LYS
1	B	237	LYS
1	B	240	LYS
1	B	283	LYS
1	C	8	LYS
1	C	12	THR
1	C	24	ASP
1	C	25	LEU
1	C	67	VAL
1	C	78	LEU
1	C	92	ASP
1	C	101	TYR
1	C	116	LEU
1	C	131	LYS
1	C	135	LEU
1	C	141	SER
1	C	145	THR
1	C	195	LEU
1	C	237	LYS
1	C	240	LYS
1	C	270	THR

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Mol	Chain	Res	Type
1	D	24	ASP
1	D	25	LEU
1	D	101	TYR
1	D	115	THR
1	D	117	THR
1	D	135	LEU
1	D	155	THR
1	D	195	LEU
1	D	237	LYS
1	D	270	THR
1	D	277	ARG
1	E	12	THR
1	E	24	ASP
1	E	25	LEU
1	E	30	LYS
1	E	66	ARG
1	E	67	VAL
1	E	75	LYS
1	E	78	LEU
1	E	95	VAL
1	E	101	TYR
1	E	116	LEU
1	E	117	THR
1	E	131	LYS
1	E	135	LEU
1	E	136	ILE
1	E	141	SER
1	E	142	ILE
1	E	155	THR
1	E	195	LEU
1	E	204	MET
1	E	230	THR
1	E	237	LYS
1	E	240	LYS
1	E	288	LYS
1	F	8	LYS
1	F	12	THR
1	F	25	LEU
1	F	66	ARG
1	F	67	VAL
1	F	101	TYR
1	F	116	LEU

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Mol	Chain	Res	Type
1	F	117	THR
1	F	135	LEU
1	F	142	ILE
1	F	169	VAL
1	F	195	LEU
1	F	200	ARG
1	F	201	ASN
1	F	232	ILE
1	F	240	LYS
1	F	248	ILE
1	F	280	GLU
1	G	21	LYS
1	G	24	ASP
1	G	25	LEU
1	G	30	LYS
1	G	75	LYS
1	G	101	TYR
1	G	116	LEU
1	G	141	SER
1	G	145	THR
1	G	190	VAL
1	G	195	LEU
1	G	201	ASN
1	G	203	SER
1	G	237	LYS
1	G	240	LYS
1	G	270	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (30) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	74	ASN
1	A	89	GLN
1	A	150	GLN
1	A	178	ASN
1	B	64	GLN
1	B	74	ASN
1	B	89	GLN
1	B	150	GLN
1	C	74	ASN
1	C	89	GLN
1	C	150	GLN

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Mol	Chain	Res	Type
1	C	178	ASN
1	C	194	GLN
1	D	74	ASN
1	D	87	GLN
1	D	123	ASN
1	D	150	GLN
1	D	178	ASN
1	E	74	ASN
1	E	150	GLN
1	E	178	ASN
1	E	194	GLN
1	F	89	GLN
1	F	150	GLN
1	F	178	ASN
1	G	74	ASN
1	G	89	GLN
1	G	150	GLN
1	G	178	ASN
1	G	194	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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

26 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	PQJ	G	401	-	11,11,24	0.84	0	15,16,29	0.78	1 (6%)
2	PQJ	C	402	-	10,10,24	1.00	1 (10%)	15,15,29	1.00	0
2	PQJ	F	304	-	10,10,24	0.98	1 (10%)	15,15,29	1.26	2 (13%)
2	PQJ	D	402	-	11,11,24	0.87	0	15,16,29	0.87	1 (6%)
2	PQJ	C	401	-	11,11,24	0.81	0	15,16,29	0.87	1 (6%)
2	PQJ	E	403	-	10,10,24	1.06	1 (10%)	15,15,29	0.87	1 (6%)
2	PQJ	B	403	-	11,11,24	0.69	0	15,16,29	1.06	0
2	PQJ	A	403	-	10,10,24	1.41	1 (10%)	15,15,29	1.19	2 (13%)
3	SO4	E	405	-	4,4,4	0.55	0	6,6,6	0.48	0
3	SO4	D	404	-	4,4,4	0.83	0	6,6,6	0.38	0
2	PQJ	B	402	-	11,11,24	0.78	0	15,16,29	0.91	1 (6%)
2	PQJ	E	404	-	10,10,24	1.41	1 (10%)	15,15,29	1.36	3 (20%)
2	PQJ	A	402	-	11,11,24	0.94	1 (9%)	15,16,29	0.85	0
2	PQJ	E	402	-	11,11,24	1.01	1 (9%)	15,16,29	0.82	0
2	PQJ	A	401	-	11,11,24	0.82	0	15,16,29	0.94	1 (6%)
3	SO4	G	403	-	4,4,4	0.72	0	6,6,6	0.37	0
2	PQJ	E	401	-	11,11,24	0.86	0	15,16,29	0.92	0
3	SO4	C	403	-	4,4,4	0.80	0	6,6,6	0.42	0
2	PQJ	F	302	-	11,11,24	0.90	1 (9%)	15,16,29	1.31	2 (13%)
2	PQJ	G	402	-	11,11,24	0.96	0	15,16,29	1.05	1 (6%)
2	PQJ	F	301	-	11,11,24	0.77	0	15,16,29	0.88	0
2	PQJ	D	403	-	11,11,24	1.05	1 (9%)	15,16,29	1.05	1 (6%)
2	PQJ	B	401	-	10,10,24	0.99	0	15,15,29	1.37	3 (20%)
3	SO4	B	404	-	4,4,4	0.44	0	6,6,6	0.14	0
2	PQJ	F	303	-	10,10,24	1.02	1 (10%)	15,15,29	1.01	2 (13%)
2	PQJ	D	401	-	10,10,24	1.46	1 (10%)	15,15,29	1.28	1 (6%)

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	PQJ	B	403	-	-	4/11/11/24	-
2	PQJ	D	403	-	-	4/11/11/24	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PQJ	A	403	-	-	2/8/8/24	-
2	PQJ	E	404	-	-	3/8/8/24	-
2	PQJ	A	402	-	-	7/11/11/24	-
2	PQJ	G	401	-	-	2/11/11/24	-
2	PQJ	C	402	-	-	4/8/8/24	-
2	PQJ	E	402	-	-	3/11/11/24	-
2	PQJ	G	402	-	-	4/11/11/24	-
2	PQJ	A	401	-	-	5/11/11/24	-
2	PQJ	F	304	-	-	3/8/8/24	-
2	PQJ	D	402	-	-	4/11/11/24	-
2	PQJ	E	401	-	-	3/11/11/24	-
2	PQJ	F	303	-	-	3/8/8/24	-
2	PQJ	D	401	-	-	3/8/8/24	-
2	PQJ	B	402	-	-	1/11/11/24	-
2	PQJ	F	302	-	-	4/11/11/24	-
2	PQJ	E	403	-	-	3/8/8/24	-
2	PQJ	C	401	-	-	7/11/11/24	-
2	PQJ	B	401	-	-	3/8/8/24	-
2	PQJ	F	301	-	-	5/11/11/24	-

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	403	PQJ	P1-O3	3.95	1.63	1.50
2	E	404	PQJ	P1-O3	3.94	1.63	1.50
2	D	401	PQJ	P1-O3	3.89	1.63	1.50
2	D	403	PQJ	P1-O1	2.45	1.68	1.59
2	F	304	PQJ	P1-O1	2.44	1.64	1.54
2	E	403	PQJ	P1-O1	2.31	1.63	1.54
2	F	303	PQJ	P1-O1	2.30	1.63	1.54
2	F	302	PQJ	P1-O1	2.24	1.67	1.59
2	C	402	PQJ	P1-O1	2.12	1.63	1.54
2	E	402	PQJ	P1-O1	2.06	1.66	1.59
2	A	402	PQJ	P1-O1	2.01	1.66	1.59

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	401	PQJ	O1-P1-O2	4.04	123.07	107.64
2	E	404	PQJ	O1-P1-O2	3.22	119.93	107.64
2	F	302	PQJ	O2-P1-O1	2.91	118.36	105.88
2	A	403	PQJ	O4-P1-O3	-2.88	98.40	106.47
2	A	403	PQJ	O1-P1-O2	2.79	118.30	107.64
2	B	401	PQJ	O1-P1-O4	-2.70	99.56	106.73
2	F	304	PQJ	O2-P1-O3	2.65	121.04	110.68
2	B	401	PQJ	P1-O4-C1	2.53	125.25	118.30
2	D	403	PQJ	C3-N1-C4	-2.39	102.84	108.97
2	A	401	PQJ	O2-P1-O1	2.36	115.98	105.88
2	B	402	PQJ	C3-N1-C5	-2.34	102.96	108.97
2	F	304	PQJ	C3-N1-C4	-2.30	103.06	108.97
2	C	401	PQJ	C3-N1-C5	-2.27	103.13	108.97
2	G	402	PQJ	O2-P1-O1	2.24	115.48	105.88
2	E	404	PQJ	C3-N1-C4	-2.23	103.25	108.97
2	F	303	PQJ	O2-P1-O3	2.19	119.27	110.68
2	G	401	PQJ	O2-P1-O3	2.14	122.80	112.24
2	B	401	PQJ	O2-P1-O3	2.09	118.87	110.68
2	E	404	PQJ	C4-N1-C2	2.04	118.28	109.92
2	F	302	PQJ	O2-P1-O4	-2.03	98.32	107.75
2	E	403	PQJ	O2-P1-O3	2.03	118.62	110.68
2	F	303	PQJ	O1-P1-O4	-2.01	101.38	106.73
2	D	402	PQJ	O4-P1-O3	-2.00	101.25	109.07

There are no chirality outliers.

All (77) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	G	401	PQJ	C1-O4-P1-O2
2	C	402	PQJ	C1-O4-P1-O2
2	C	402	PQJ	C1-O4-P1-O3
2	C	402	PQJ	C1-O4-P1-O1
2	C	402	PQJ	O4-C1-C2-N1
2	B	403	PQJ	C1-O4-P1-O3
2	B	402	PQJ	O4-C1-C2-N1
2	A	402	PQJ	C1-O4-P1-O2
2	A	402	PQJ	C1-O4-P1-O3
2	A	402	PQJ	C1-O4-P1-O1
2	A	402	PQJ	C6-O1-P1-O2
2	E	401	PQJ	C1-O4-P1-O3
2	F	302	PQJ	C1-O4-P1-O3
2	F	302	PQJ	C6-O1-P1-O3
2	D	403	PQJ	C6-O1-P1-O2

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Mol	Chain	Res	Type	Atoms
2	D	403	PQJ	C6-O1-P1-O3
2	D	403	PQJ	C6-O1-P1-O4
2	G	402	PQJ	C1-C2-N1-C4
2	G	402	PQJ	C1-C2-N1-C5
2	D	402	PQJ	C1-C2-N1-C4
2	E	404	PQJ	C1-C2-N1-C5
2	E	404	PQJ	C1-C2-N1-C4
2	E	402	PQJ	C1-O4-P1-O1
2	D	402	PQJ	C1-C2-N1-C3
2	C	401	PQJ	C6-O1-P1-O3
2	F	301	PQJ	C6-O1-P1-O3
2	D	402	PQJ	C1-C2-N1-C5
2	E	404	PQJ	C1-C2-N1-C3
2	G	402	PQJ	C1-C2-N1-C3
2	B	401	PQJ	C1-C2-N1-C5
2	C	401	PQJ	C1-C2-N1-C5
2	A	403	PQJ	C1-O4-P1-O3
2	F	304	PQJ	C1-C2-N1-C3
2	A	402	PQJ	C6-O1-P1-O3
2	D	401	PQJ	C1-C2-N1-C5
2	A	401	PQJ	C6-O1-P1-O3
2	E	401	PQJ	C1-O4-P1-O1
2	E	402	PQJ	C1-O4-P1-O2
2	E	402	PQJ	C1-O4-P1-O3
2	E	401	PQJ	C1-O4-P1-O2
2	F	301	PQJ	C1-C2-N1-C3
2	C	401	PQJ	C1-C2-N1-C4
2	F	304	PQJ	C1-C2-N1-C4
2	F	301	PQJ	C1-C2-N1-C4
2	B	401	PQJ	C1-C2-N1-C4
2	D	401	PQJ	C1-C2-N1-C4
2	C	401	PQJ	C6-O1-P1-O4
2	E	403	PQJ	C1-C2-N1-C3
2	B	401	PQJ	C1-C2-N1-C3
2	D	401	PQJ	C1-C2-N1-C3
2	B	403	PQJ	C1-O4-P1-O1
2	F	304	PQJ	C1-C2-N1-C5
2	D	402	PQJ	C6-O1-P1-O2
2	C	401	PQJ	C6-O1-P1-O2
2	B	403	PQJ	C6-O1-P1-O2
2	F	301	PQJ	C6-O1-P1-O2
2	C	401	PQJ	C1-C2-N1-C3

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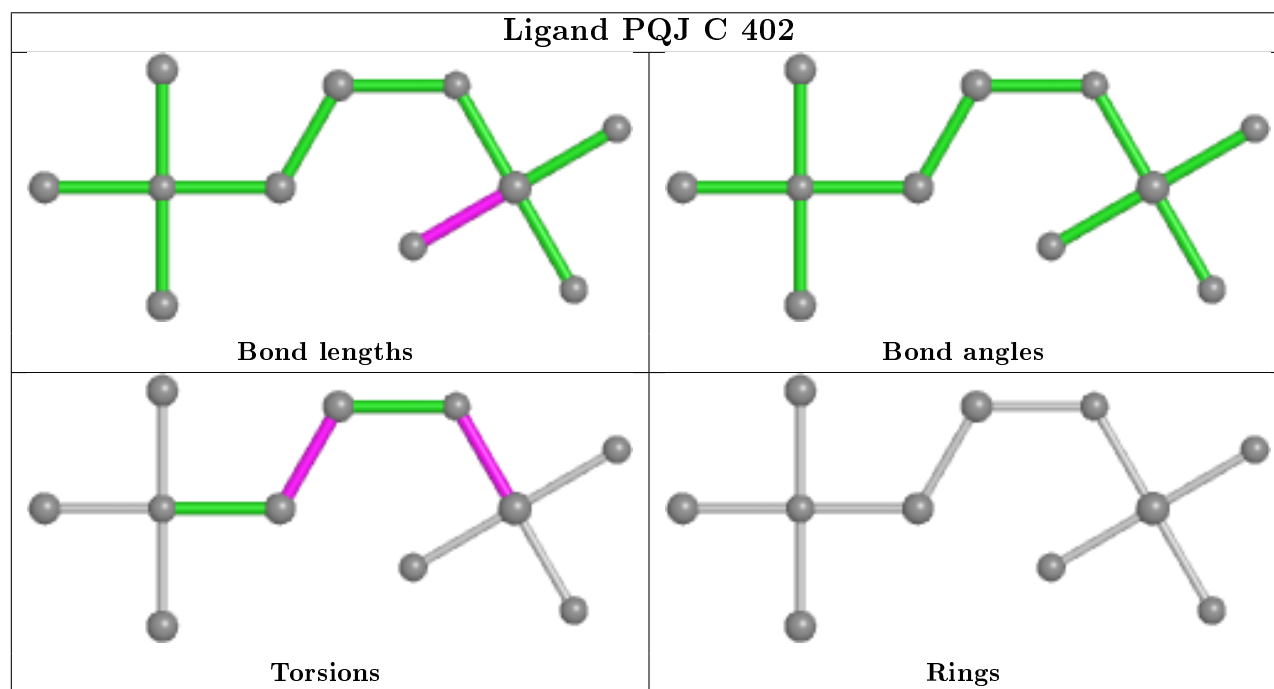
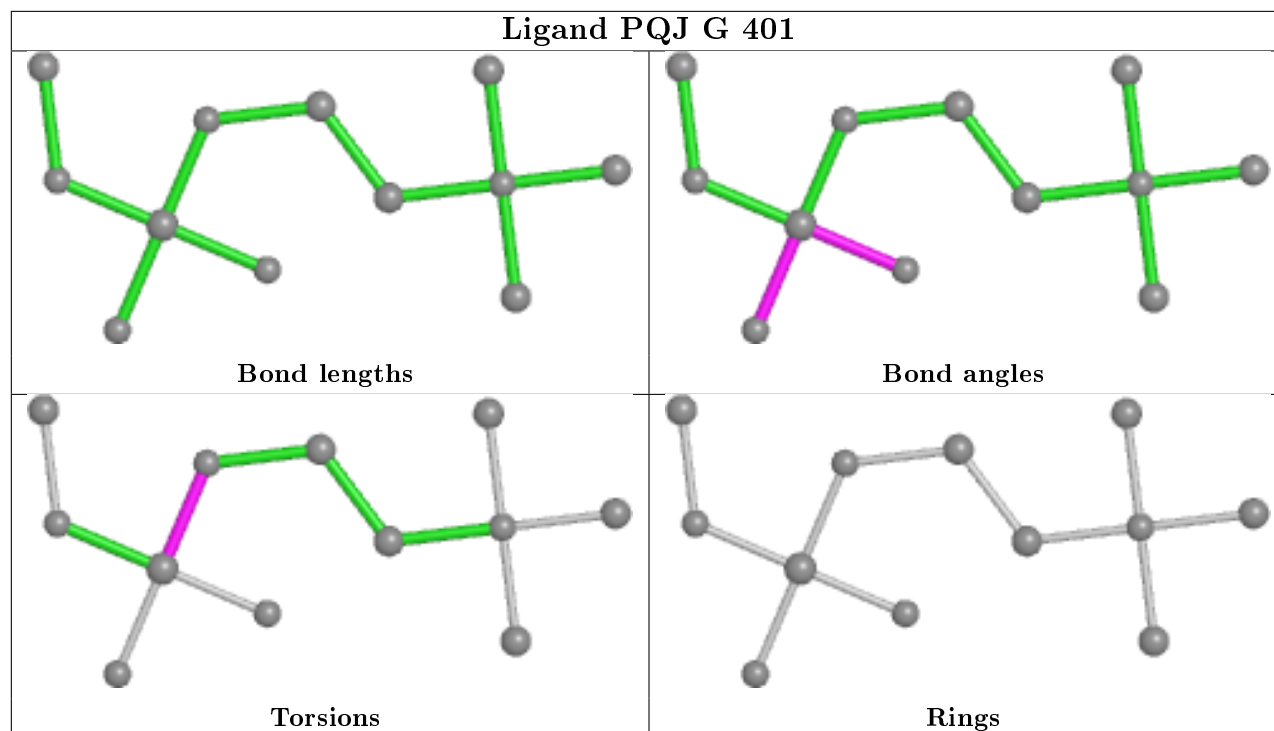
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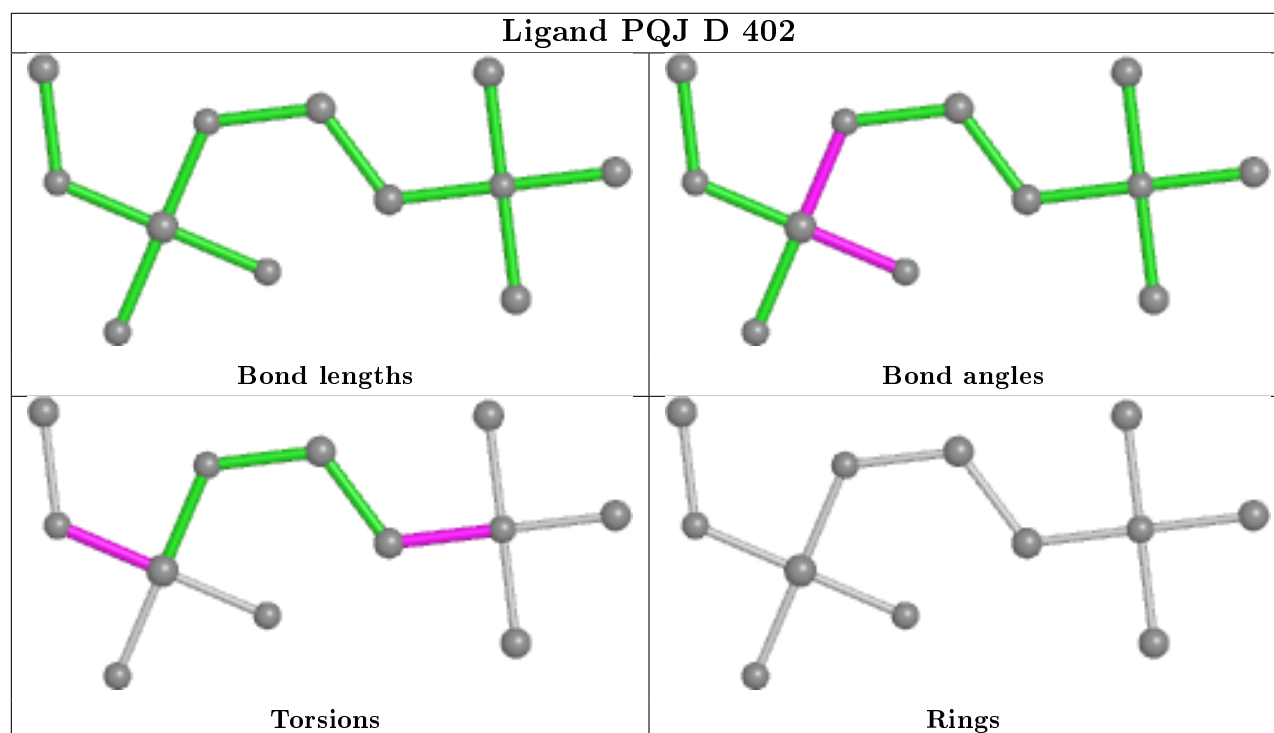
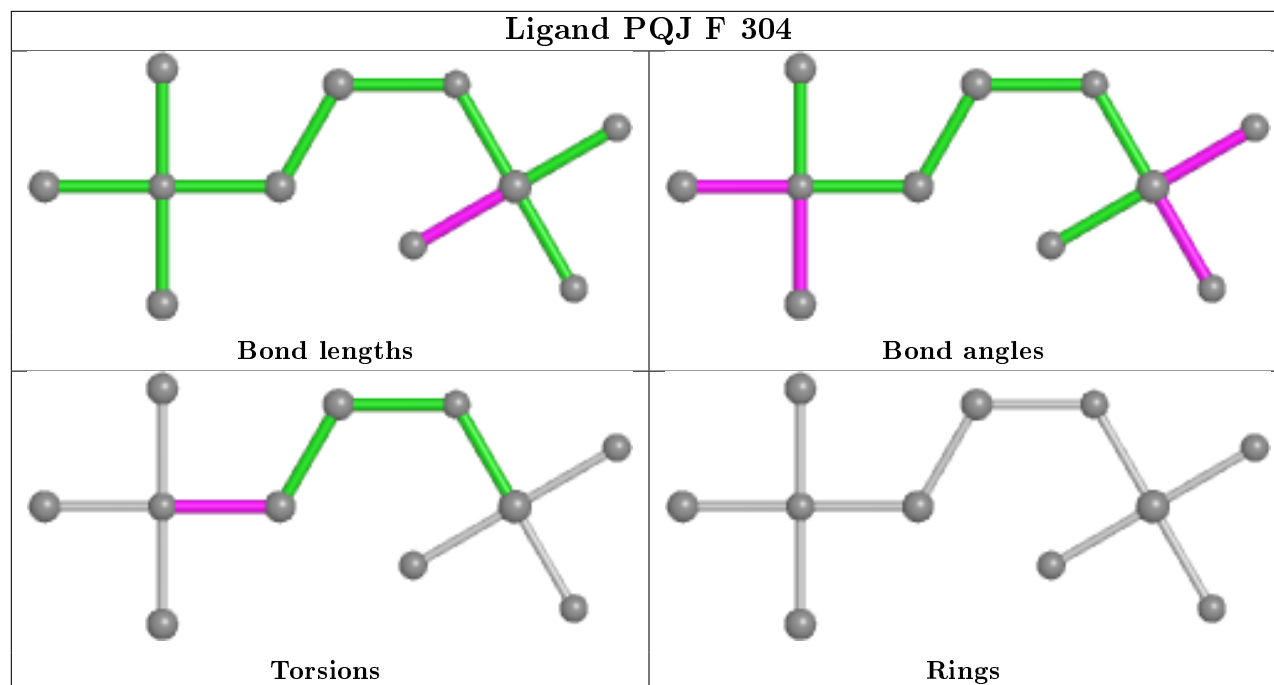
Mol	Chain	Res	Type	Atoms
2	A	401	PQJ	C1-C2-N1-C5
2	F	301	PQJ	C1-C2-N1-C5
2	F	303	PQJ	C1-C2-N1-C3
2	A	402	PQJ	C1-C2-N1-C5
2	E	403	PQJ	C1-C2-N1-C4
2	F	302	PQJ	C1-O4-P1-O1
2	E	403	PQJ	C1-C2-N1-C5
2	A	401	PQJ	C1-C2-N1-C3
2	A	402	PQJ	C1-C2-N1-C4
2	F	303	PQJ	C1-C2-N1-C4
2	F	302	PQJ	C1-C2-N1-C5
2	G	401	PQJ	C1-O4-P1-O3
2	G	402	PQJ	C1-O4-P1-O2
2	C	401	PQJ	C1-O4-P1-O3
2	A	403	PQJ	C1-C2-N1-C4
2	A	401	PQJ	C6-O1-P1-O4
2	A	401	PQJ	C1-C2-N1-C4
2	D	403	PQJ	C1-O4-P1-O3
2	B	403	PQJ	C1-C2-N1-C3
2	F	303	PQJ	C1-C2-N1-C5

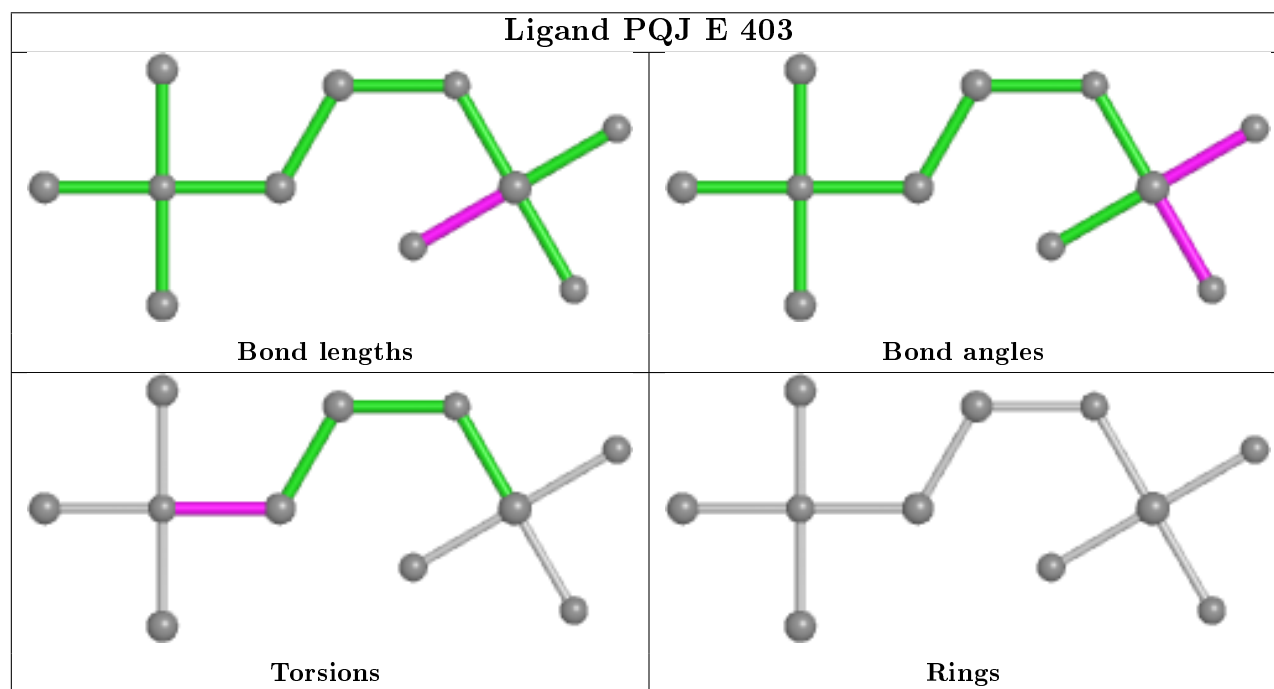
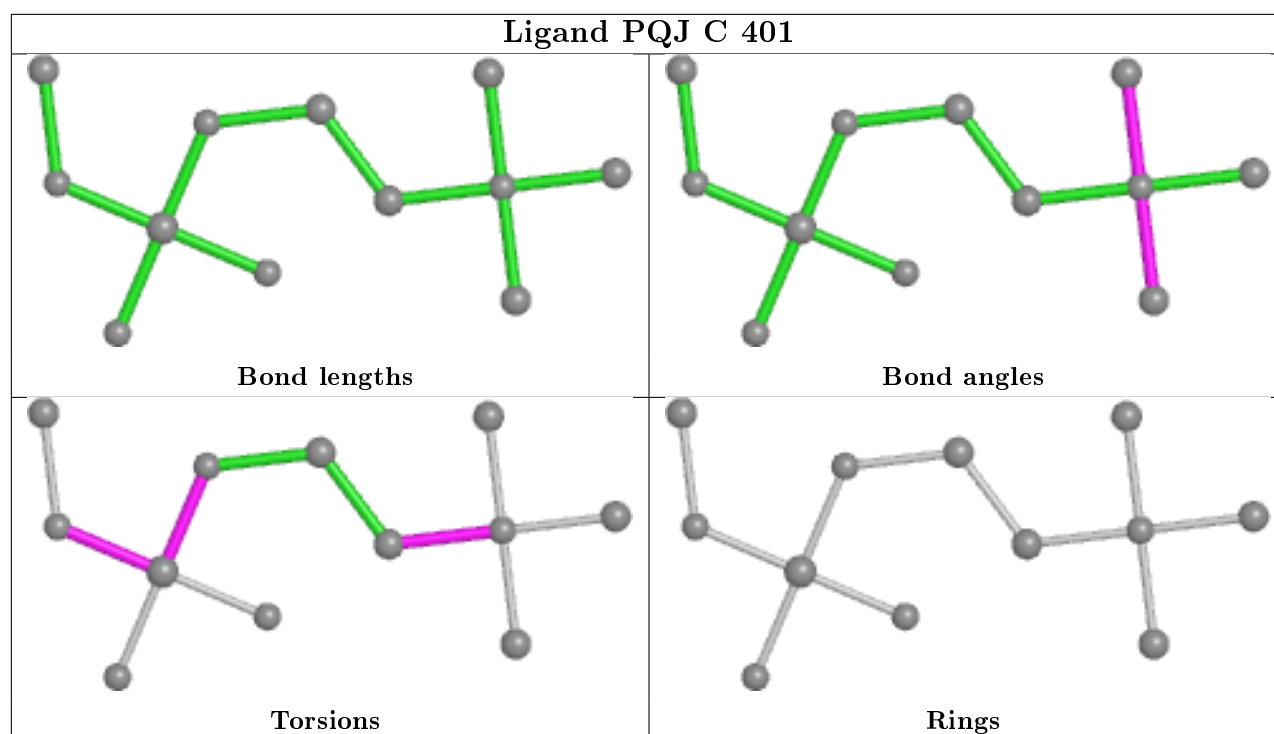
There are no ring outliers.

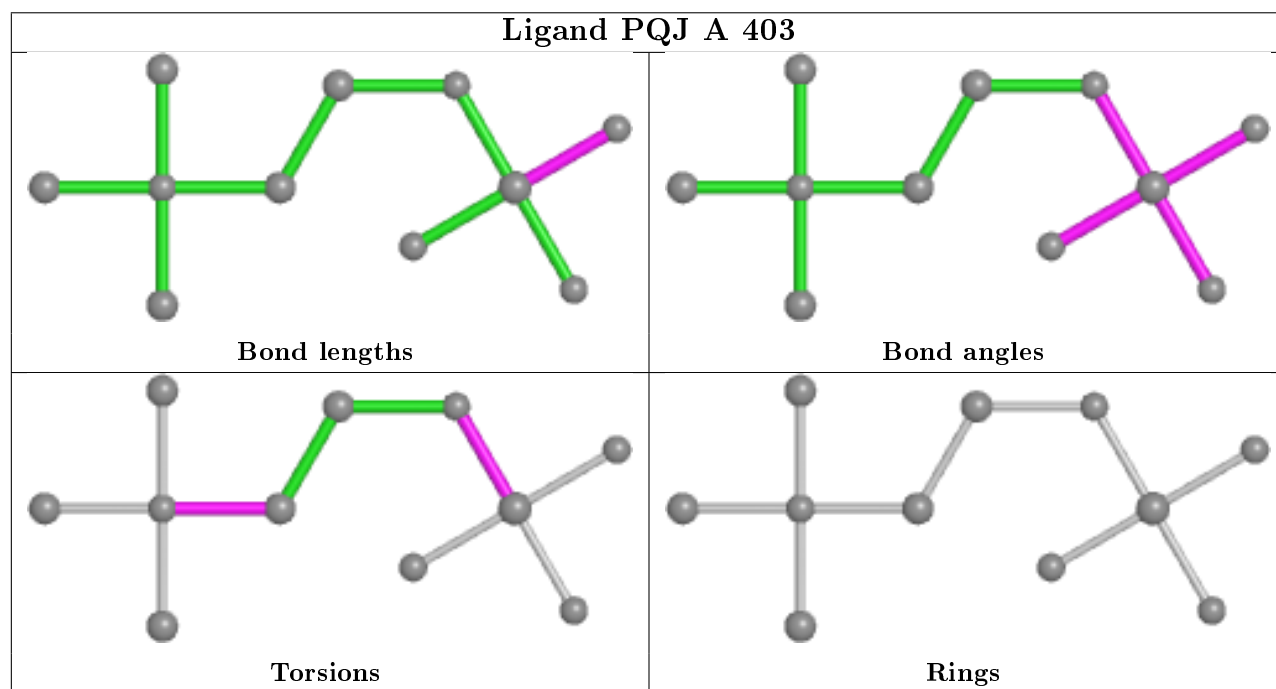
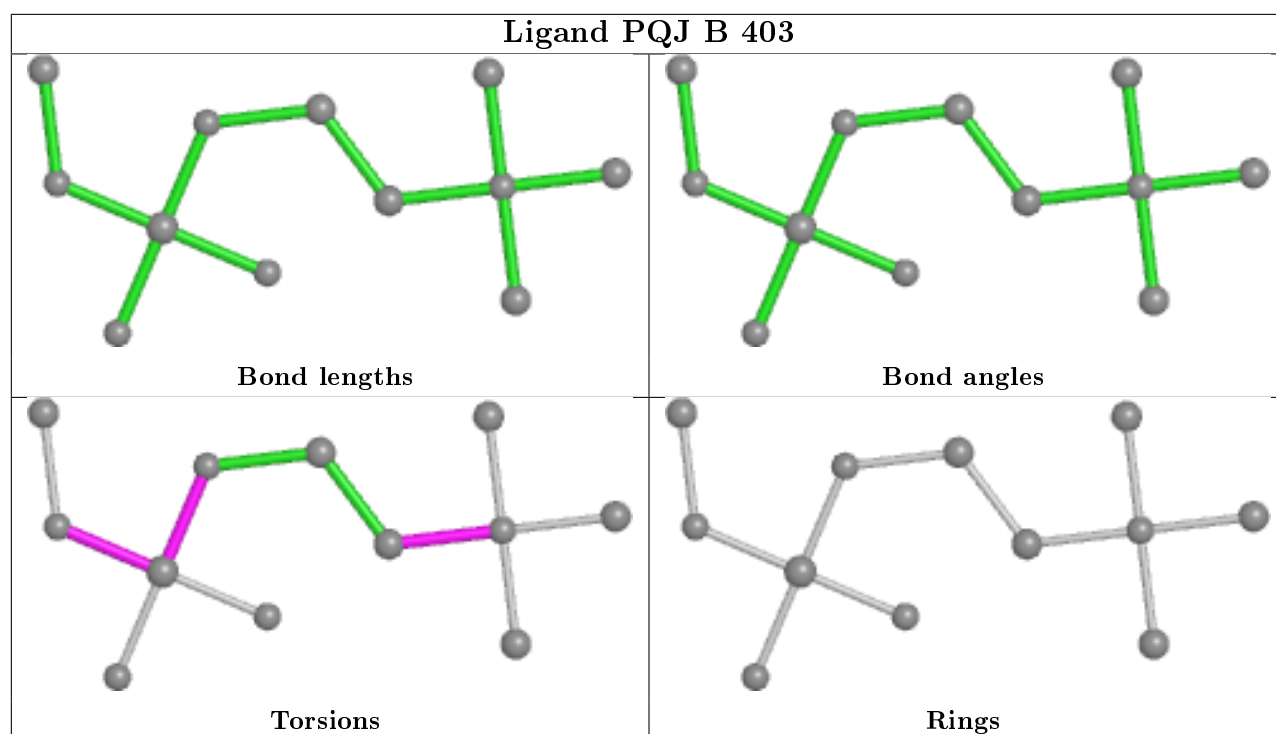
No monomer is involved in short contacts.

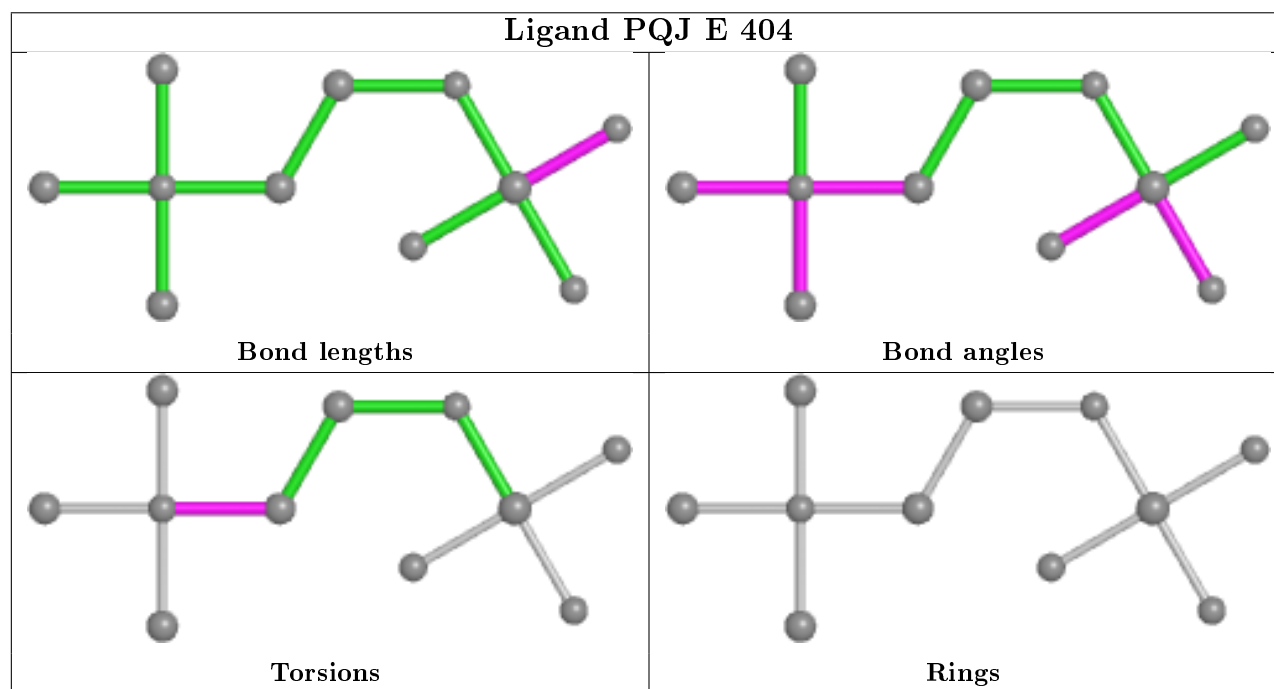
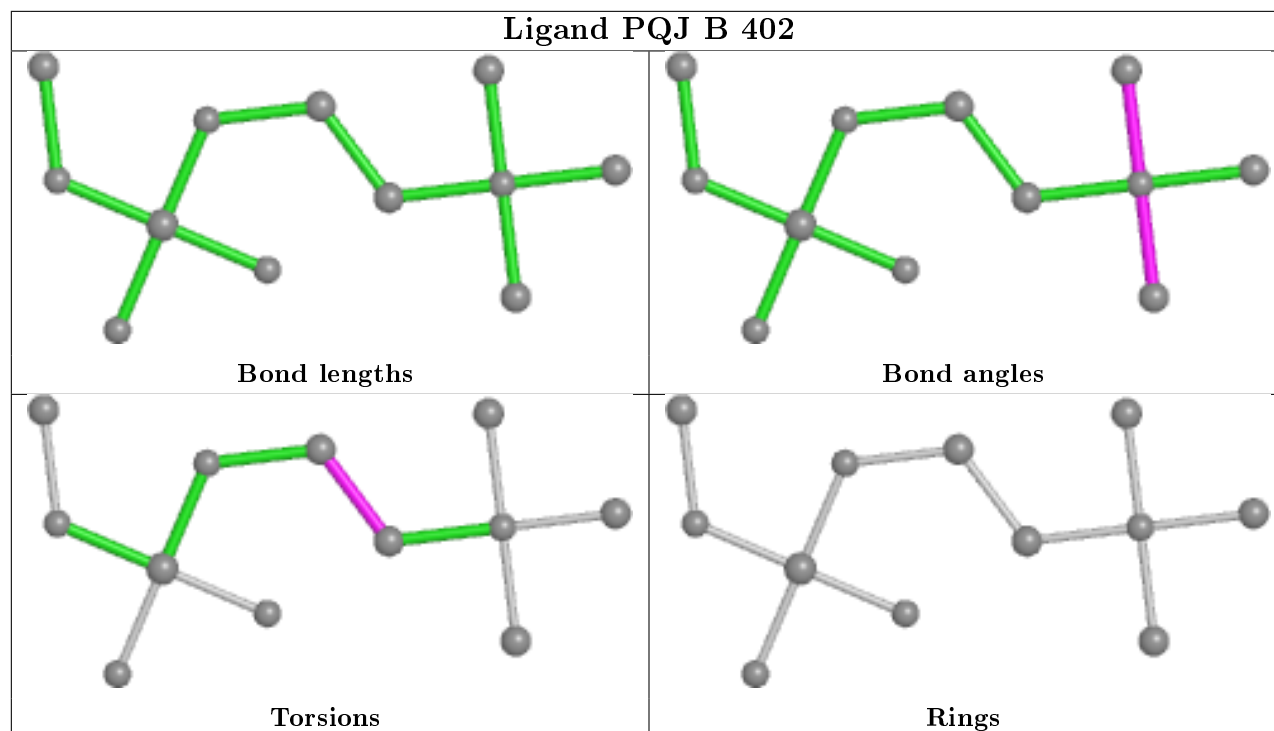
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



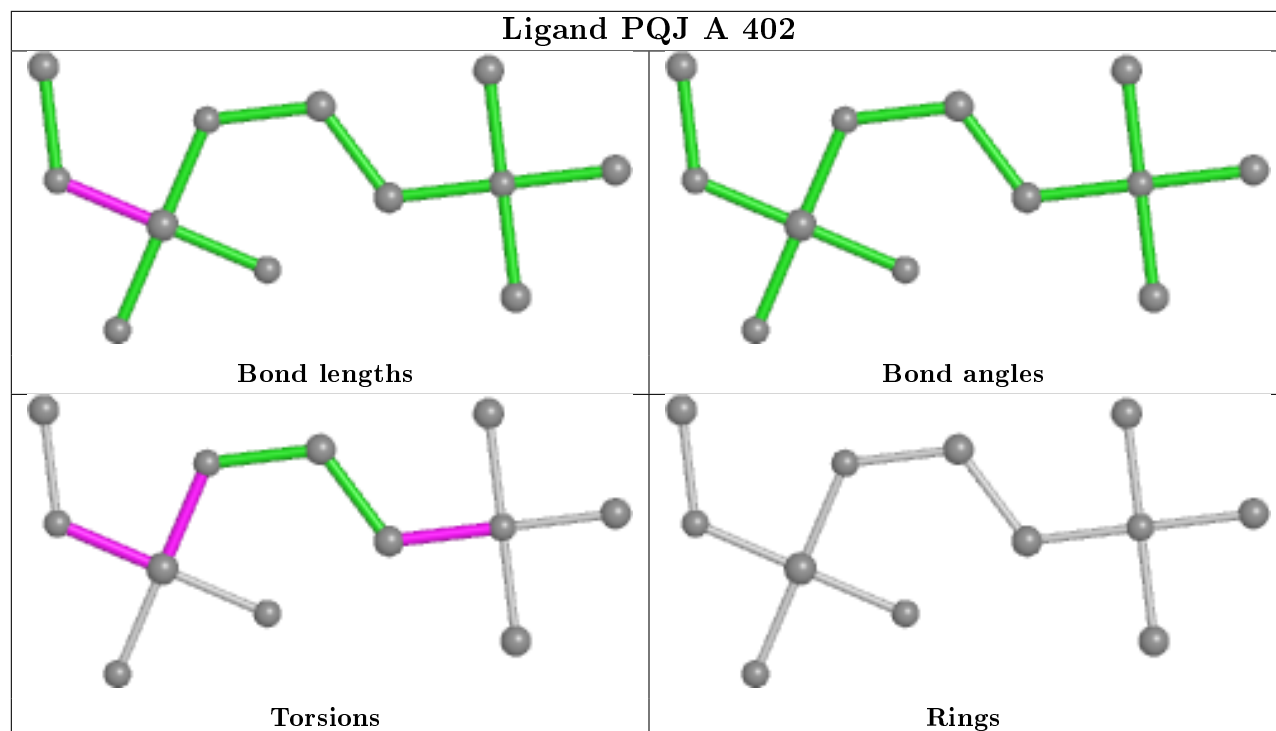




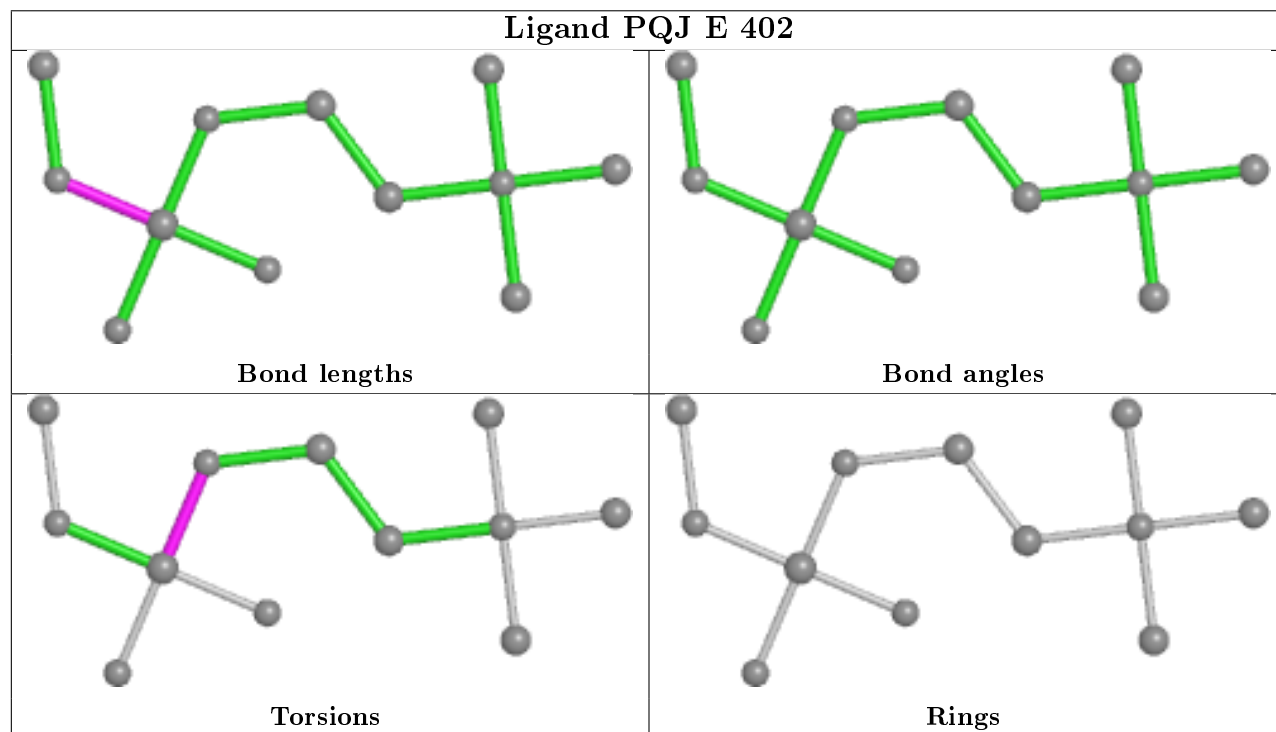




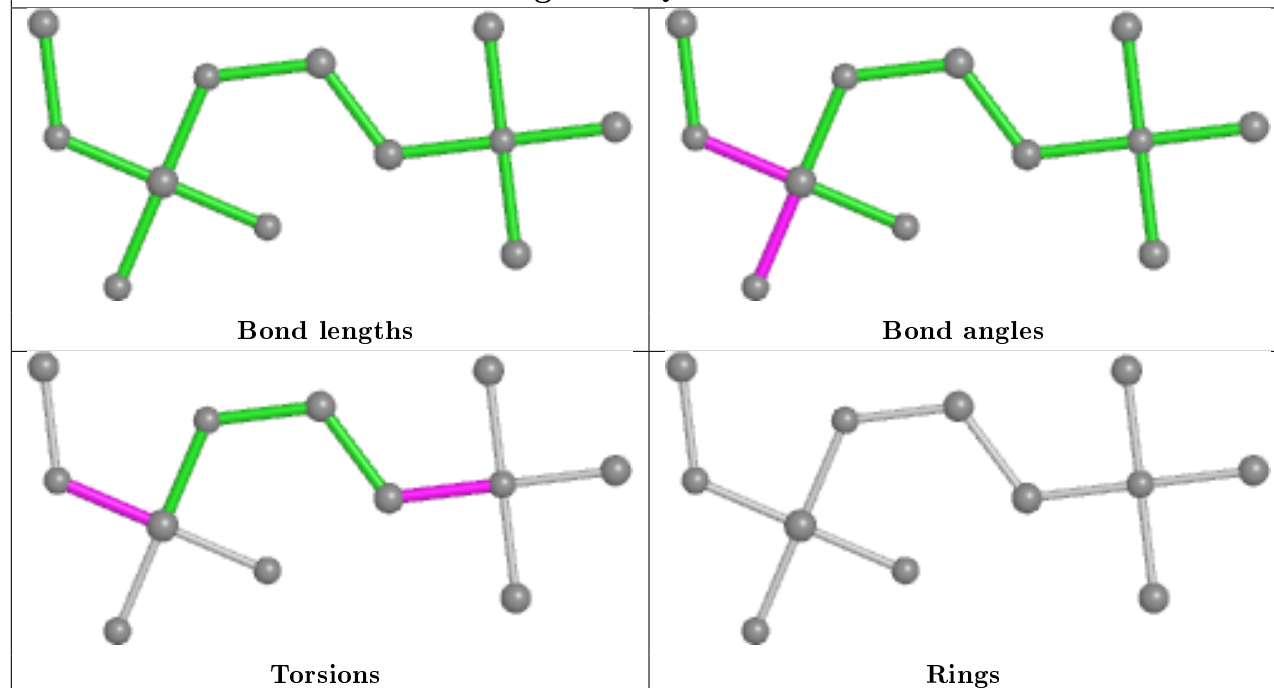
Ligand PQJ A 402



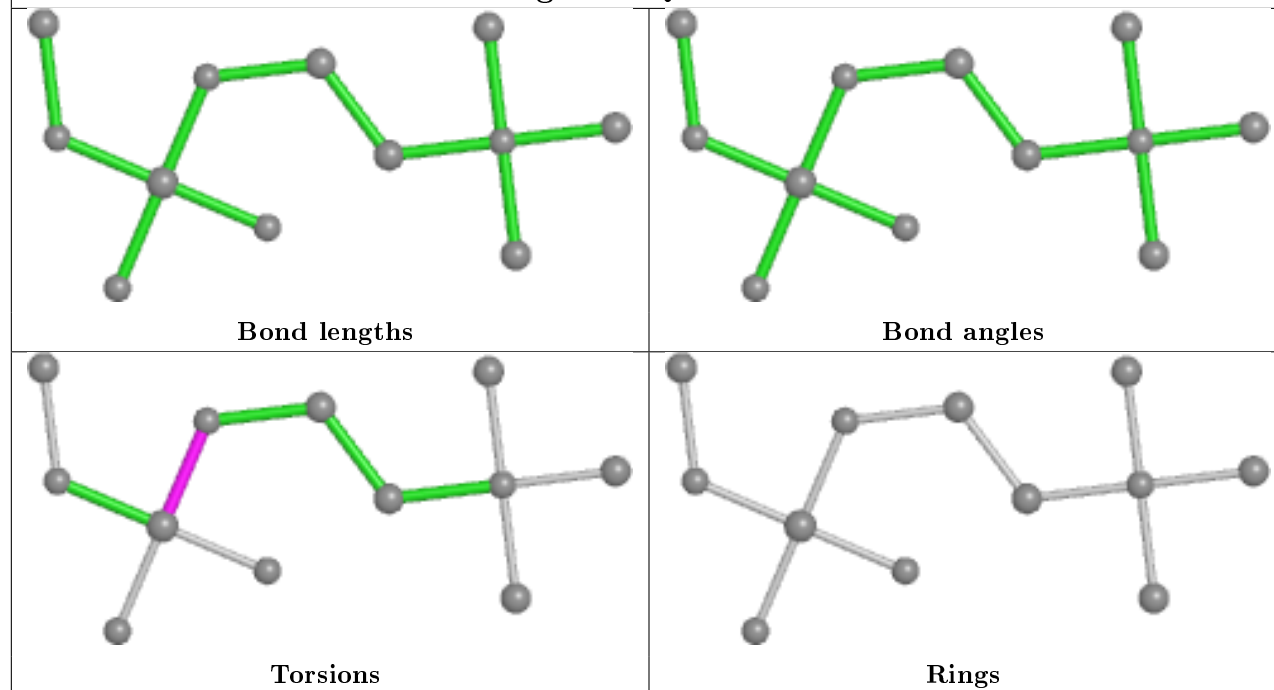
Ligand PQJ E 402



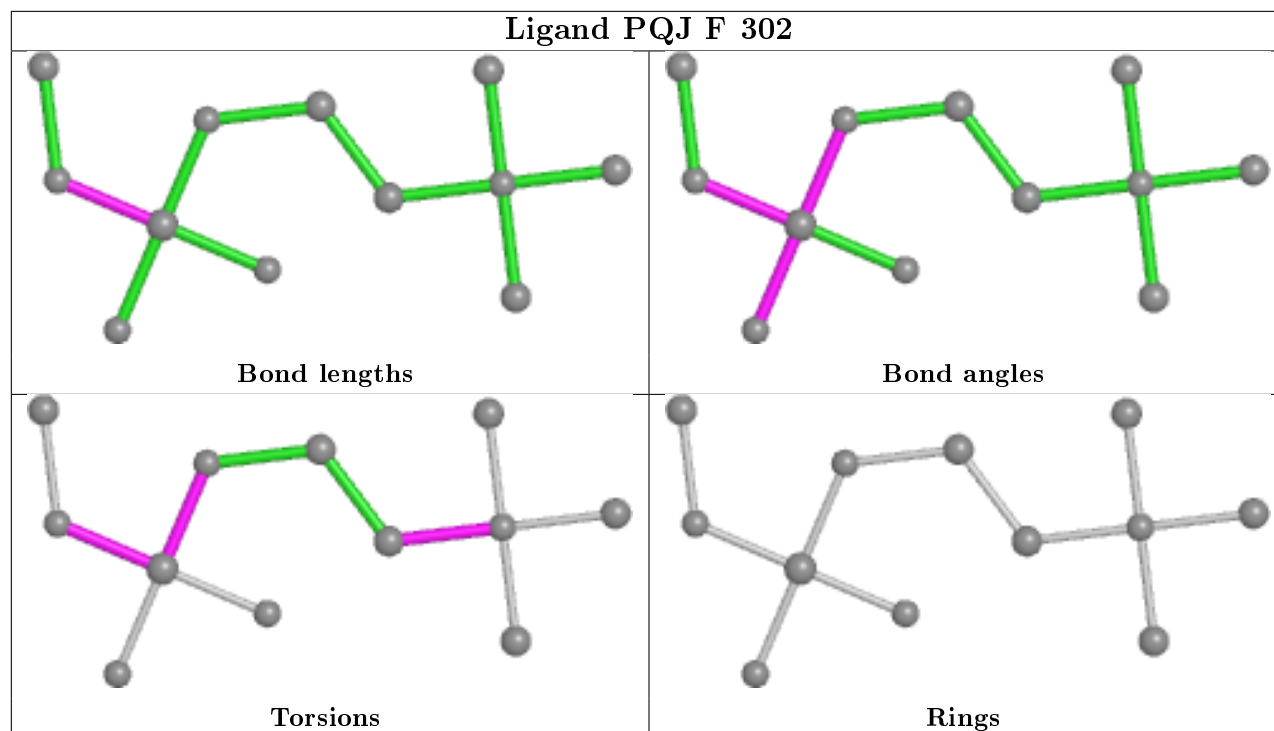
Ligand PQJ A 401



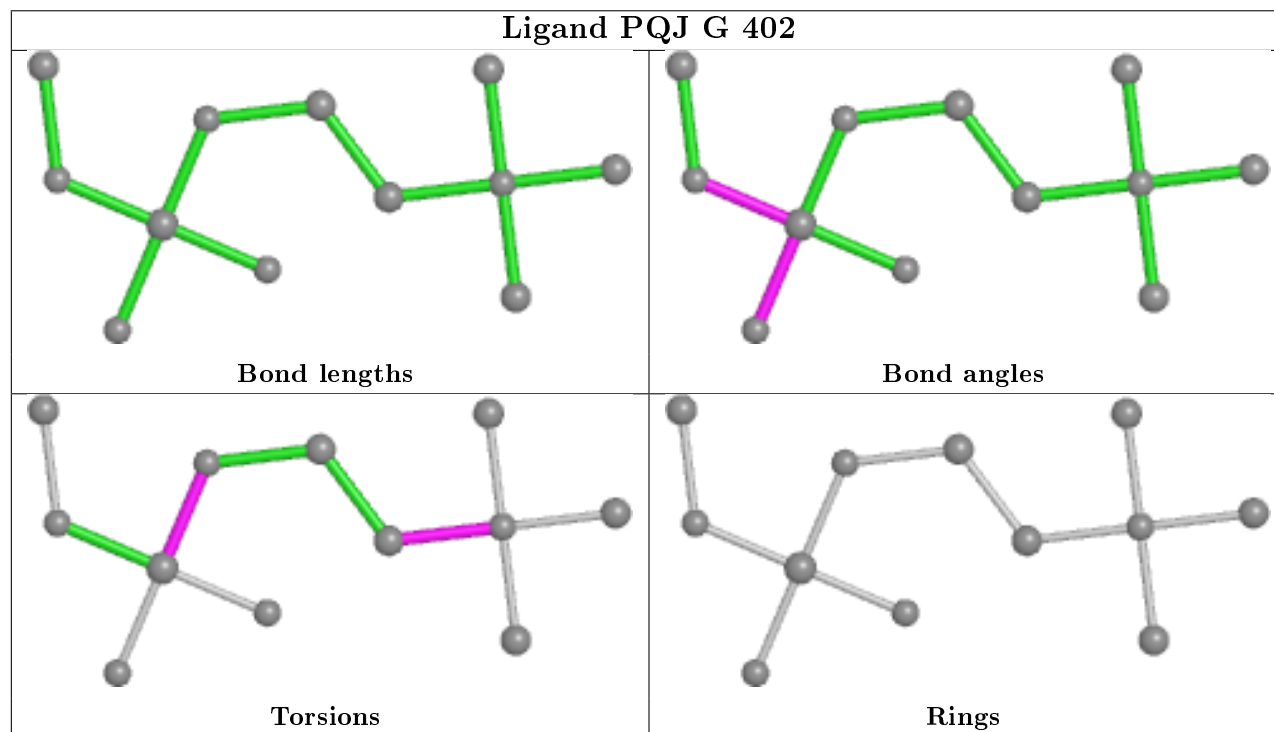
Ligand PQJ E 401



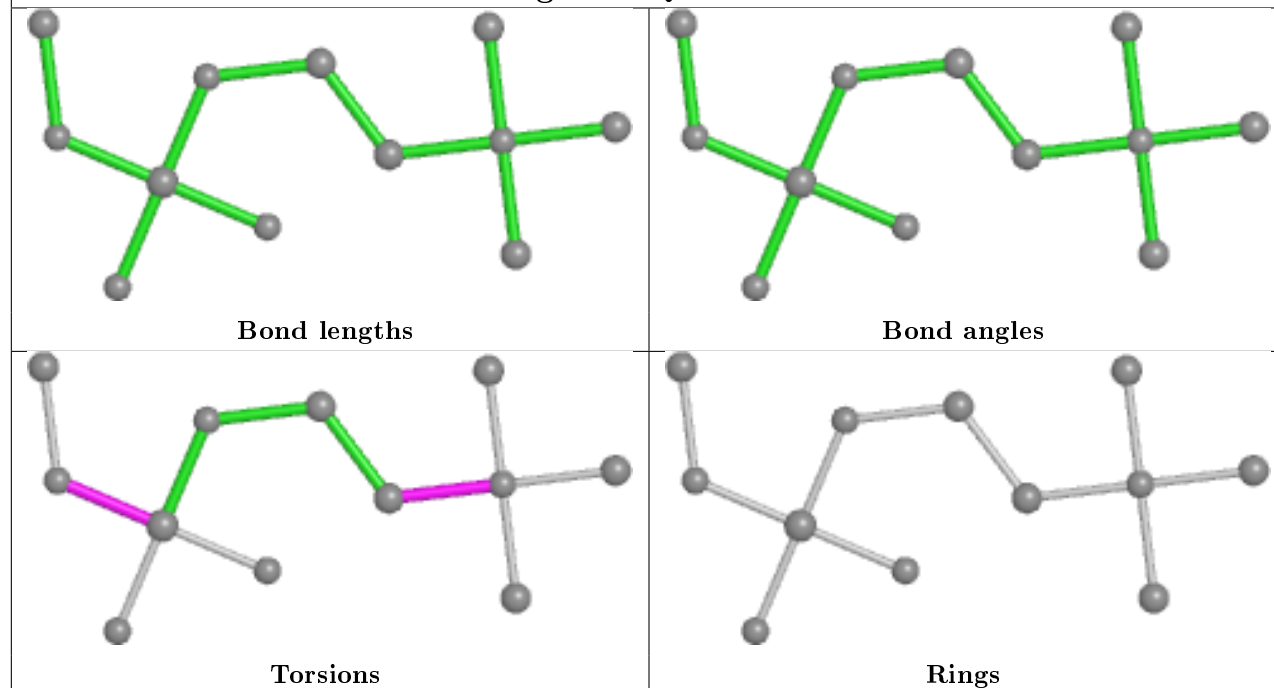
Ligand PQJ F 302



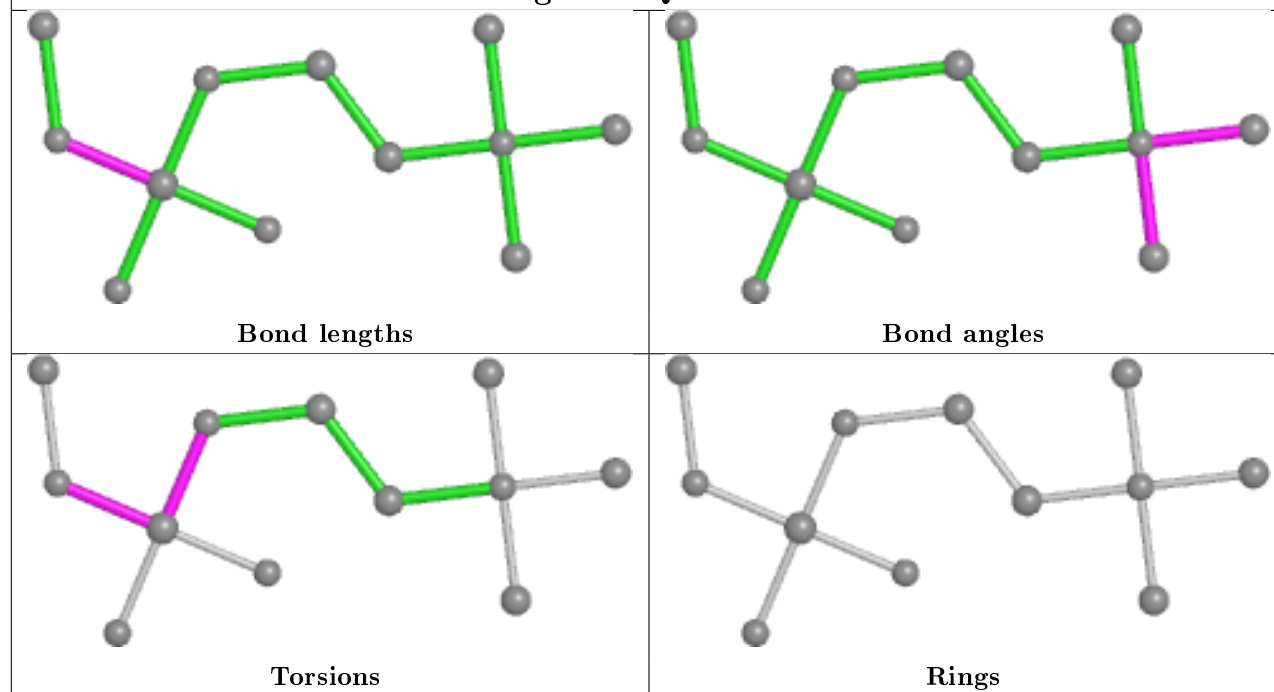
Ligand PQJ G 402



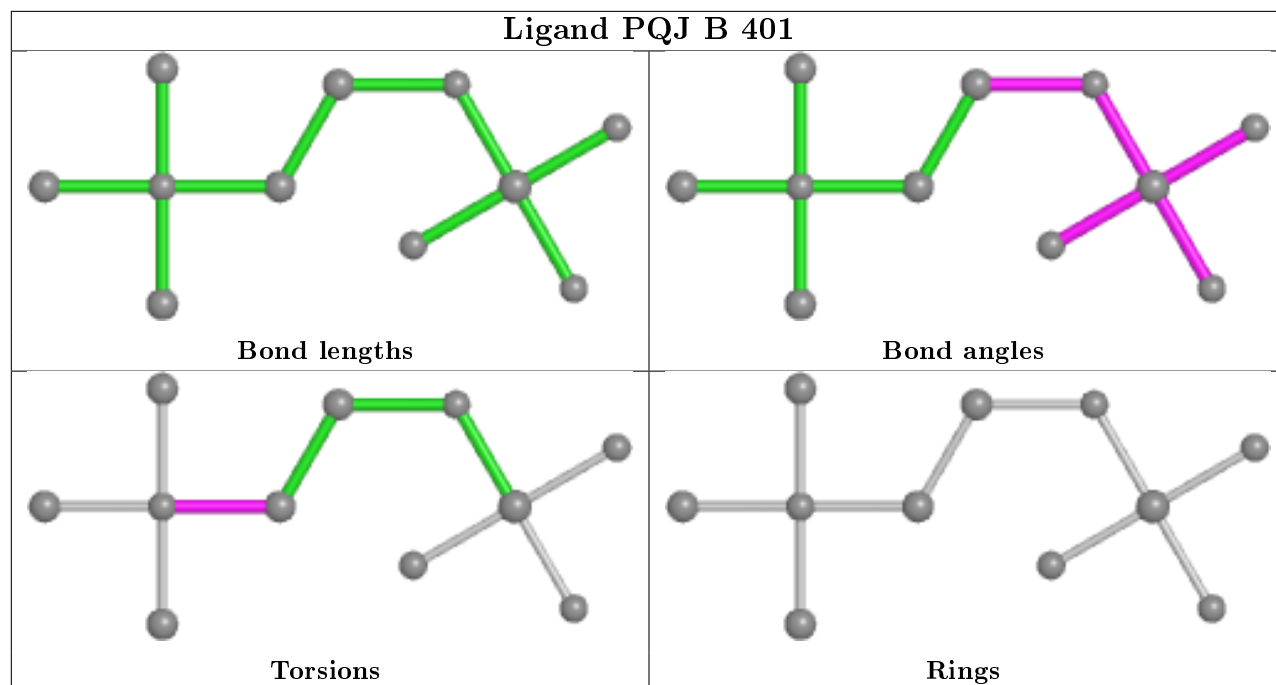
Ligand PQJ F 301



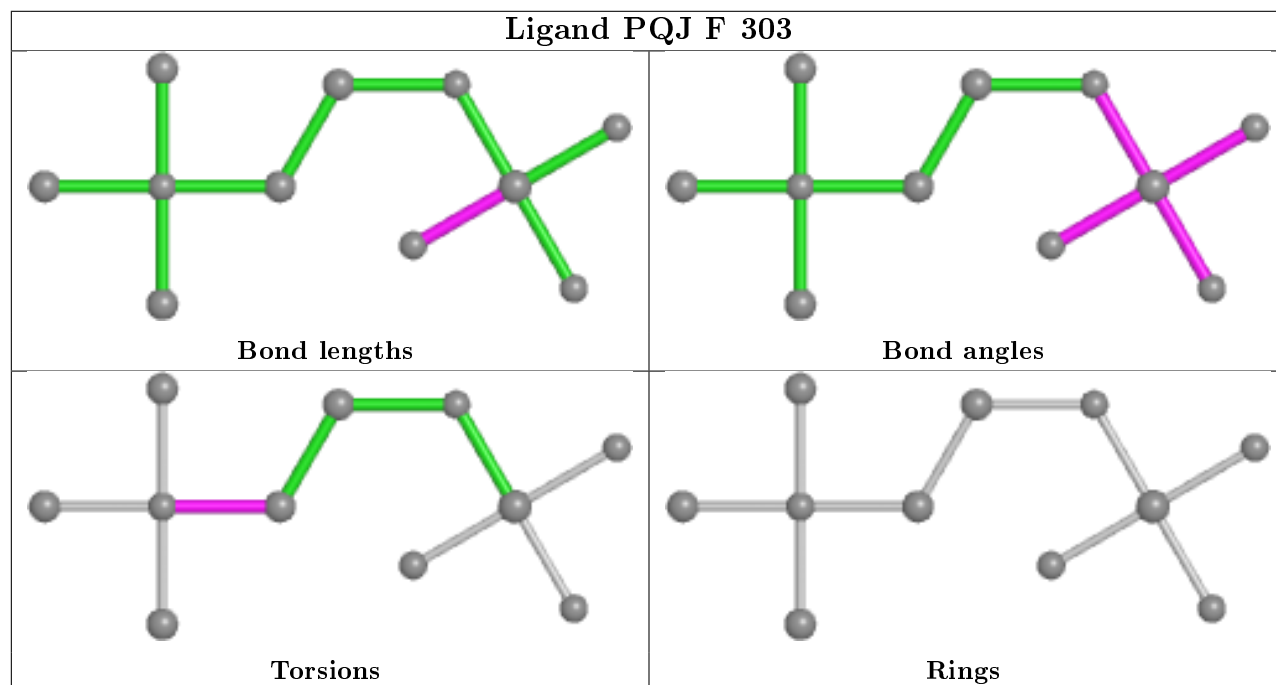
Ligand PQJ D 403

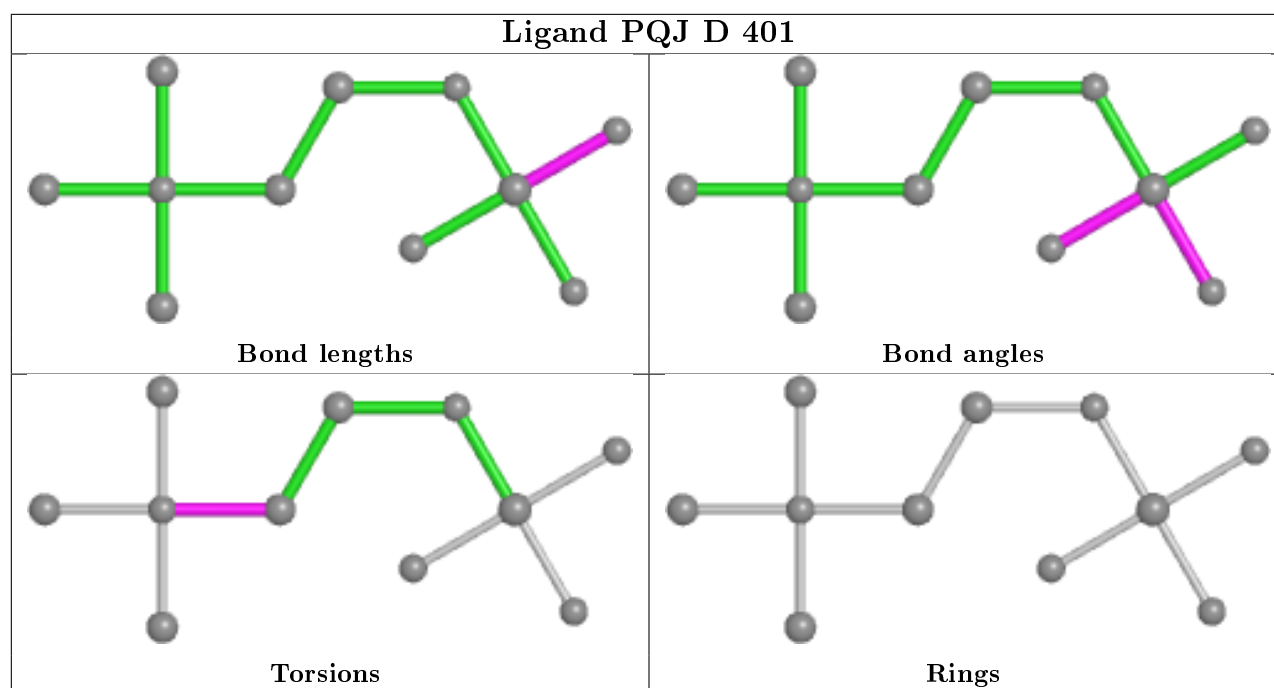


Ligand PQJ B 401



Ligand PQJ F 303





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	293/293 (100%)	0.03	7 (2%) 59 68	31, 43, 72, 107	0
1	B	293/293 (100%)	-0.02	6 (2%) 65 75	30, 42, 68, 98	0
1	C	293/293 (100%)	0.05	15 (5%) 28 40	31, 45, 82, 123	0
1	D	293/293 (100%)	0.17	14 (4%) 30 43	30, 41, 80, 137	0
1	E	293/293 (100%)	-0.09	8 (2%) 54 64	29, 40, 73, 124	0
1	F	293/293 (100%)	0.07	9 (3%) 49 61	28, 41, 78, 166	0
1	G	293/293 (100%)	-0.12	5 (1%) 70 78	28, 41, 72, 121	0
All	All	2051/2051 (100%)	0.01	64 (3%) 49 61	28, 42, 75, 166	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	73	ALA	6.2
1	C	120	PHE	5.0
1	E	132	ILE	4.7
1	D	120	PHE	4.6
1	D	129	THR	4.5
1	G	68	TYR	3.7
1	C	68	TYR	3.6
1	F	120	PHE	3.6
1	B	68	TYR	3.5
1	C	69	SER	3.4
1	F	130	GLY	3.4
1	G	120	PHE	3.4
1	A	68	TYR	3.1
1	D	72	GLY	3.1
1	C	132	ILE	3.1
1	D	260	TRP	3.0
1	E	120	PHE	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	128	ASP	3.0
1	C	130	GLY	3.0
1	C	129	THR	2.9
1	F	68	TYR	2.8
1	E	69	SER	2.8
1	A	74	ASN	2.8
1	D	130	GLY	2.8
1	D	132	ILE	2.8
1	F	69	SER	2.8
1	G	132	ILE	2.8
1	A	71	GLU	2.7
1	A	129	THR	2.6
1	C	126	GLY	2.6
1	B	120	PHE	2.6
1	E	68	TYR	2.6
1	G	131	LYS	2.6
1	E	74	ASN	2.5
1	D	201	ASN	2.5
1	A	73	ALA	2.5
1	C	71	GLU	2.5
1	B	73	ALA	2.4
1	F	263	THR	2.4
1	F	261	THR	2.4
1	A	120	PHE	2.3
1	C	73	ALA	2.3
1	F	73	ALA	2.3
1	D	128	ASP	2.3
1	F	191	TYR	2.3
1	D	203	SER	2.3
1	F	201	ASN	2.2
1	E	131	LYS	2.2
1	C	136	ILE	2.2
1	D	136	ILE	2.2
1	A	136	ILE	2.1
1	C	128	ASP	2.1
1	D	124	VAL	2.1
1	E	125	THR	2.1
1	D	262	SER	2.1
1	D	205	LYS	2.1
1	G	69	SER	2.1
1	C	262	SER	2.1
1	C	131	LYS	2.1

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Mol	Chain	Res	Type	RSRZ
1	E	130	GLY	2.1
1	B	132	ILE	2.1
1	C	93	ASN	2.0
1	C	118	TYR	2.0
1	B	126	GLY	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	PQJ	G	402	12/25	0.78	0.23	62,71,95,96	0
2	PQJ	E	402	12/25	0.82	0.21	66,78,94,97	0
2	PQJ	C	402	11/25	0.85	0.16	64,73,103,106	0
2	PQJ	D	402	12/25	0.86	0.18	74,79,91,94	0
3	SO4	D	404	5/5	0.87	0.19	56,70,83,84	0
2	PQJ	F	303	11/25	0.90	0.16	65,80,84,87	0
2	PQJ	E	401	12/25	0.91	0.17	44,60,77,79	0
3	SO4	B	404	5/5	0.91	0.12	71,90,95,97	0
3	SO4	E	405	5/5	0.91	0.13	59,67,77,83	0
3	SO4	C	403	5/5	0.92	0.18	52,56,72,75	0
2	PQJ	D	403	12/25	0.92	0.16	56,59,71,72	0
2	PQJ	B	402	12/25	0.92	0.16	53,72,87,88	0
2	PQJ	A	402	12/25	0.92	0.18	50,70,74,76	0
2	PQJ	G	401	12/25	0.93	0.15	52,60,71,79	0
2	PQJ	E	403	11/25	0.93	0.21	60,76,82,83	0
2	PQJ	B	403	12/25	0.93	0.16	60,69,79,81	0
2	PQJ	A	403	11/25	0.94	0.14	53,62,78,79	0
2	PQJ	E	404	11/25	0.94	0.20	59,69,81,84	0

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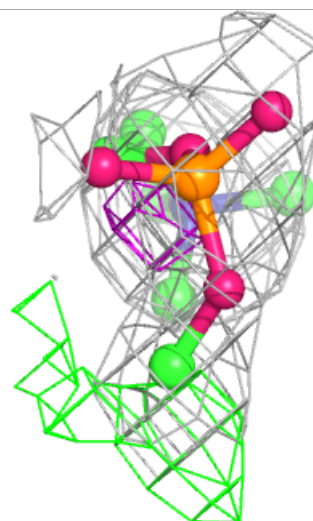
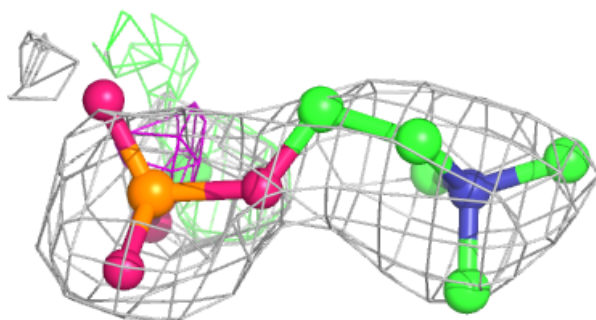
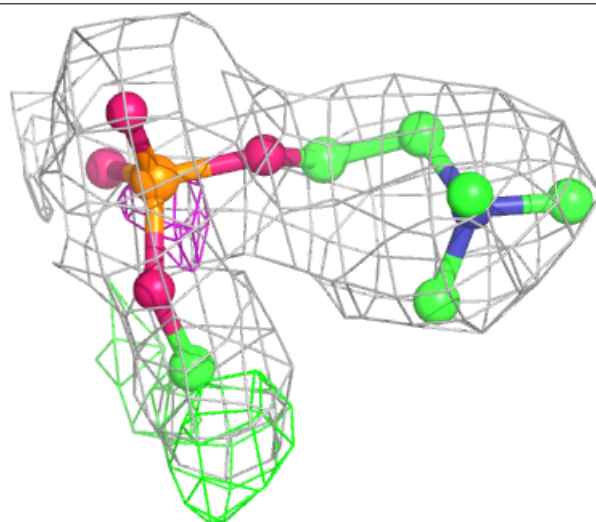
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	PQJ	F	302	12/25	0.94	0.15	53,57,65,67	0
2	PQJ	C	401	12/25	0.94	0.13	56,61,74,80	0
2	PQJ	F	304	11/25	0.94	0.20	55,62,72,73	0
3	SO4	G	403	5/5	0.94	0.12	54,65,66,68	0
2	PQJ	D	401	11/25	0.94	0.13	53,57,76,78	0
2	PQJ	F	301	12/25	0.96	0.12	52,58,61,64	0
2	PQJ	A	401	12/25	0.96	0.10	48,51,58,63	0
2	PQJ	B	401	11/25	0.96	0.09	49,54,73,74	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.

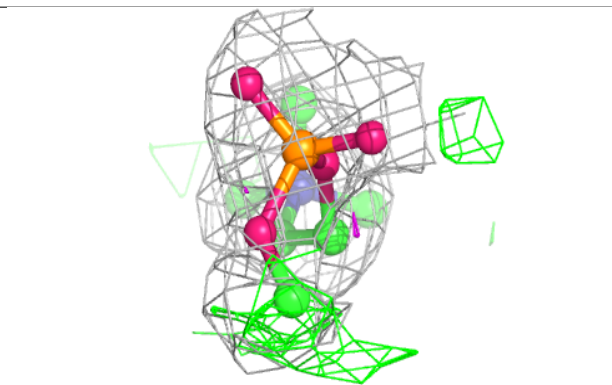
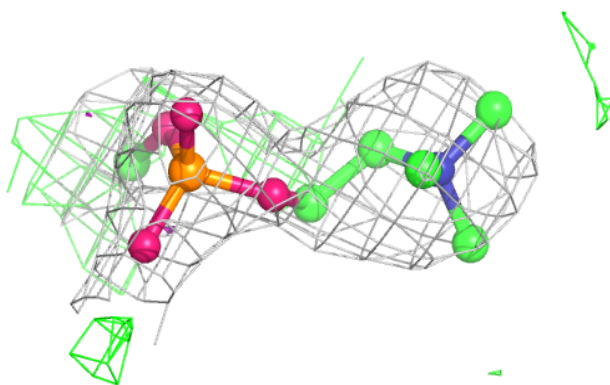
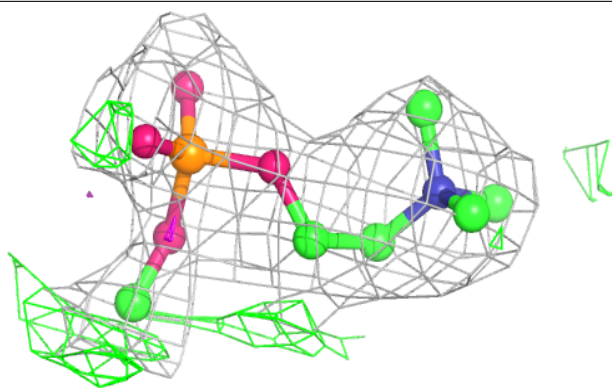
Electron density around PQJ G 402:

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

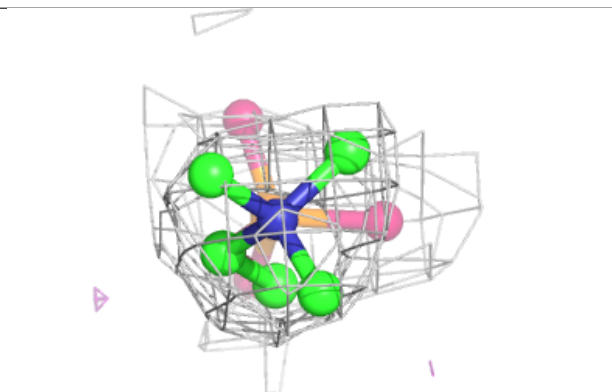
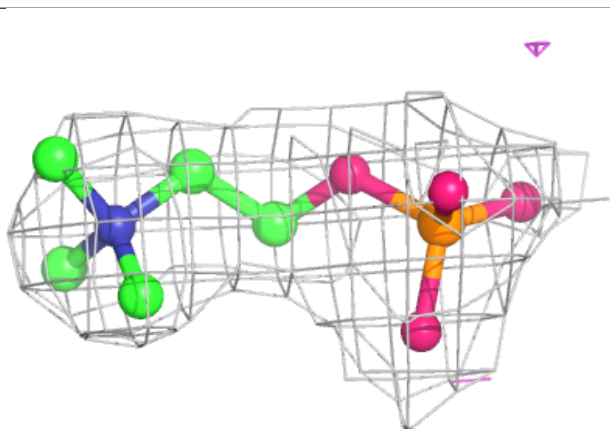
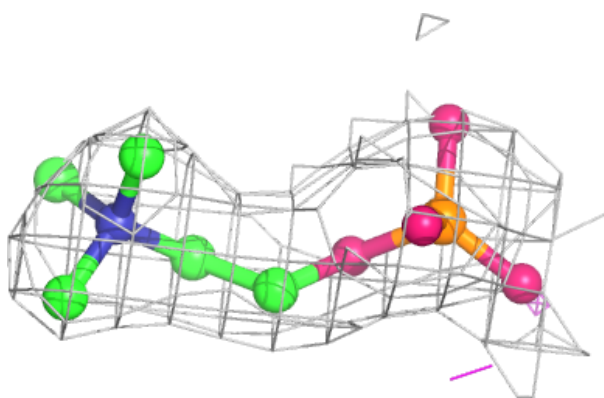


Electron density around PQJ E 402:

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

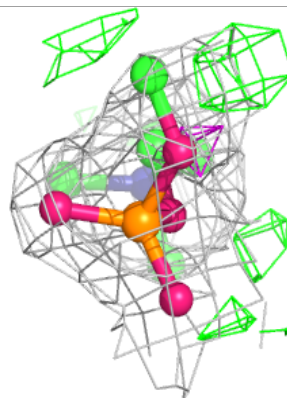
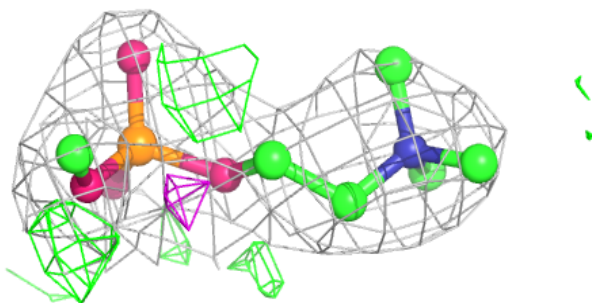
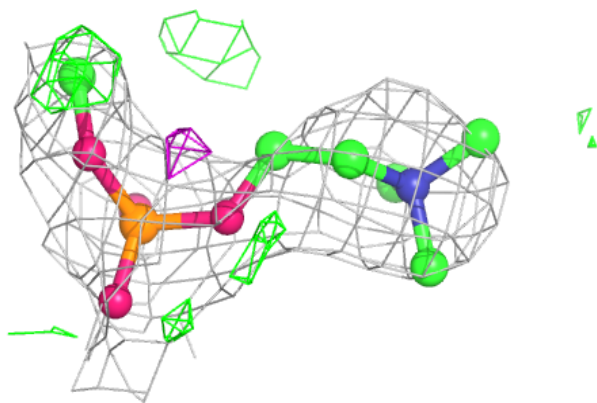
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and green (positive)

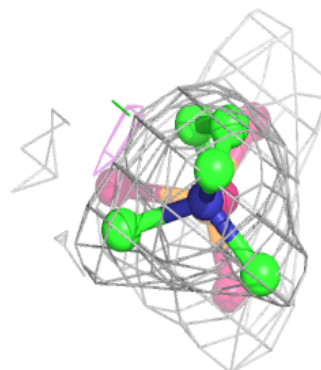
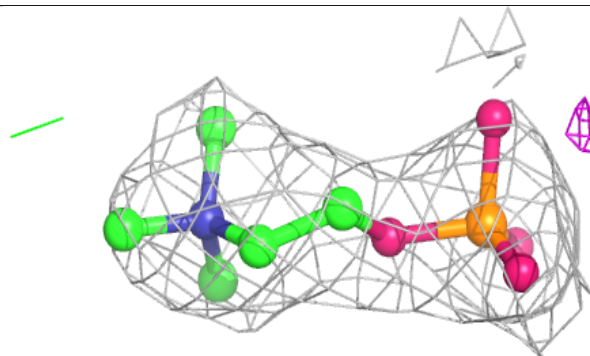
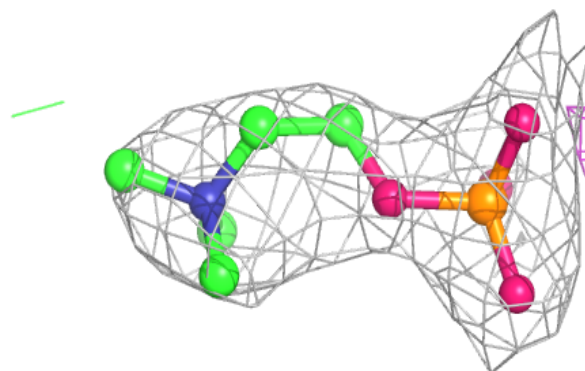


Electron density around PQJ D 402:

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and green (positive)

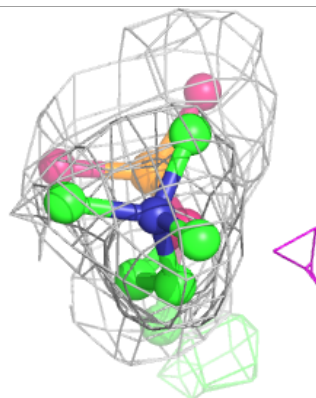
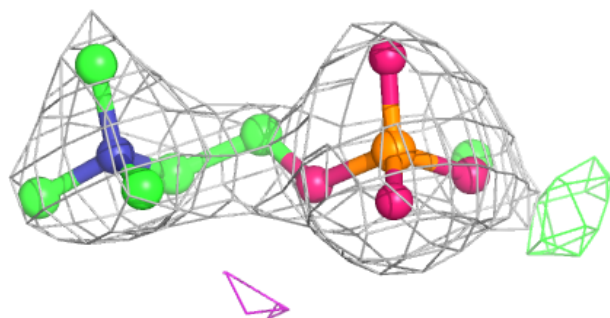
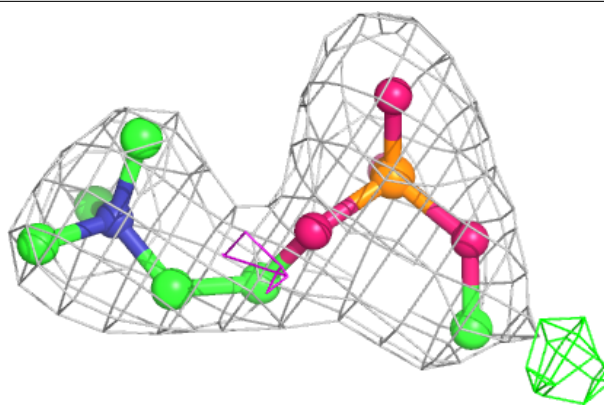
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and green (positive)



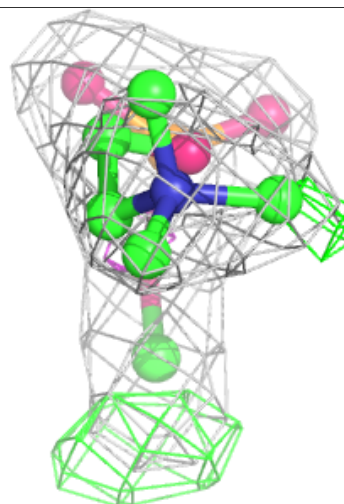
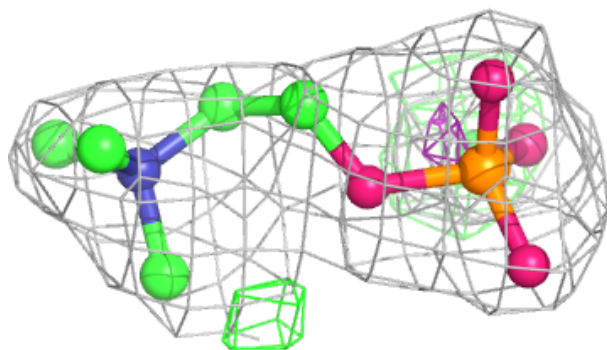
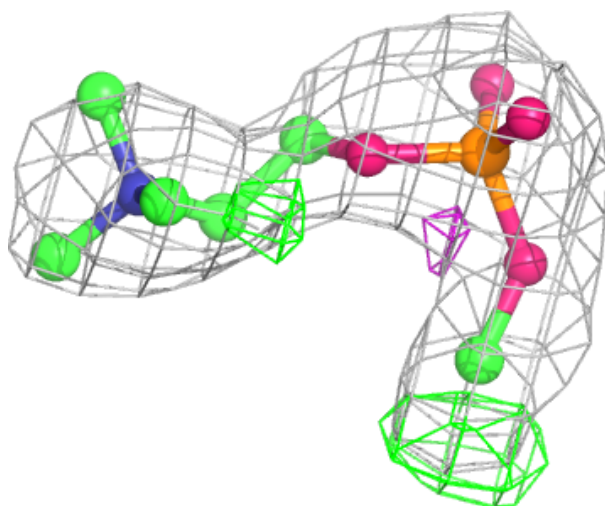
Electron density around PQJ E 401:

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and green (positive)



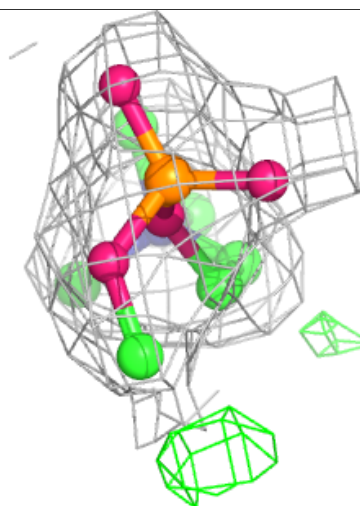
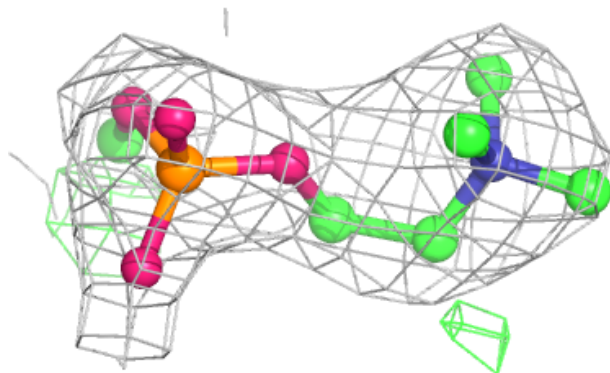
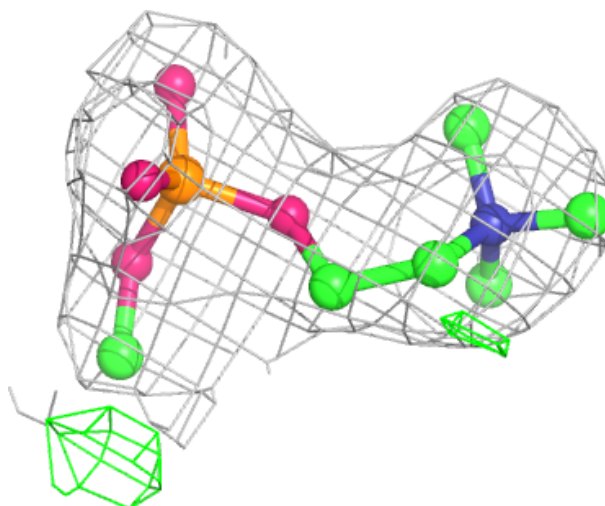
Electron density around PQJ D 403:

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



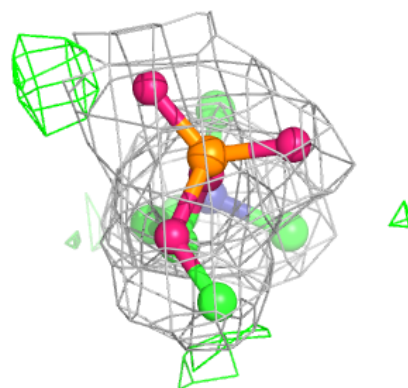
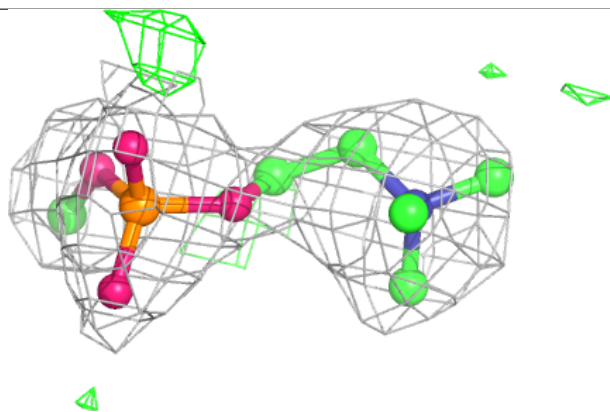
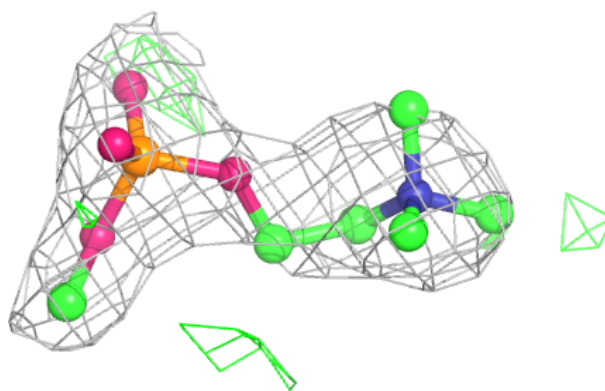
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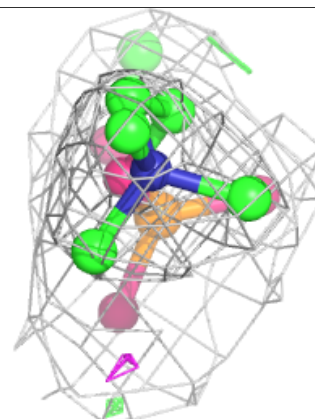
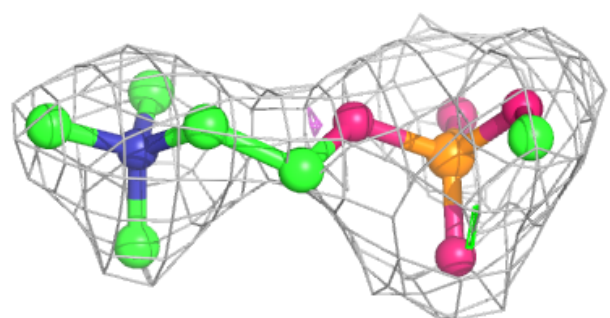
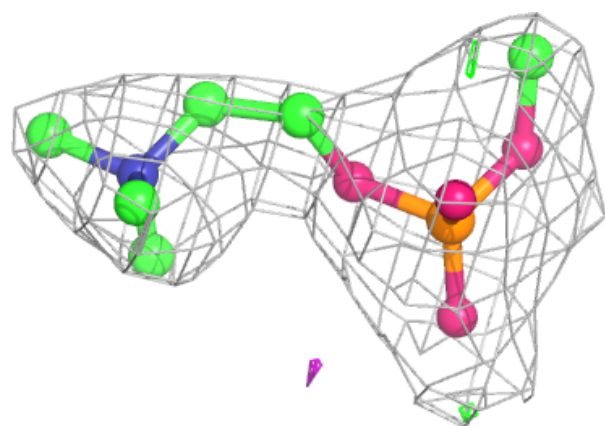


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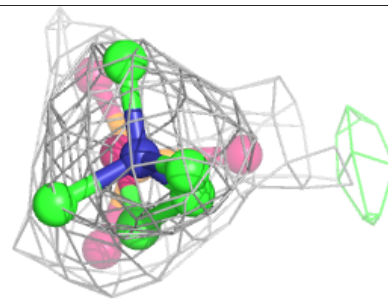
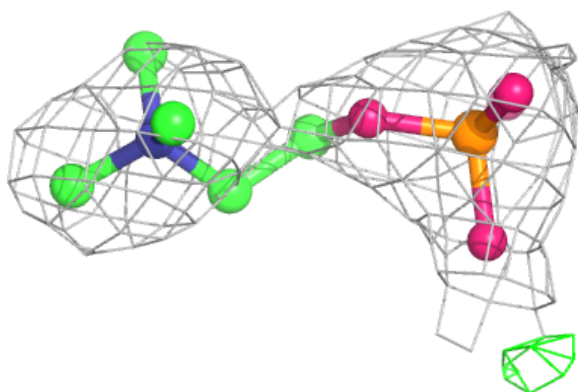
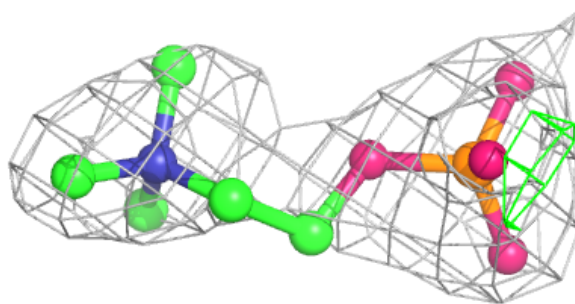
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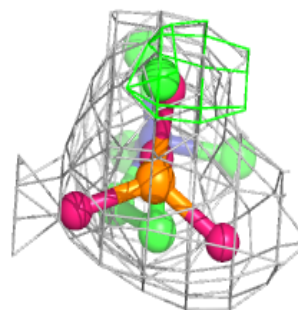
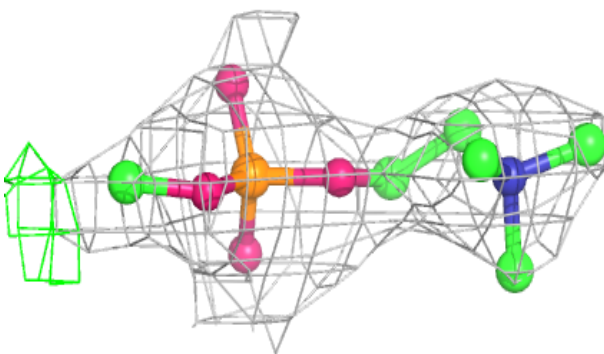
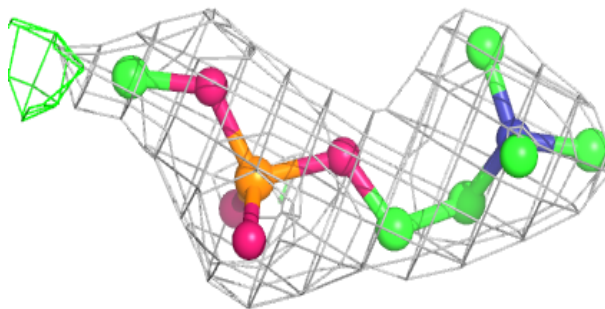


Electron density around PQJ E 403:

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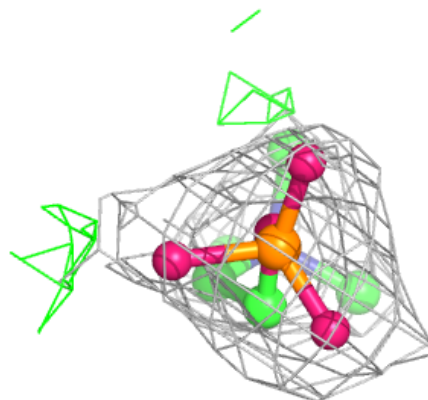
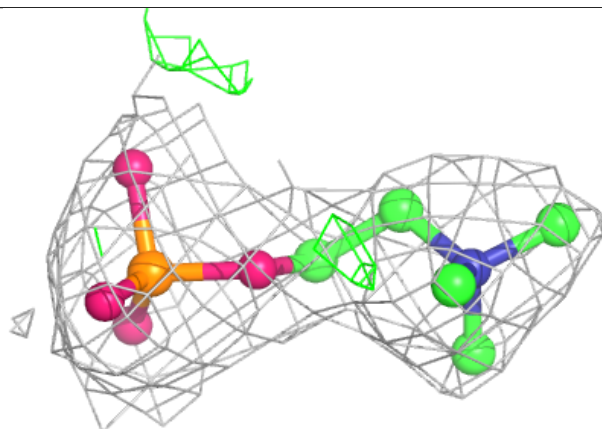
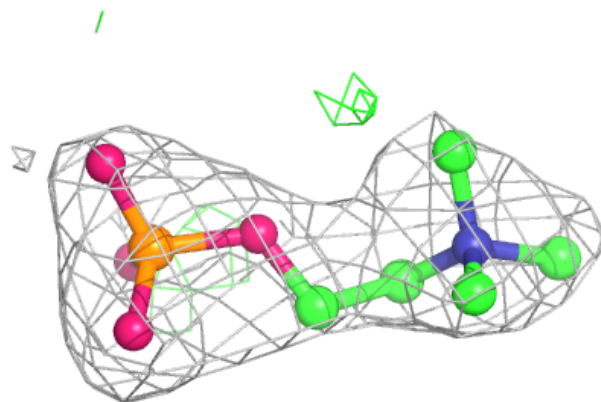
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and green (positive)



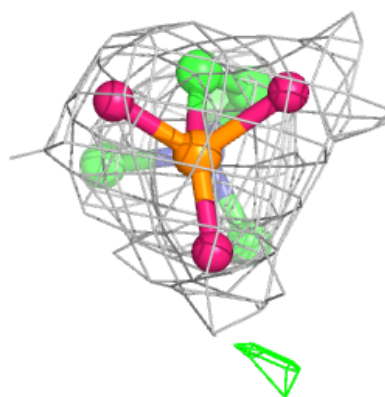
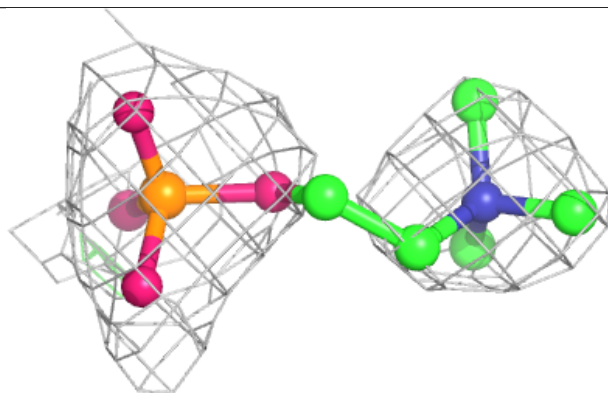
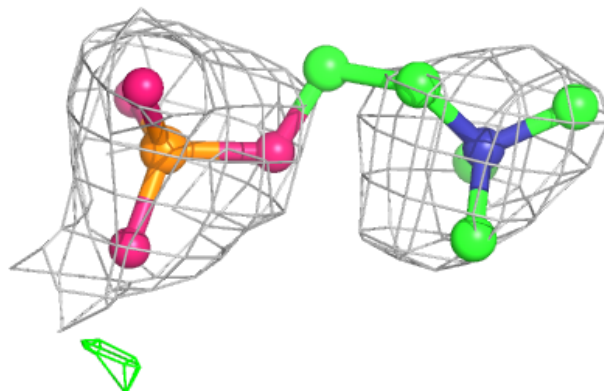
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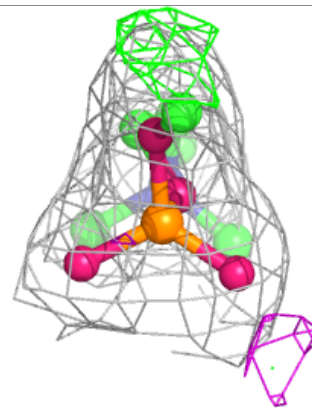
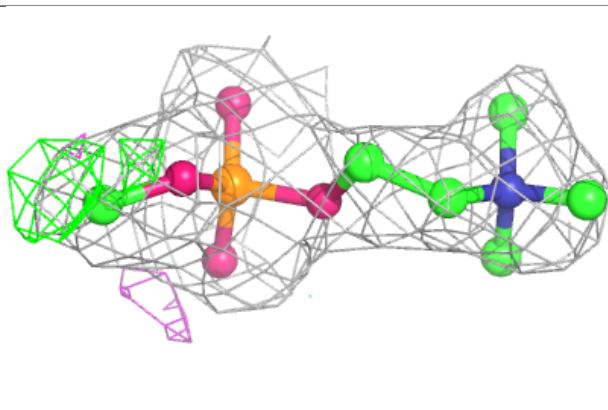
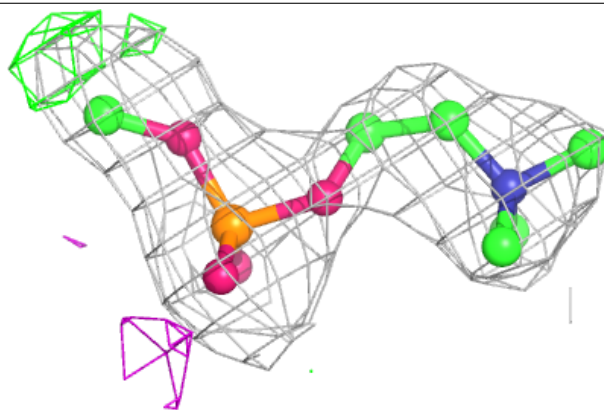


Electron density around PQJ E 404:

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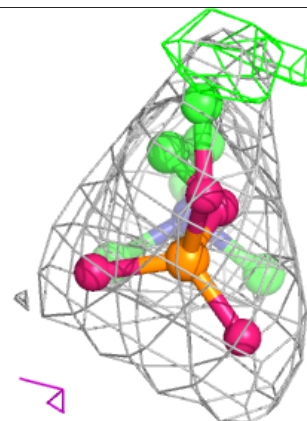
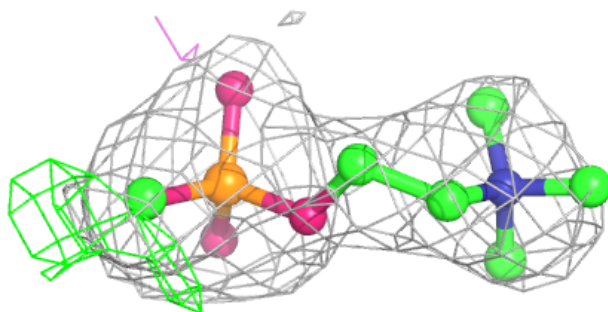
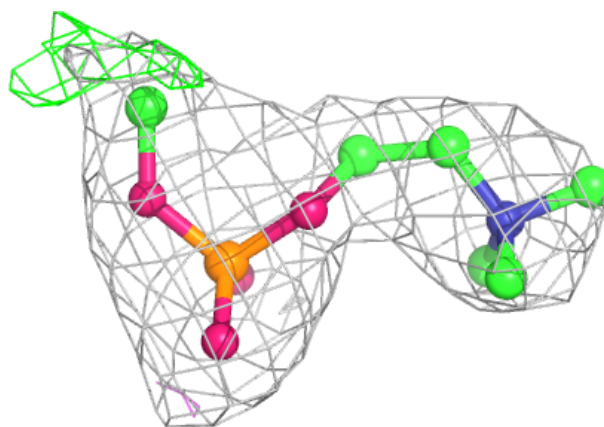
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and green (positive)

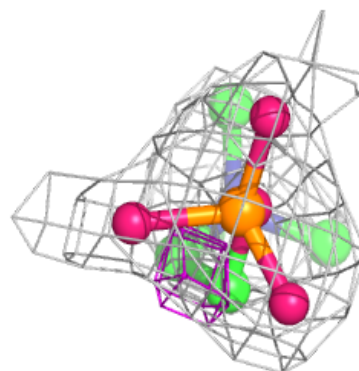
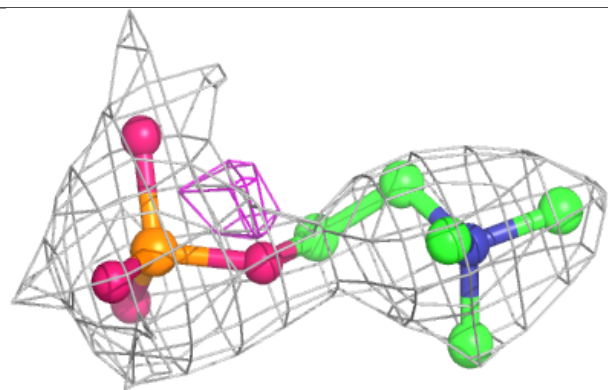
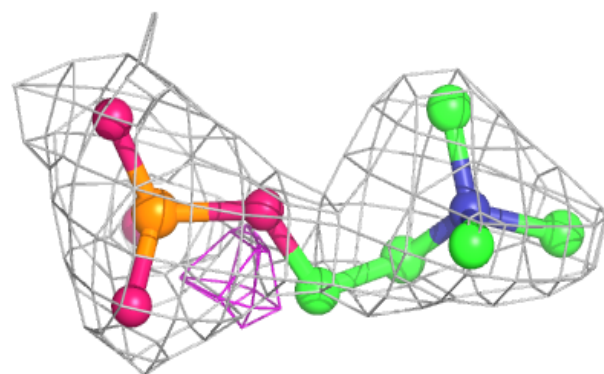


Electron density around PQJ C 401:

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

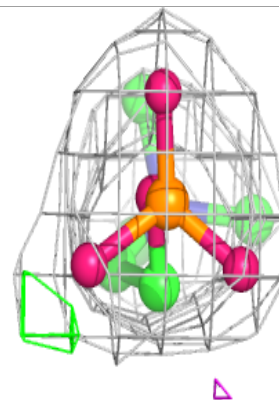
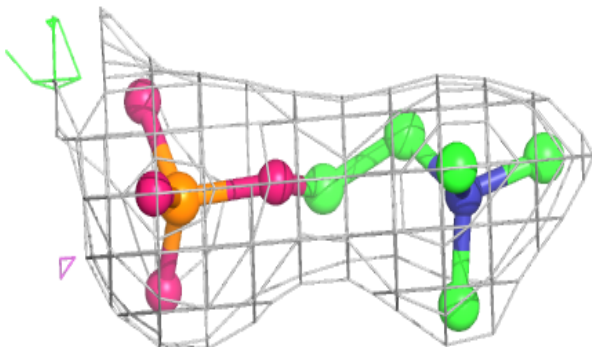
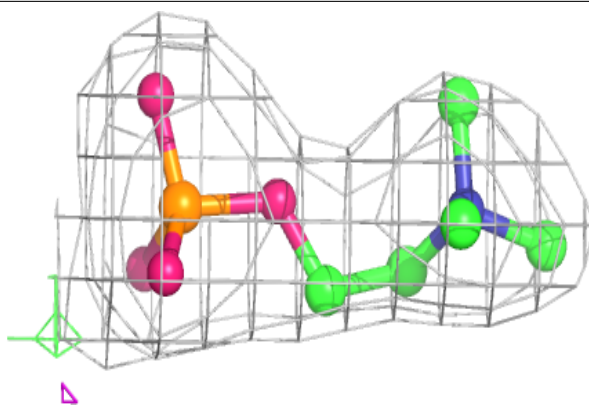
**Electron density around PQJ F 304:**

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



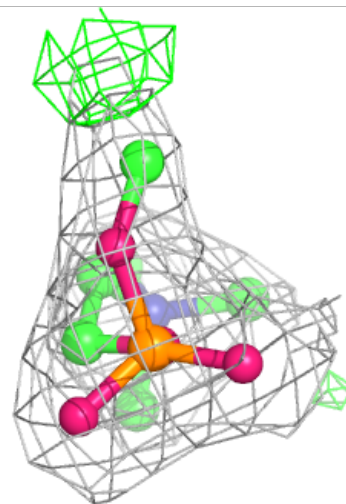
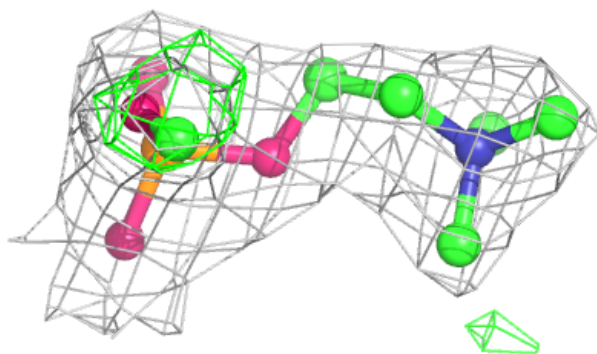
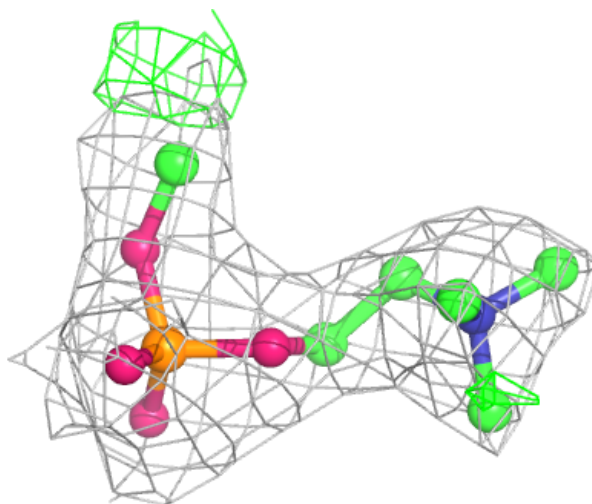
Electron density around PQJ D 401:

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



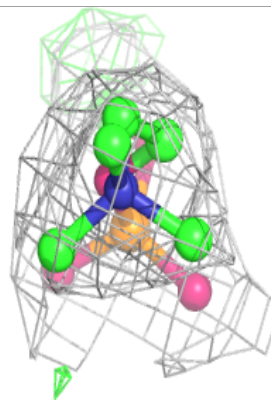
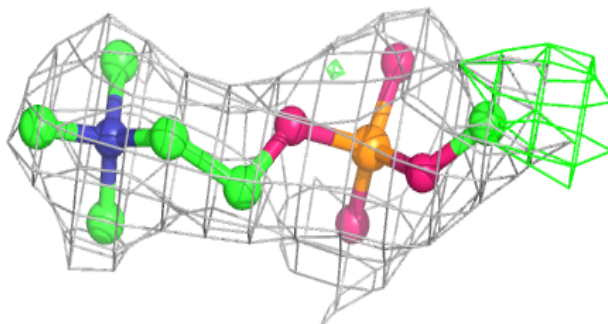
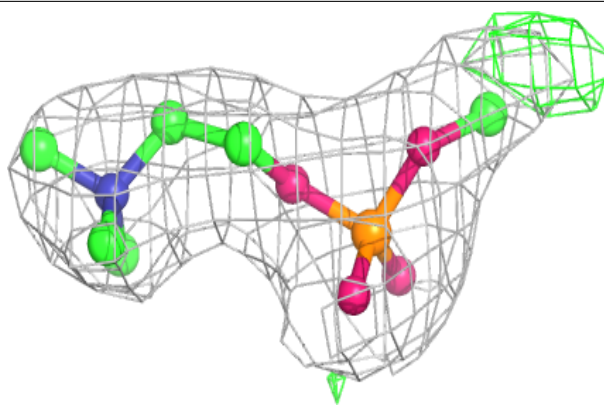
Electron density around PQJ F 301:

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



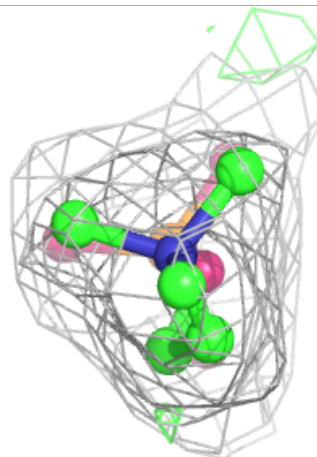
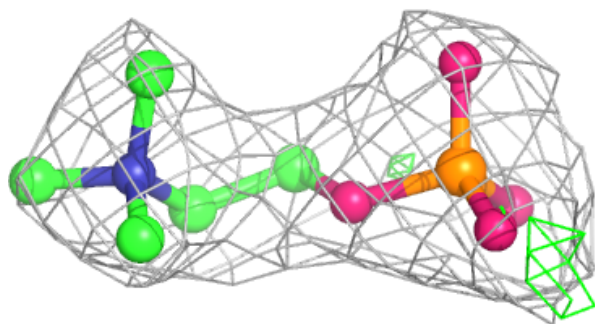
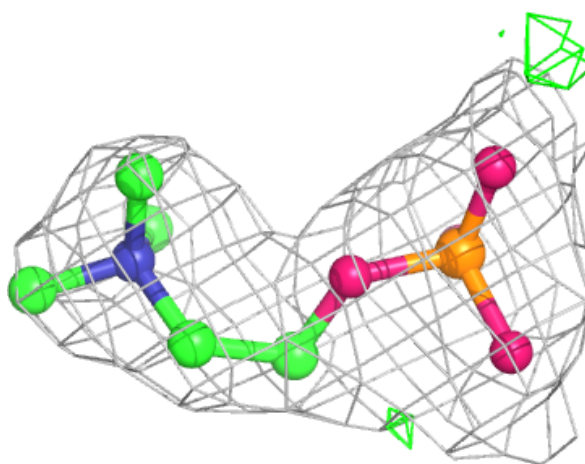
Electron density around PQJ A 401:

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



Electron density around PQJ B 401:

$2mF_o-DF_c$ (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.