



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 02:24 PM UTC

PDB ID : 3GOK / pdb_00003gok
Title : Binding site mapping of protein ligands
Authors : Scheich, C.
Deposited on : 2009-03-19
Resolution : 3.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

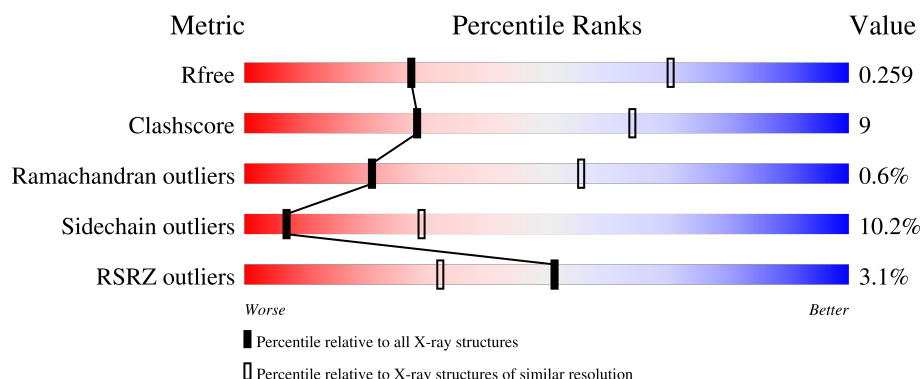
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



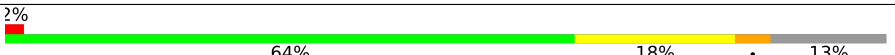
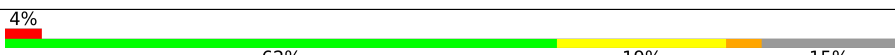
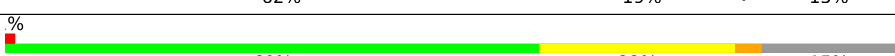
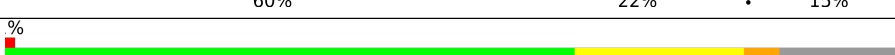
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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

Mol	Chain	Length	Quality of chain
1	A	334	3% 65% 17% • 15%
1	B	334	2% 64% 19% • 13%
1	C	334	4% 66% 16% • 15%
1	D	334	3% 60% 21% •• 15%
1	E	334	2% 62% 20% •• 13%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	334	
1	G	334	
1	H	334	
1	I	334	
1	J	334	
1	K	334	
1	L	334	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 28332 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 MAP kinase-activated protein kinase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	285	Total	C	N	O	S	0	0	0
			2317	1481	401	418	17			
1	B	290	Total	C	N	O	S	0	0	0
			2361	1510	407	427	17			
1	C	285	Total	C	N	O	S	0	0	0
			2322	1488	400	417	17			
1	D	283	Total	C	N	O	S	0	0	0
			2298	1467	399	415	17			
1	E	290	Total	C	N	O	S	0	0	0
			2361	1510	407	427	17			
1	F	284	Total	C	N	O	S	0	0	0
			2316	1485	399	415	17			
1	G	286	Total	C	N	O	S	0	0	0
			2329	1490	402	420	17			
1	H	290	Total	C	N	O	S	0	0	0
			2361	1510	407	427	17			
1	I	284	Total	C	N	O	S	0	0	0
			2316	1485	399	415	17			
1	J	283	Total	C	N	O	S	0	0	0
			2298	1467	399	415	17			
1	K	290	Total	C	N	O	S	0	0	0
			2361	1510	407	427	17			
1	L	284	Total	C	N	O	S	0	0	0
			2316	1485	399	415	17			

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	31	GLY	-	expression tag	UNP P49137
A	32	ALA	-	expression tag	UNP P49137
A	33	MET	-	expression tag	UNP P49137
A	34	GLY	-	expression tag	UNP P49137
A	35	SER	-	expression tag	UNP P49137

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	36	GLY	-	expression tag	UNP P49137
A	37	ALA	-	expression tag	UNP P49137
A	38	MET	-	expression tag	UNP P49137
A	39	GLY	-	expression tag	UNP P49137
A	40	SER	-	expression tag	UNP P49137
B	31	GLY	-	expression tag	UNP P49137
B	32	ALA	-	expression tag	UNP P49137
B	33	MET	-	expression tag	UNP P49137
B	34	GLY	-	expression tag	UNP P49137
B	35	SER	-	expression tag	UNP P49137
B	36	GLY	-	expression tag	UNP P49137
B	37	ALA	-	expression tag	UNP P49137
B	38	MET	-	expression tag	UNP P49137
B	39	GLY	-	expression tag	UNP P49137
B	40	SER	-	expression tag	UNP P49137
C	31	GLY	-	expression tag	UNP P49137
C	32	ALA	-	expression tag	UNP P49137
C	33	MET	-	expression tag	UNP P49137
C	34	GLY	-	expression tag	UNP P49137
C	35	SER	-	expression tag	UNP P49137
C	36	GLY	-	expression tag	UNP P49137
C	37	ALA	-	expression tag	UNP P49137
C	38	MET	-	expression tag	UNP P49137
C	39	GLY	-	expression tag	UNP P49137
C	40	SER	-	expression tag	UNP P49137
D	31	GLY	-	expression tag	UNP P49137
D	32	ALA	-	expression tag	UNP P49137
D	33	MET	-	expression tag	UNP P49137
D	34	GLY	-	expression tag	UNP P49137
D	35	SER	-	expression tag	UNP P49137
D	36	GLY	-	expression tag	UNP P49137
D	37	ALA	-	expression tag	UNP P49137
D	38	MET	-	expression tag	UNP P49137
D	39	GLY	-	expression tag	UNP P49137
D	40	SER	-	expression tag	UNP P49137
E	31	GLY	-	expression tag	UNP P49137
E	32	ALA	-	expression tag	UNP P49137
E	33	MET	-	expression tag	UNP P49137
E	34	GLY	-	expression tag	UNP P49137
E	35	SER	-	expression tag	UNP P49137
E	36	GLY	-	expression tag	UNP P49137
E	37	ALA	-	expression tag	UNP P49137

Continued on next page...

Continued from previous page...

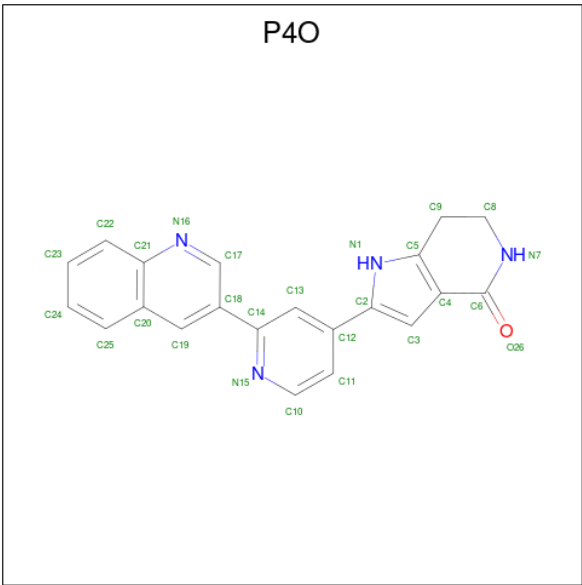
Chain	Residue	Modelled	Actual	Comment	Reference
E	38	MET	-	expression tag	UNP P49137
E	39	GLY	-	expression tag	UNP P49137
E	40	SER	-	expression tag	UNP P49137
F	31	GLY	-	expression tag	UNP P49137
F	32	ALA	-	expression tag	UNP P49137
F	33	MET	-	expression tag	UNP P49137
F	34	GLY	-	expression tag	UNP P49137
F	35	SER	-	expression tag	UNP P49137
F	36	GLY	-	expression tag	UNP P49137
F	37	ALA	-	expression tag	UNP P49137
F	38	MET	-	expression tag	UNP P49137
F	39	GLY	-	expression tag	UNP P49137
F	40	SER	-	expression tag	UNP P49137
G	31	GLY	-	expression tag	UNP P49137
G	32	ALA	-	expression tag	UNP P49137
G	33	MET	-	expression tag	UNP P49137
G	34	GLY	-	expression tag	UNP P49137
G	35	SER	-	expression tag	UNP P49137
G	36	GLY	-	expression tag	UNP P49137
G	37	ALA	-	expression tag	UNP P49137
G	38	MET	-	expression tag	UNP P49137
G	39	GLY	-	expression tag	UNP P49137
G	40	SER	-	expression tag	UNP P49137
H	31	GLY	-	expression tag	UNP P49137
H	32	ALA	-	expression tag	UNP P49137
H	33	MET	-	expression tag	UNP P49137
H	34	GLY	-	expression tag	UNP P49137
H	35	SER	-	expression tag	UNP P49137
H	36	GLY	-	expression tag	UNP P49137
H	37	ALA	-	expression tag	UNP P49137
H	38	MET	-	expression tag	UNP P49137
H	39	GLY	-	expression tag	UNP P49137
H	40	SER	-	expression tag	UNP P49137
I	31	GLY	-	expression tag	UNP P49137
I	32	ALA	-	expression tag	UNP P49137
I	33	MET	-	expression tag	UNP P49137
I	34	GLY	-	expression tag	UNP P49137
I	35	SER	-	expression tag	UNP P49137
I	36	GLY	-	expression tag	UNP P49137
I	37	ALA	-	expression tag	UNP P49137
I	38	MET	-	expression tag	UNP P49137
I	39	GLY	-	expression tag	UNP P49137

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
I	40	SER	-	expression tag	UNP P49137
J	31	GLY	-	expression tag	UNP P49137
J	32	ALA	-	expression tag	UNP P49137
J	33	MET	-	expression tag	UNP P49137
J	34	GLY	-	expression tag	UNP P49137
J	35	SER	-	expression tag	UNP P49137
J	36	GLY	-	expression tag	UNP P49137
J	37	ALA	-	expression tag	UNP P49137
J	38	MET	-	expression tag	UNP P49137
J	39	GLY	-	expression tag	UNP P49137
J	40	SER	-	expression tag	UNP P49137
K	31	GLY	-	expression tag	UNP P49137
K	32	ALA	-	expression tag	UNP P49137
K	33	MET	-	expression tag	UNP P49137
K	34	GLY	-	expression tag	UNP P49137
K	35	SER	-	expression tag	UNP P49137
K	36	GLY	-	expression tag	UNP P49137
K	37	ALA	-	expression tag	UNP P49137
K	38	MET	-	expression tag	UNP P49137
K	39	GLY	-	expression tag	UNP P49137
K	40	SER	-	expression tag	UNP P49137
L	31	GLY	-	expression tag	UNP P49137
L	32	ALA	-	expression tag	UNP P49137
L	33	MET	-	expression tag	UNP P49137
L	34	GLY	-	expression tag	UNP P49137
L	35	SER	-	expression tag	UNP P49137
L	36	GLY	-	expression tag	UNP P49137
L	37	ALA	-	expression tag	UNP P49137
L	38	MET	-	expression tag	UNP P49137
L	39	GLY	-	expression tag	UNP P49137
L	40	SER	-	expression tag	UNP P49137

- Molecule 2 is 2-(2-QUINOLIN-3-YLPYRIDIN-4-YL)-1,5,6,7-TETRAHYDRO-4H-PYRROLO[3,2-C]PYRIDIN-4-ONE (CCD ID: P4O) (formula: C₂₁H₁₆N₄O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			26	21	4	1		
2	B	1	Total	C	N	O	0	0
			26	21	4	1		
2	C	1	Total	C	N	O	0	0
			26	21	4	1		
2	D	1	Total	C	N	O	0	0
			26	21	4	1		
2	E	1	Total	C	N	O	0	0
			26	21	4	1		
2	F	1	Total	C	N	O	0	0
			26	21	4	1		
2	G	1	Total	C	N	O	0	0
			26	21	4	1		
2	H	1	Total	C	N	O	0	0
			26	21	4	1		
2	I	1	Total	C	N	O	0	0
			26	21	4	1		
2	J	1	Total	C	N	O	0	0
			26	21	4	1		
2	K	1	Total	C	N	O	0	0
			26	21	4	1		
2	L	1	Total	C	N	O	0	0
			26	21	4	1		

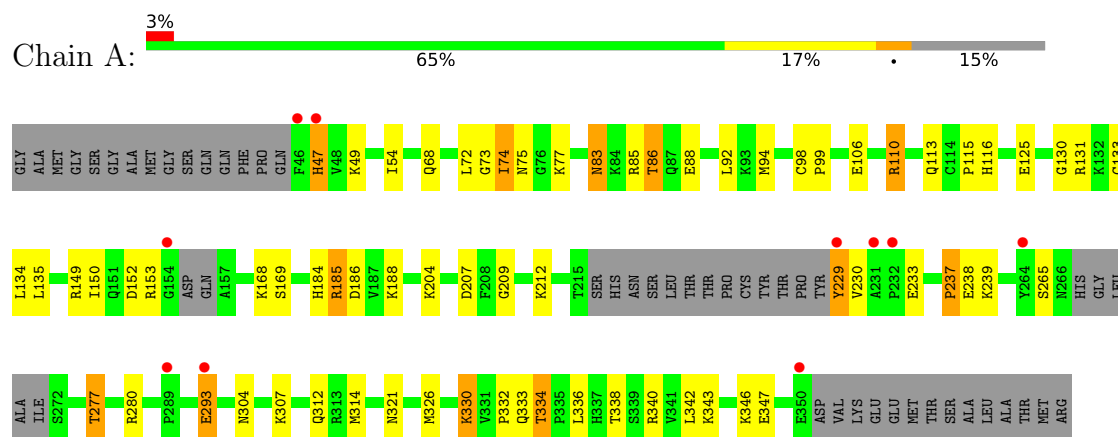
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	3	Total O 3 3	0	0
3	B	8	Total O 8 8	0	0
3	C	6	Total O 6 6	0	0
3	D	8	Total O 8 8	0	0
3	E	5	Total O 5 5	0	0
3	F	2	Total O 2 2	0	0
3	G	6	Total O 6 6	0	0
3	H	7	Total O 7 7	0	0
3	I	2	Total O 2 2	0	0
3	J	6	Total O 6 6	0	0
3	K	4	Total O 4 4	0	0
3	L	7	Total O 7 7	0	0

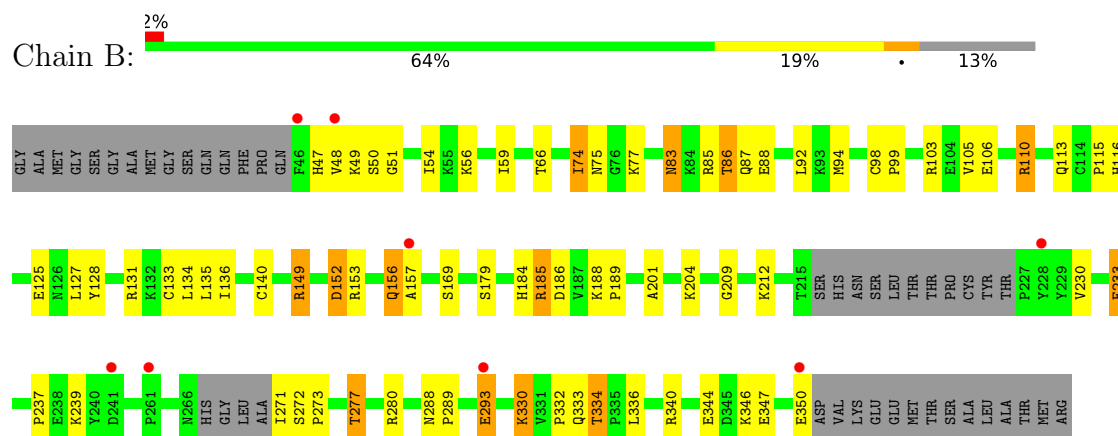
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

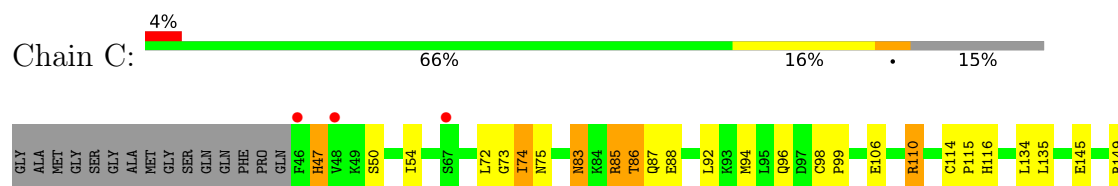
- Molecule 1: MAP kinase-activated protein kinase 2

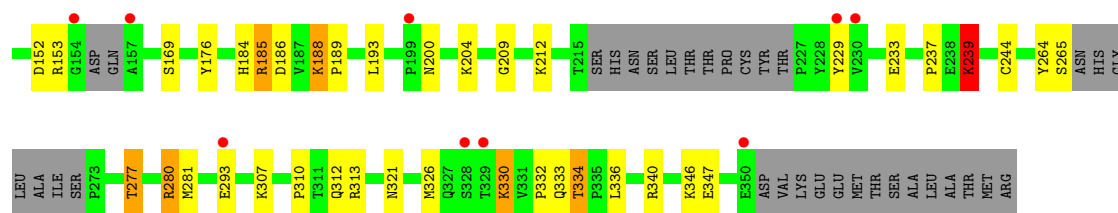


- Molecule 1: MAP kinase-activated protein kinase 2

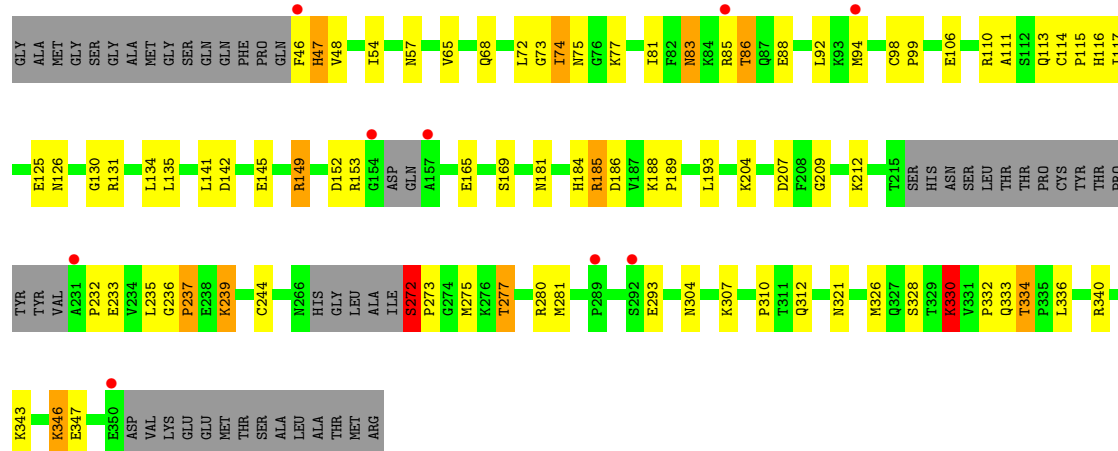


- Molecule 1: MAP kinase-activated protein kinase 2

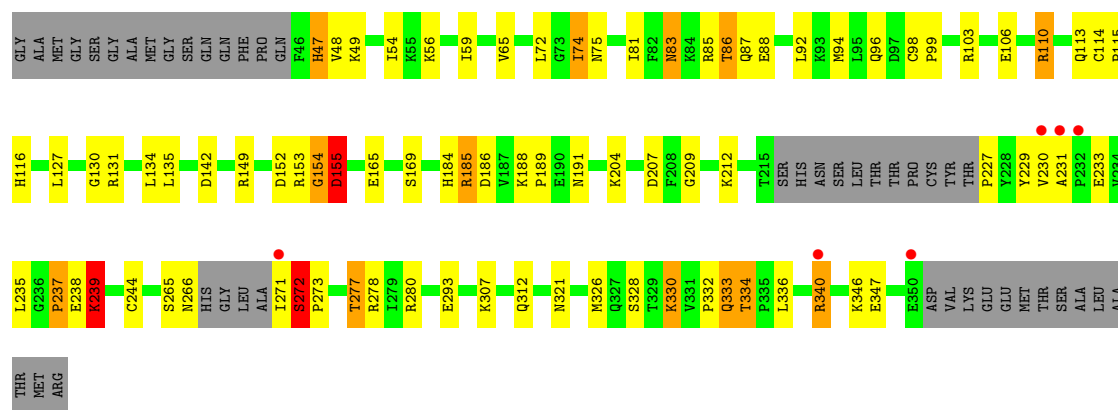




• Molecule 1: MAP kinase-activated protein kinase 2

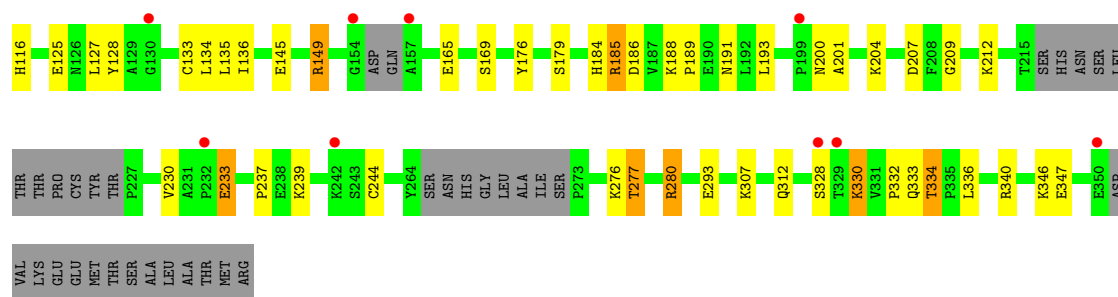


• Molecule 1: MAP kinase-activated protein kinase 2

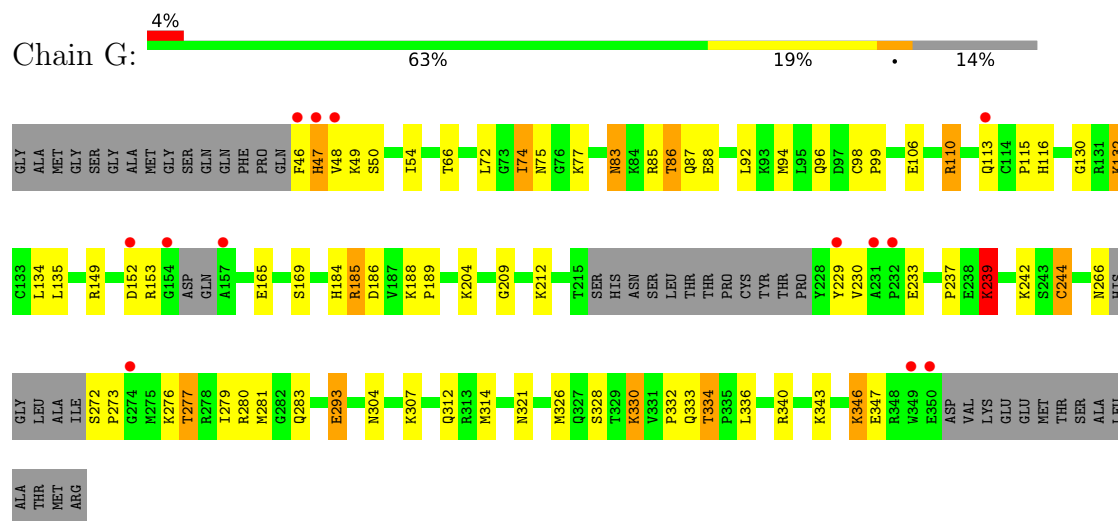


• Molecule 1: MAP kinase-activated protein kinase 2

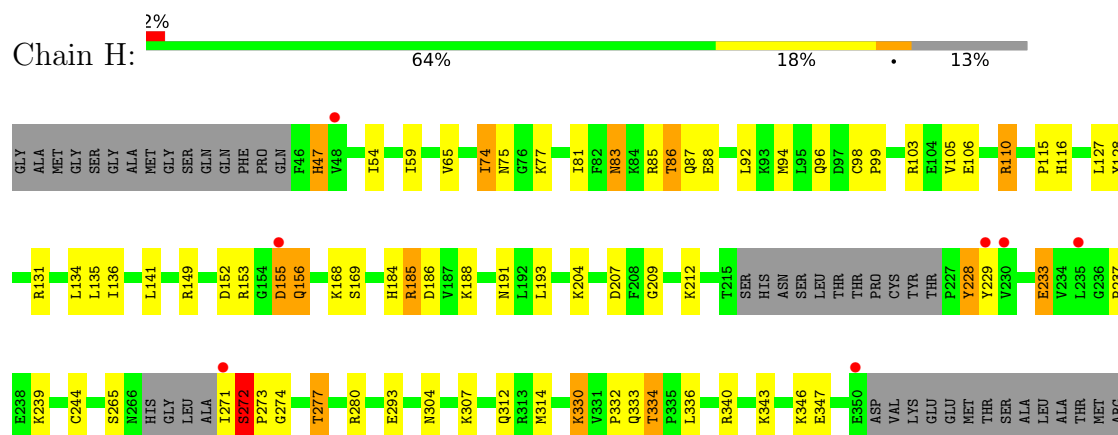




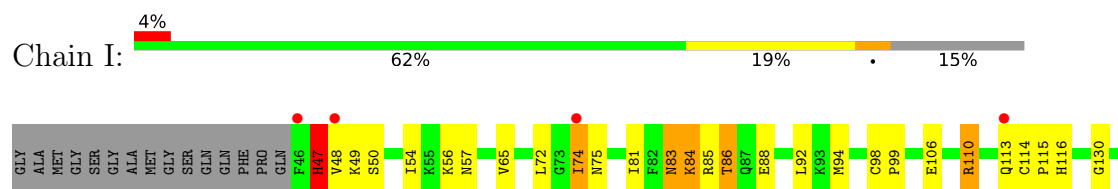
- Molecule 1: MAP kinase-activated protein kinase 2

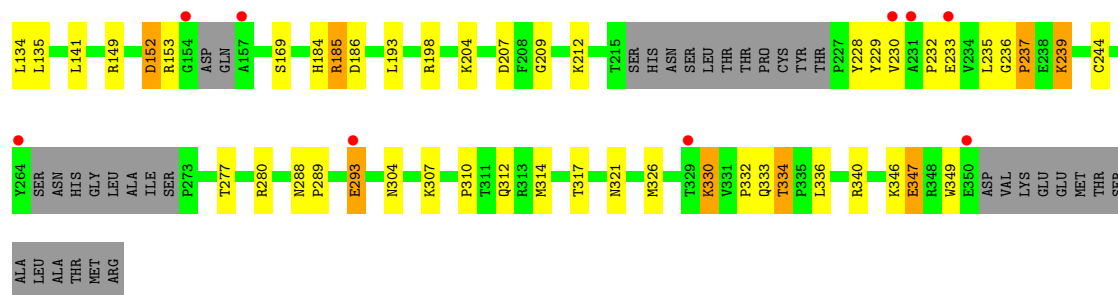


- Molecule 1: MAP kinase-activated protein kinase 2

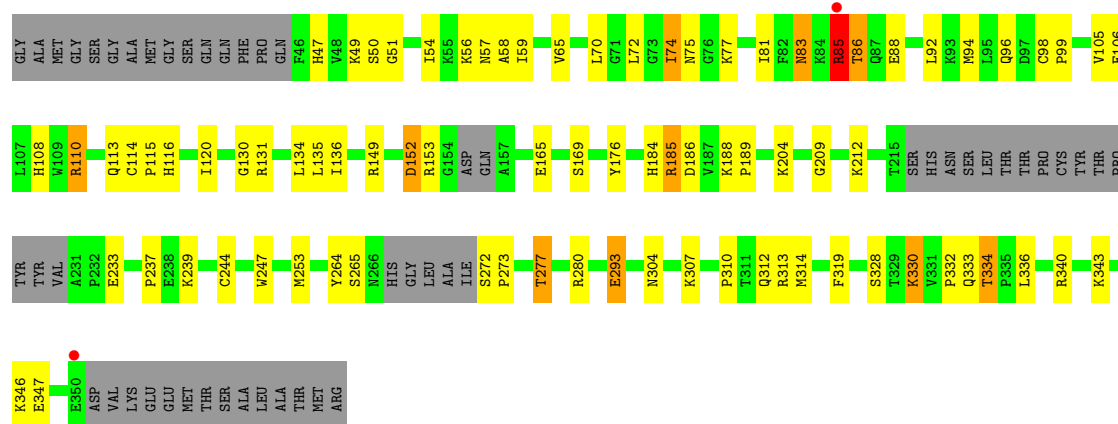


- Molecule 1: MAP kinase-activated protein kinase 2

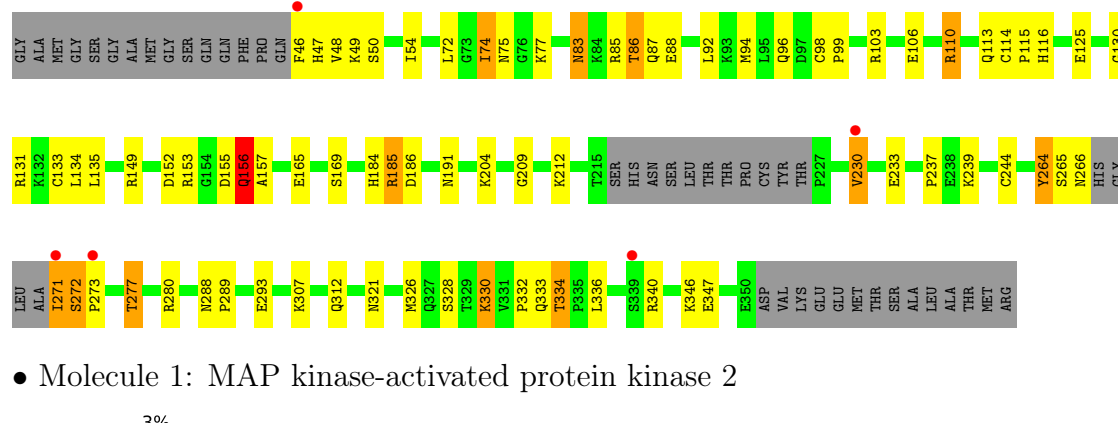




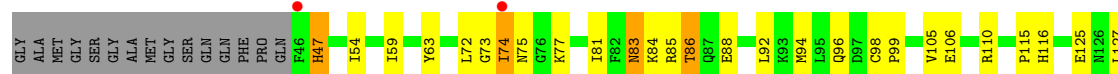
- Molecule 1: MAP kinase-activated protein kinase 2

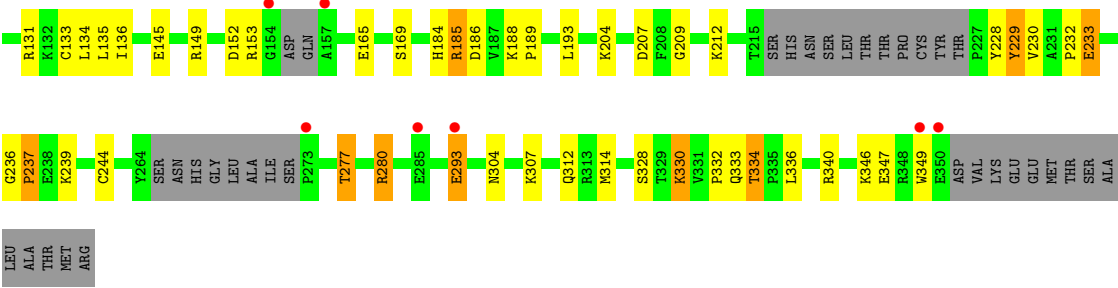


- Molecule 1: MAP kinase-activated protein kinase 2



- Molecule 1: MAP kinase-activated protein kinase 2





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	140.21Å 183.19Å 217.66Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.73 – 3.20 46.73 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.8 (46.73-3.20) 99.7 (46.73-3.20)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	0.17	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.11 (at 3.19Å)	Xtriage
Refinement program	REFMAC 5.1	Depositor
R, R_{free}	0.238 , 0.258 (Not available) , 0.259	Depositor DCC
R_{free} test set	4642 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	91.4	Xtriage
Anisotropy	0.027	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 96.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	28332	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.88% 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: P4O

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	0.95	0/2366	1.05	7/3188 (0.2%)
1	B	0.86	0/2413	1.05	8/3254 (0.2%)
1	C	0.89	0/2373	1.10	14/3197 (0.4%)
1	D	0.91	0/2346	1.08	14/3160 (0.4%)
1	E	0.82	1/2413 (0.0%)	1.08	14/3254 (0.4%)
1	F	0.92	0/2367	1.10	13/3189 (0.4%)
1	G	0.86	0/2379	1.07	8/3206 (0.2%)
1	H	0.80	0/2413	1.06	8/3254 (0.2%)
1	I	0.87	0/2367	1.12	15/3189 (0.5%)
1	J	0.77	0/2346	1.05	9/3160 (0.3%)
1	K	0.78	0/2413	1.06	10/3254 (0.3%)
1	L	0.82	2/2367 (0.1%)	1.11	15/3189 (0.5%)
All	All	0.86	3/28563 (0.0%)	1.08	135/38494 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	D	0	1
1	E	0	1
All	All	0	2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	L	230	VAL	CA-CB	5.92	1.60	1.54
1	E	272	SER	CA-C	5.38	1.59	1.52
1	L	47	HIS	CA-CB	5.06	1.59	1.53

The worst 5 of 135 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	47	HIS	CB-CA-C	-10.55	93.90	110.78
1	L	47	HIS	CB-CA-C	-10.17	94.50	110.78
1	E	272	SER	CA-C-N	10.07	130.35	119.87
1	E	272	SER	C-N-CA	10.07	130.35	119.87
1	I	280	ARG	NE-CZ-NH2	9.98	128.19	119.20

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	272	SER	Peptide
1	E	154	GLY	Peptide

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	2317	0	2344	35	2
1	B	2361	0	2385	54	2
1	C	2322	0	2351	41	1
1	D	2298	0	2326	50	1
1	E	2361	0	2385	55	8
1	F	2316	0	2346	50	1
1	G	2329	0	2353	48	0
1	H	2361	0	2385	43	2
1	I	2316	0	2346	48	3
1	J	2298	0	2326	52	8
1	K	2361	0	2385	43	0
1	L	2316	0	2346	42	2
2	A	26	0	16	1	0
2	B	26	0	16	1	0
2	C	26	0	16	1	0
2	D	26	0	16	3	0
2	E	26	0	16	2	0
2	F	26	0	16	3	0
2	G	26	0	16	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	H	26	0	16	1	0
2	I	26	0	16	0	0
2	J	26	0	16	2	0
2	K	26	0	16	1	0
2	L	26	0	16	1	0
3	A	3	0	0	1	0
3	B	8	0	0	2	0
3	C	6	0	0	0	0
3	D	8	0	0	3	0
3	E	5	0	0	1	0
3	F	2	0	0	0	0
3	G	6	0	0	1	0
3	H	7	0	0	0	0
3	I	2	0	0	0	0
3	J	6	0	0	1	0
3	K	4	0	0	1	0
3	L	7	0	0	1	0
All	All	28332	0	28470	498	15

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 9.

The worst 5 of 498 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:A:47:HIS:HA	3:A:366:HOH:O	1.52	1.08
1:H:265:SER:O	1:H:272:SER:HA	1.71	0.88
1:H:271:ILE:HG12	1:H:274:GLY:HA3	1.53	0.88
1:F:332:PRO:HB2	1:F:334:THR:HG22	1.55	0.88
1:I:332:PRO:HB2	1:I:334:THR:HG22	1.53	0.87

The worst 5 of 15 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)
1:I:198:ARG:NH2	1:L:84:LYS:O[2_555]	1.26	0.94
1:E:340:ARG:NE	1:J:85:ARG:NE[2_554]	1.50	0.70
1:E:340:ARG:NH1	1:J:85:ARG:CZ[2_554]	1.57	0.63
1:E:340:ARG:CB	1:J:85:ARG:CD[2_554]	1.66	0.54
1:E:340:ARG:NH1	1:J:85:ARG:NH2[2_554]	1.70	0.50

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	277/334 (83%)	257 (93%)	18 (6%)	2 (1%)	18	52
1	B	284/334 (85%)	260 (92%)	21 (7%)	3 (1%)	11	43
1	C	277/334 (83%)	259 (94%)	17 (6%)	1 (0%)	30	62
1	D	275/334 (82%)	258 (94%)	16 (6%)	1 (0%)	30	62
1	E	284/334 (85%)	260 (92%)	21 (7%)	3 (1%)	11	43
1	F	276/334 (83%)	257 (93%)	18 (6%)	1 (0%)	30	62
1	G	278/334 (83%)	260 (94%)	17 (6%)	1 (0%)	30	62
1	H	284/334 (85%)	258 (91%)	23 (8%)	3 (1%)	11	43
1	I	276/334 (83%)	260 (94%)	15 (5%)	1 (0%)	30	62
1	J	275/334 (82%)	258 (94%)	16 (6%)	1 (0%)	30	62
1	K	284/334 (85%)	260 (92%)	21 (7%)	3 (1%)	11	43
1	L	276/334 (83%)	258 (94%)	17 (6%)	1 (0%)	30	62
All	All	3346/4008 (84%)	3105 (93%)	220 (7%)	21 (1%)	21	56

5 of 21 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	230	VAL
1	A	237	PRO
1	B	157	ALA
1	B	237	PRO
1	C	237	PRO

5.3.2 Protein sidechains [i](#)

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	257/297 (86%)	231 (90%)	26 (10%)	7	30
1	B	262/297 (88%)	238 (91%)	24 (9%)	8	33
1	C	257/297 (86%)	233 (91%)	24 (9%)	8	33
1	D	255/297 (86%)	229 (90%)	26 (10%)	7	29
1	E	262/297 (88%)	236 (90%)	26 (10%)	7	31
1	F	256/297 (86%)	229 (90%)	27 (10%)	6	28
1	G	258/297 (87%)	229 (89%)	29 (11%)	6	25
1	H	262/297 (88%)	234 (89%)	28 (11%)	6	27
1	I	256/297 (86%)	231 (90%)	25 (10%)	7	31
1	J	255/297 (86%)	228 (89%)	27 (11%)	6	27
1	K	262/297 (88%)	234 (89%)	28 (11%)	6	27
1	L	256/297 (86%)	231 (90%)	25 (10%)	7	31
All	All	3098/3564 (87%)	2783 (90%)	315 (10%)	7	29

5 of 315 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	334	THR
1	K	334	THR
1	J	75	ASN
1	J	346	LYS
1	L	106	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 91 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	184	HIS
1	J	75	ASN
1	H	200	ASN
1	I	151	GLN
1	J	200	ASN

5.3.3 RNA ⓘ

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](#)

12 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	P4O	D	1	-	29,30,30	1.59	3 (10%)	39,43,43	1.55	8 (20%)
2	P4O	I	1	-	29,30,30	1.43	5 (17%)	39,43,43	1.98	13 (33%)
2	P4O	A	1	-	29,30,30	1.38	4 (13%)	39,43,43	1.76	10 (25%)
2	P4O	B	1	-	29,30,30	1.39	2 (6%)	39,43,43	1.80	11 (28%)
2	P4O	F	1	-	29,30,30	1.50	4 (13%)	39,43,43	1.94	9 (23%)
2	P4O	H	1	-	29,30,30	1.45	2 (6%)	39,43,43	1.77	12 (30%)
2	P4O	J	1	-	29,30,30	1.50	3 (10%)	39,43,43	2.02	11 (28%)
2	P4O	K	1	-	29,30,30	1.55	3 (10%)	39,43,43	1.54	6 (15%)
2	P4O	E	1	-	29,30,30	1.43	4 (13%)	39,43,43	1.62	8 (20%)
2	P4O	G	1	-	29,30,30	1.45	3 (10%)	39,43,43	1.79	9 (23%)
2	P4O	L	1	-	29,30,30	1.45	4 (13%)	39,43,43	2.11	13 (33%)
2	P4O	C	1	-	29,30,30	1.42	4 (13%)	39,43,43	1.81	8 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	P4O	D	1	-	-	0/8/18/18	0/5/5/5
2	P4O	I	1	-	-	0/8/18/18	0/5/5/5
2	P4O	A	1	-	-	0/8/18/18	0/5/5/5
2	P4O	B	1	-	-	0/8/18/18	0/5/5/5
2	P4O	F	1	-	-	0/8/18/18	0/5/5/5
2	P4O	H	1	-	-	0/8/18/18	0/5/5/5
2	P4O	J	1	-	-	0/8/18/18	0/5/5/5
2	P4O	K	1	-	-	0/8/18/18	0/5/5/5
2	P4O	E	1	-	-	0/8/18/18	0/5/5/5
2	P4O	G	1	-	-	0/8/18/18	0/5/5/5
2	P4O	L	1	-	-	0/8/18/18	0/5/5/5
2	P4O	C	1	-	-	0/8/18/18	0/5/5/5

The worst 5 of 41 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	J	1	P4O	C20-C21	6.02	1.51	1.42
2	D	1	P4O	C20-C21	5.87	1.50	1.42
2	F	1	P4O	C20-C21	5.25	1.50	1.42
2	H	1	P4O	C20-C21	5.21	1.49	1.42
2	C	1	P4O	C20-C21	5.19	1.49	1.42

The worst 5 of 118 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	1	P4O	C19-C18-C17	5.29	122.82	116.26
2	C	1	P4O	C18-C17-N16	-5.23	120.87	125.48
2	F	1	P4O	C12-C2-C3	-4.95	123.42	131.03
2	J	1	P4O	C18-C17-N16	-4.80	121.25	125.48
2	J	1	P4O	C19-C18-C17	4.79	122.20	116.26

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

10 monomers are involved in 16 short contacts:

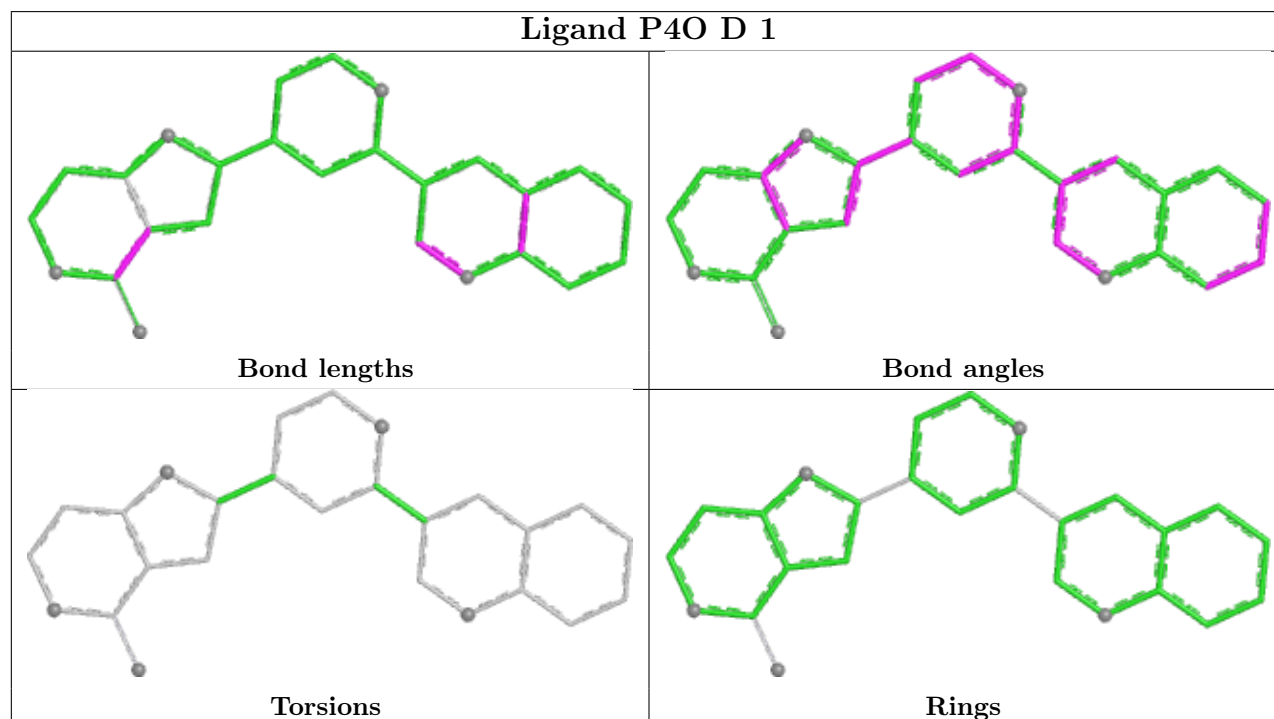
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1	P4O	3	0
2	A	1	P4O	1	0
2	B	1	P4O	1	0
2	F	1	P4O	3	0

Continued on next page...

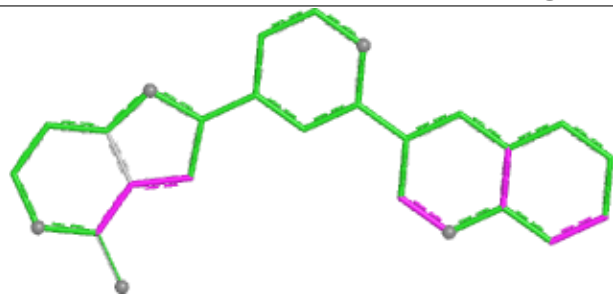
Continued from previous page...

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	H	1	P4O	1	0
2	J	1	P4O	2	0
2	K	1	P4O	1	0
2	E	1	P4O	2	0
2	L	1	P4O	1	0
2	C	1	P4O	1	0

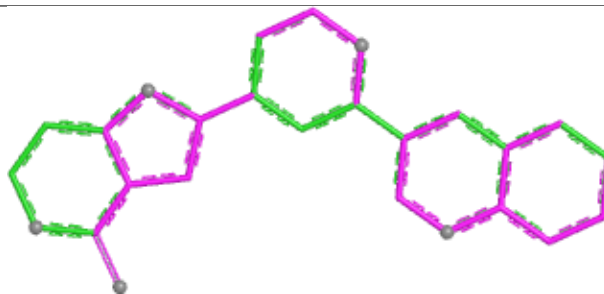
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



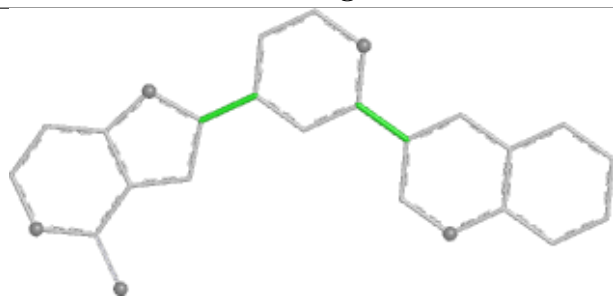
Ligand P4O I 1



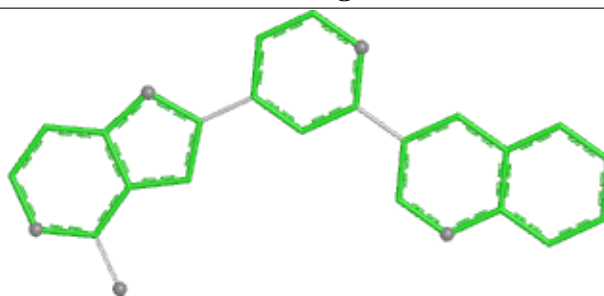
Bond lengths



Bond angles

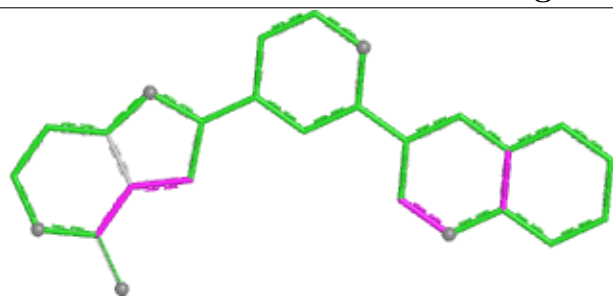


Torsions

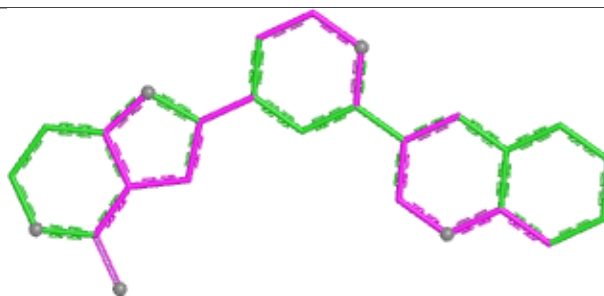


Rings

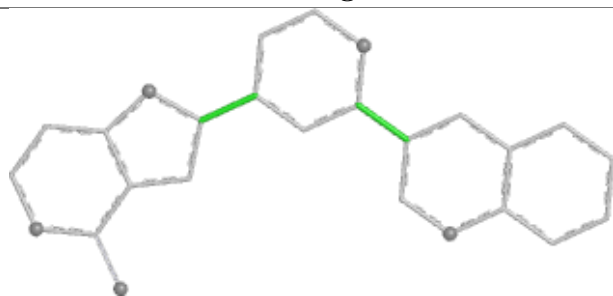
Ligand P4O A 1



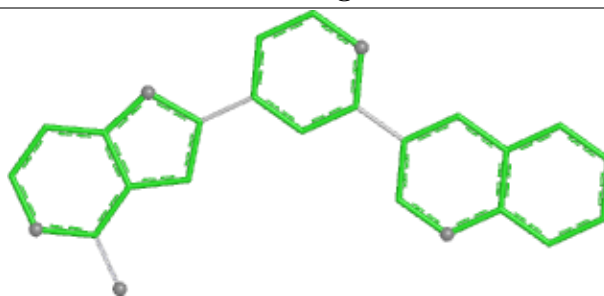
Bond lengths



Bond angles

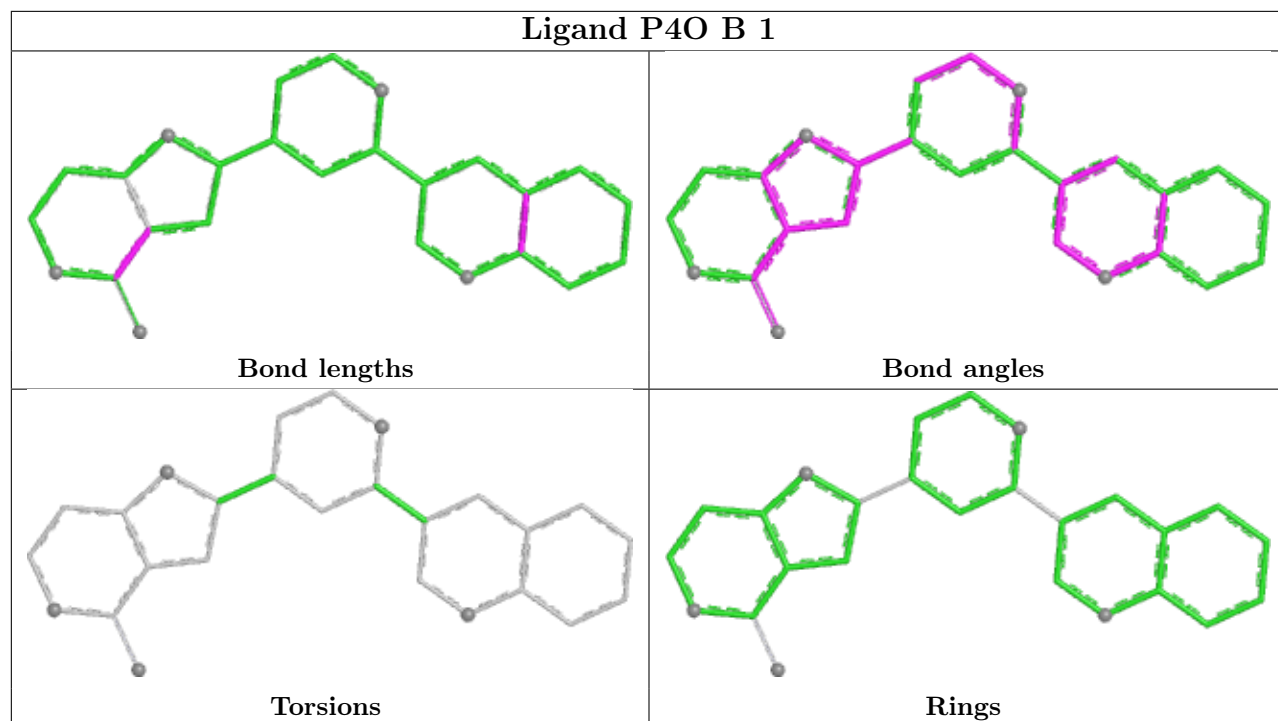


Torsions

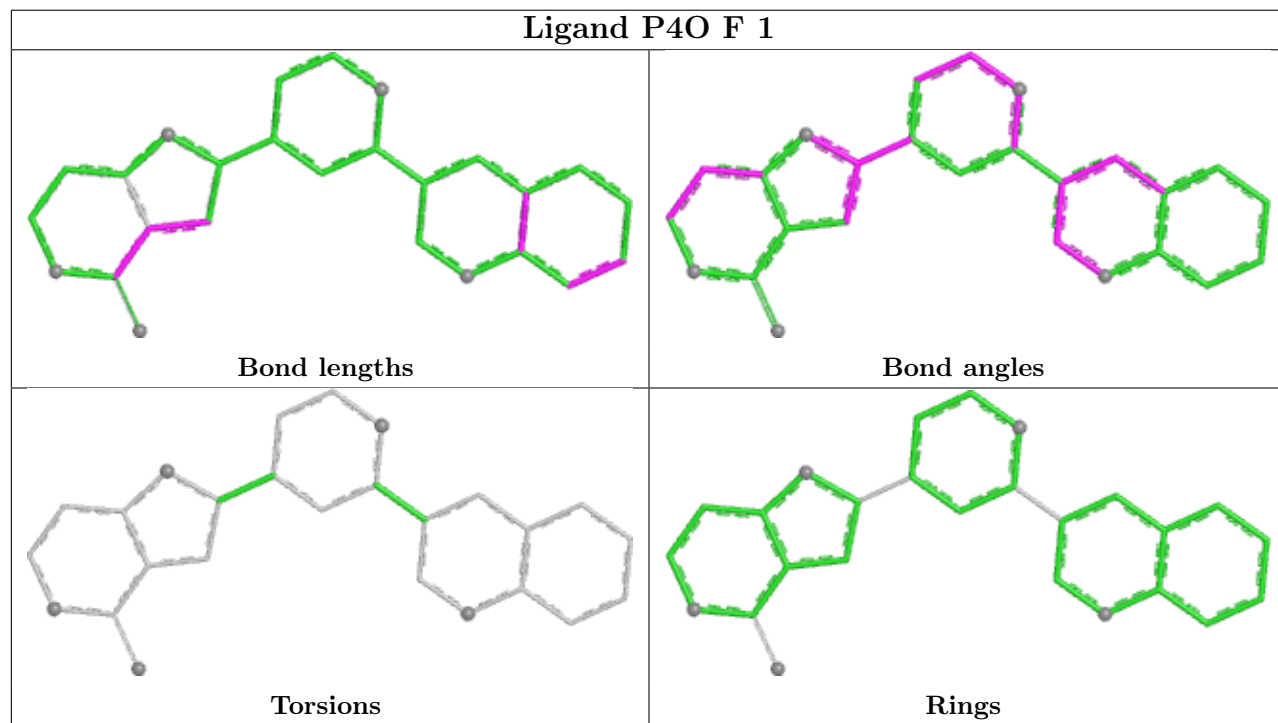


Rings

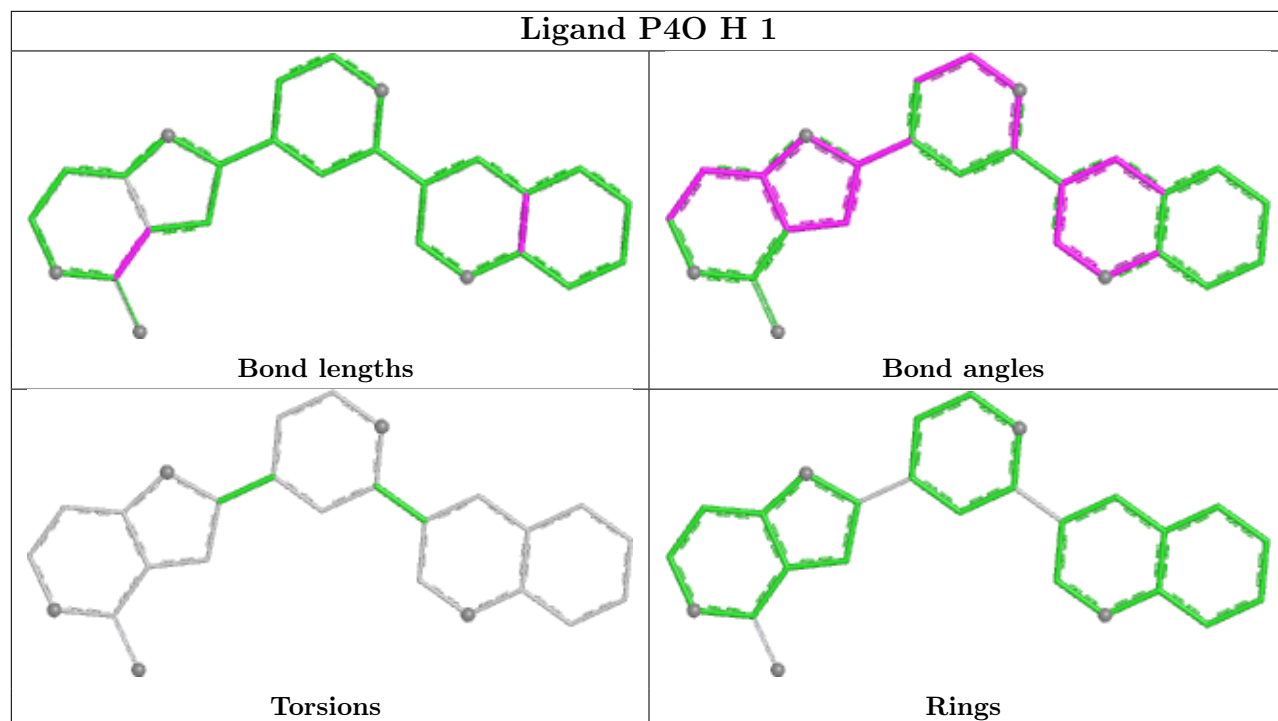
Ligand P4O B 1



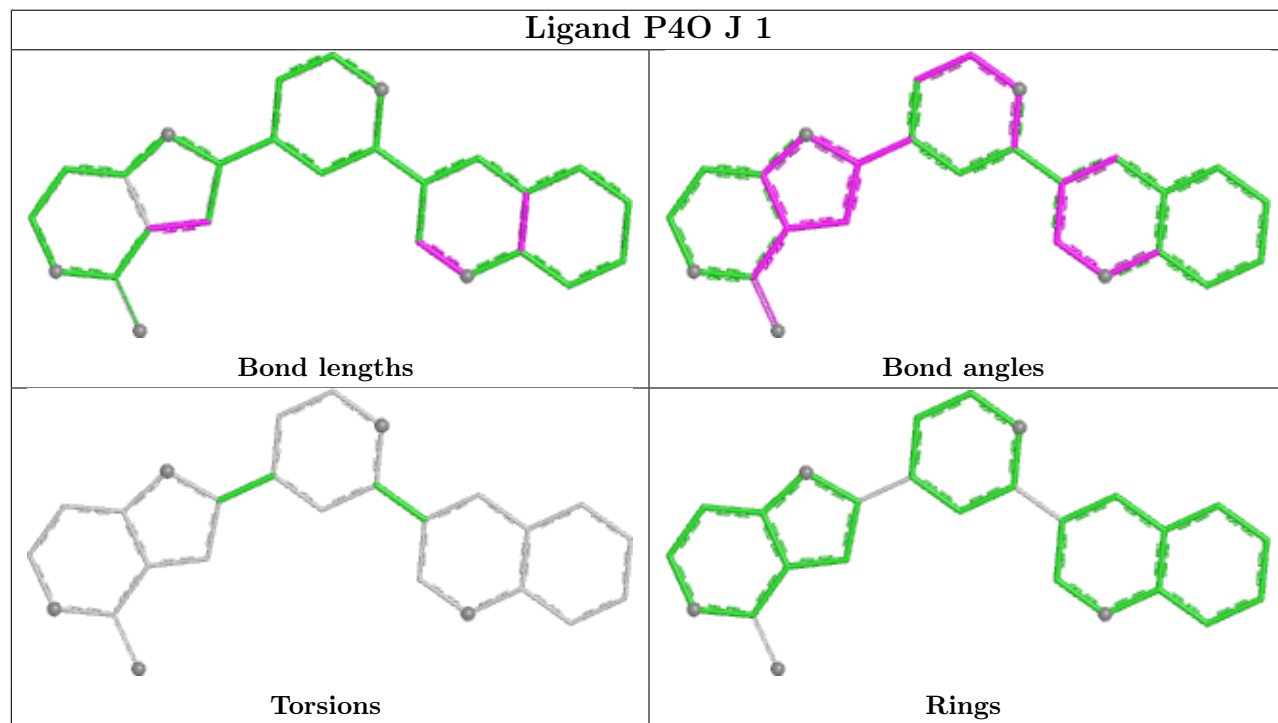
Ligand P4O F 1



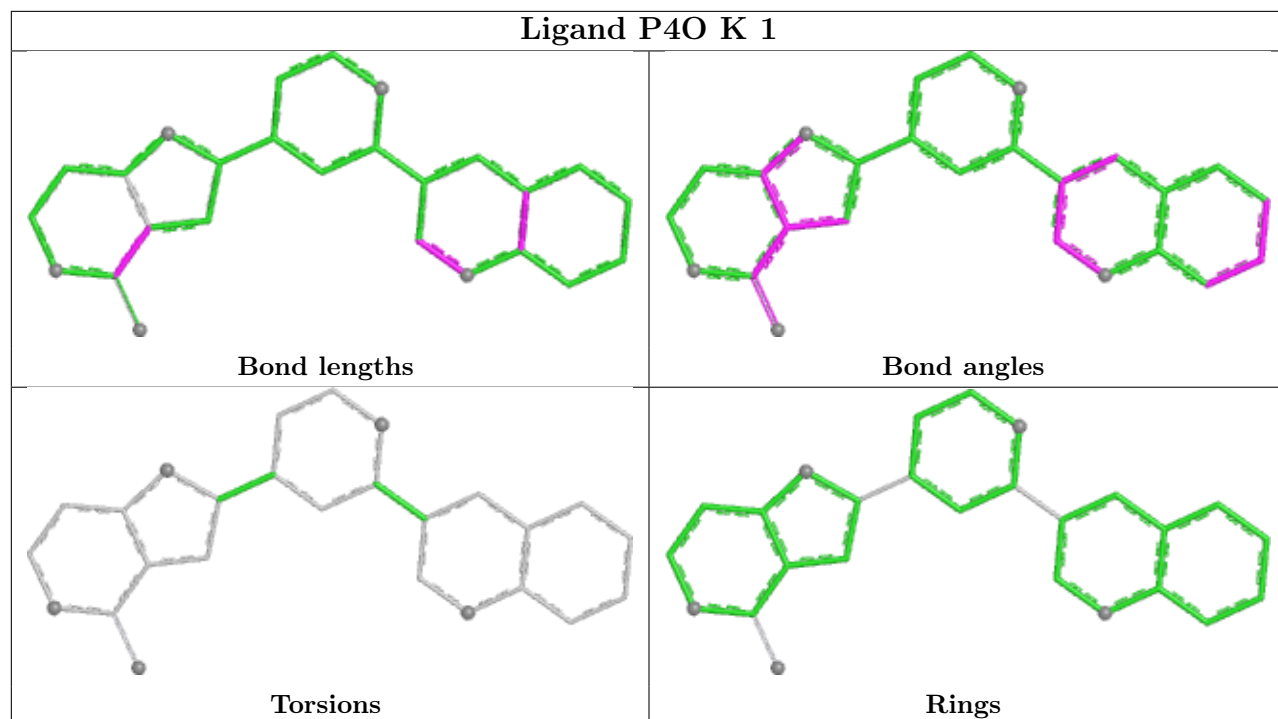
Ligand P4O H 1



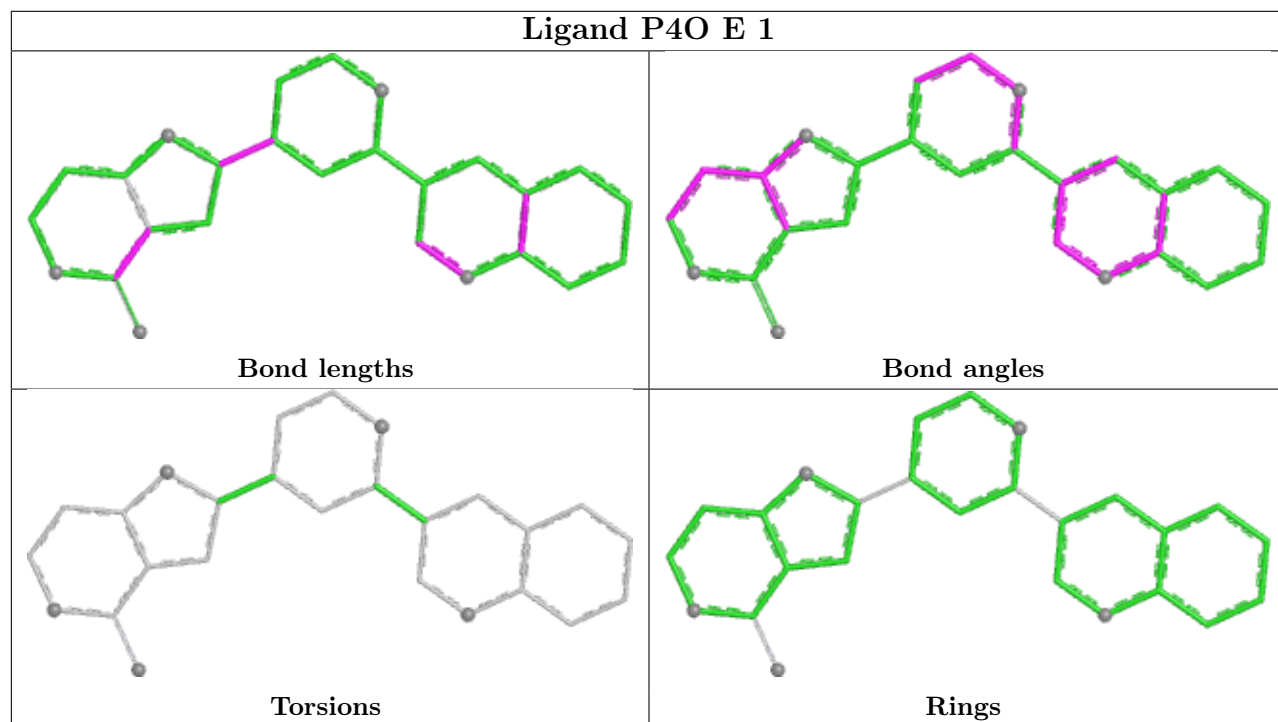
Ligand P4O J 1



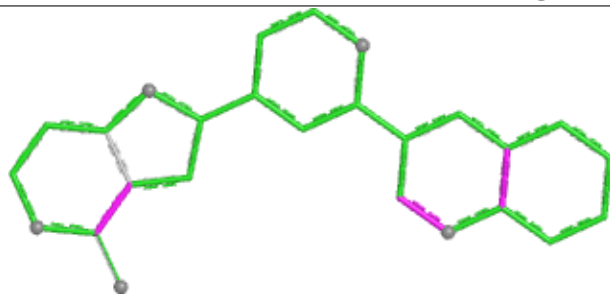
Ligand P4O K 1



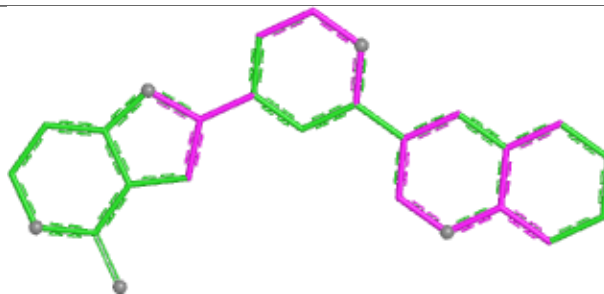
Ligand P4O E 1



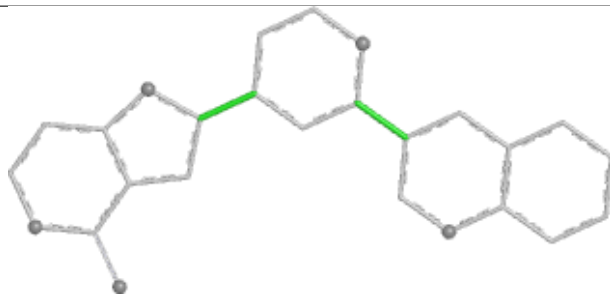
Ligand P4O G 1



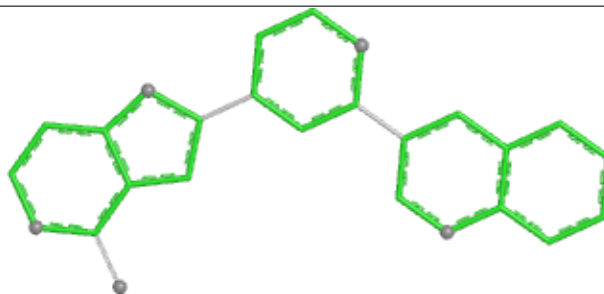
Bond lengths



Bond angles

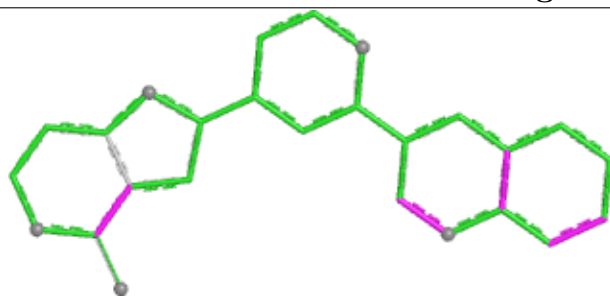


Torsions

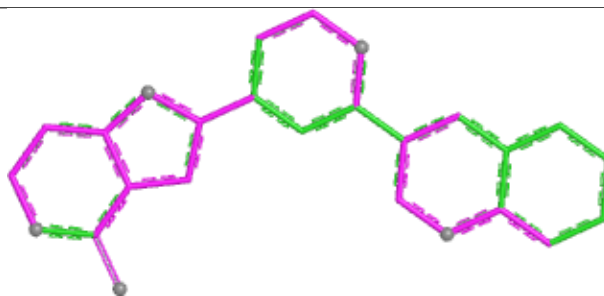


Rings

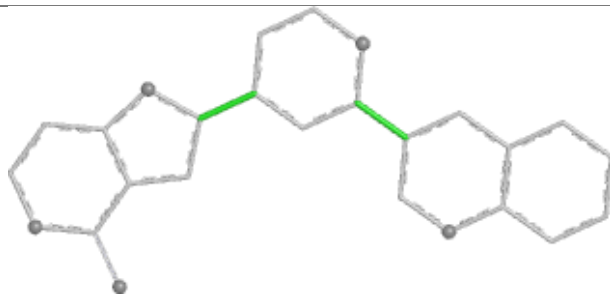
Ligand P4O L 1



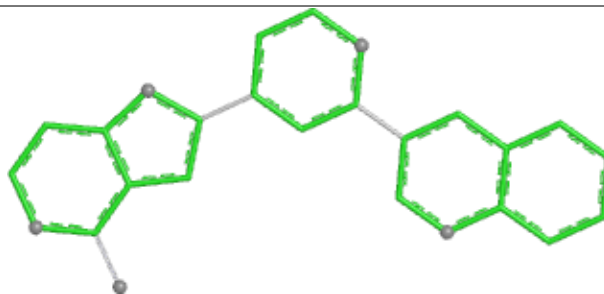
Bond lengths



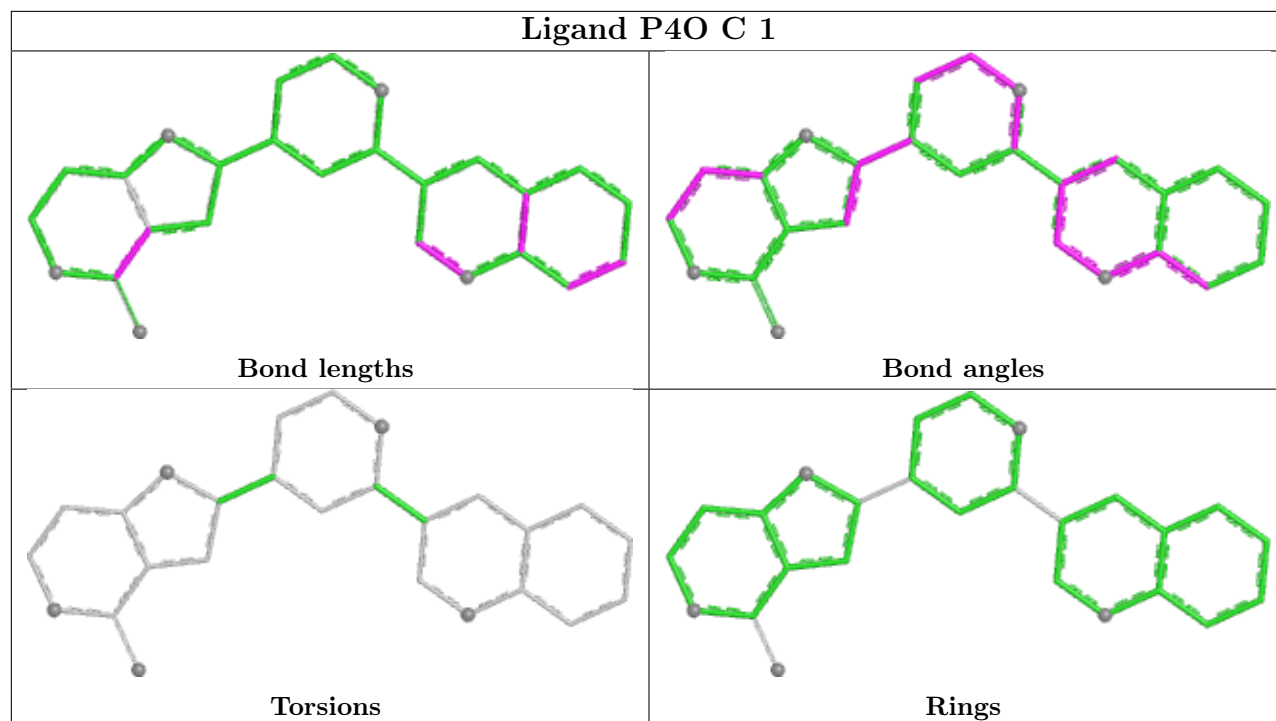
Bond angles



Torsions



Rings



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 [i](#)

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	A	285/334 (85%)	0.19	10 (3%)	47	29	42, 63, 95, 119	0
1	B	290/334 (86%)	0.12	8 (2%)	55	35	42, 64, 94, 118	0
1	C	285/334 (85%)	0.20	12 (4%)	40	25	42, 63, 93, 118	0
1	D	283/334 (84%)	0.22	9 (3%)	50	31	42, 63, 93, 118	0
1	E	290/334 (86%)	0.04	6 (2%)	63	43	42, 64, 95, 118	0
1	F	284/334 (85%)	0.29	12 (4%)	40	25	42, 63, 93, 118	0
1	G	286/334 (85%)	0.20	13 (4%)	38	24	42, 63, 93, 118	0
1	H	290/334 (86%)	-0.03	7 (2%)	59	40	42, 64, 94, 118	0
1	I	284/334 (85%)	0.18	13 (4%)	37	23	42, 63, 93, 118	0
1	J	283/334 (84%)	-0.04	2 (0%)	84	69	42, 63, 93, 119	0
1	K	290/334 (86%)	0.02	5 (1%)	69	49	42, 64, 95, 119	0
1	L	284/334 (85%)	0.06	9 (3%)	50	31	42, 63, 93, 118	0
All	All	3434/4008 (85%)	0.12	106 (3%)	51	32	42, 63, 95, 119	0

The worst 5 of 106 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	157	ALA	6.3
1	C	157	ALA	5.3
1	I	154	GLY	4.9
1	C	154	GLY	4.9
1	F	154	GLY	4.4

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

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

6.3 Carbohydrates

There are no oligosaccharides in this entry.

6.4 Ligands

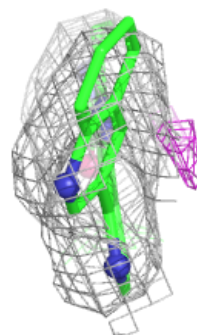
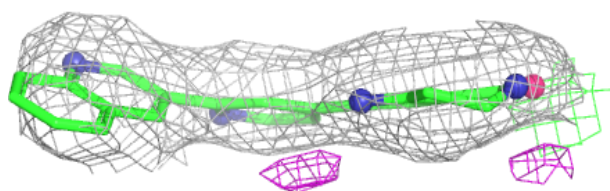
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	P4O	K	1	26/26	0.90	0.14	95,97,106,107	0
2	P4O	J	1	26/26	0.92	0.11	97,110,120,120	0
2	P4O	G	1	26/26	0.92	0.11	71,77,88,88	0
2	P4O	L	1	26/26	0.92	0.11	93,97,105,106	0
2	P4O	F	1	26/26	0.93	0.09	70,74,86,88	0
2	P4O	B	1	26/26	0.93	0.09	70,77,95,96	0
2	P4O	H	1	26/26	0.93	0.10	78,82,92,93	0
2	P4O	I	1	26/26	0.95	0.09	83,86,93,95	0
2	P4O	E	1	26/26	0.96	0.08	87,91,98,100	0
2	P4O	A	1	26/26	0.96	0.08	62,68,78,78	0
2	P4O	C	1	26/26	0.96	0.08	70,79,93,95	0
2	P4O	D	1	26/26	0.96	0.08	62,71,80,81	0

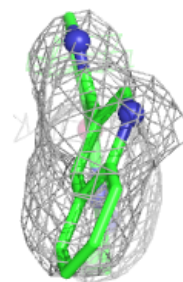
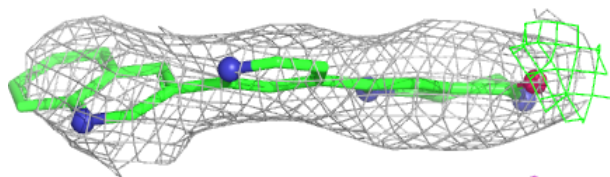
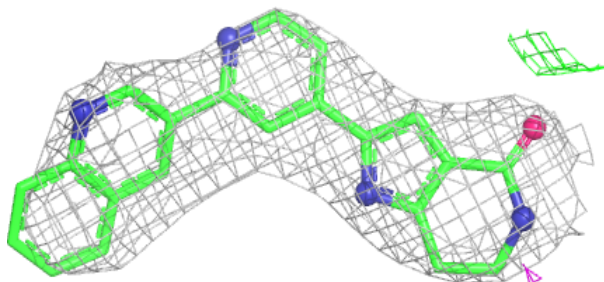
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around P4O K 1:

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

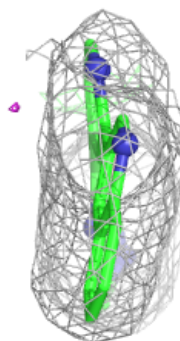
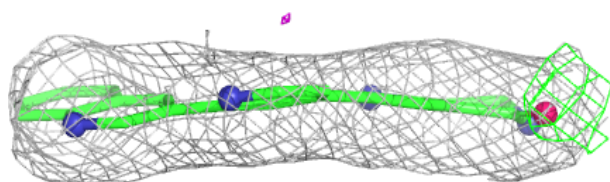
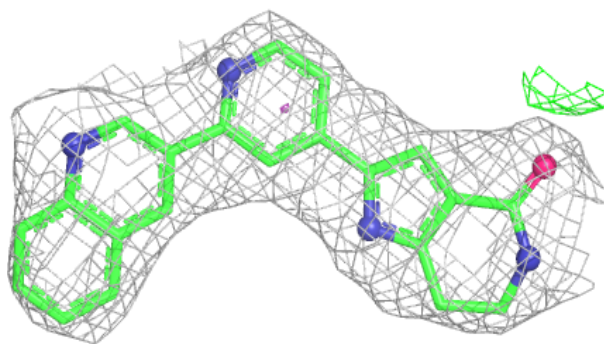
**Electron density around P4O J 1:**

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

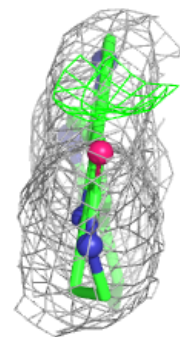
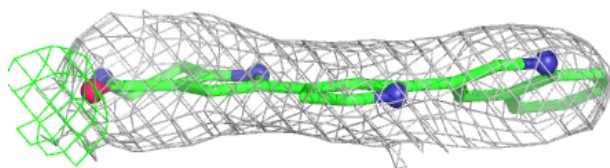
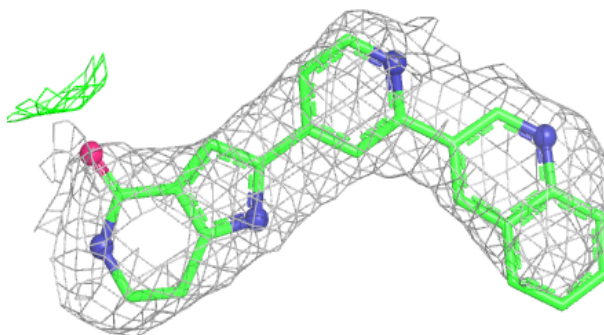


Electron density around P4O G 1:

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

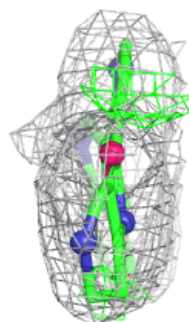
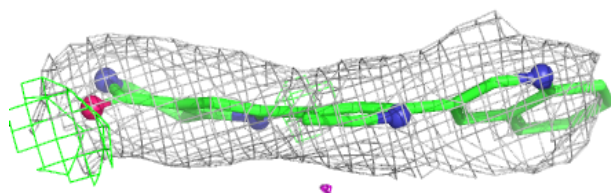
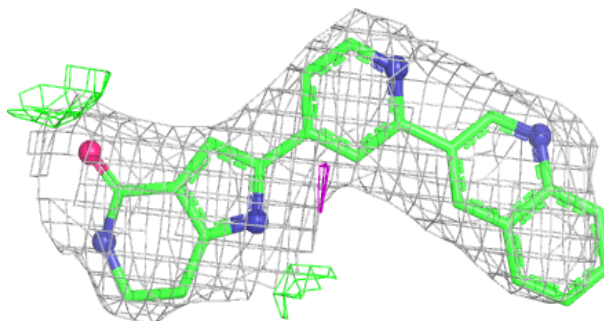
**Electron density around P4O L 1:**

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

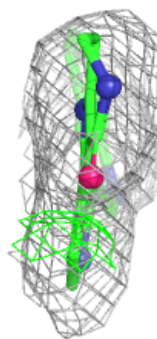
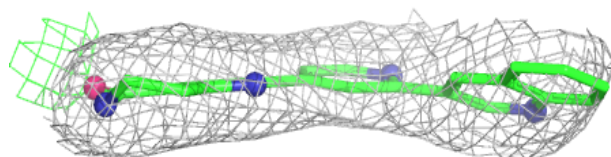
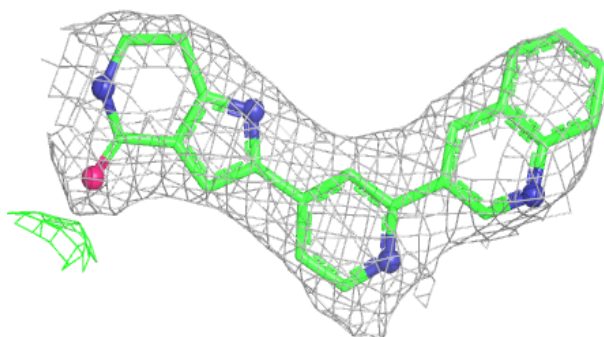


Electron density around P4O F 1:

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

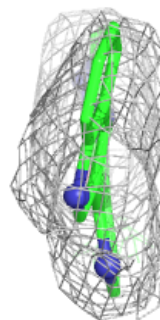
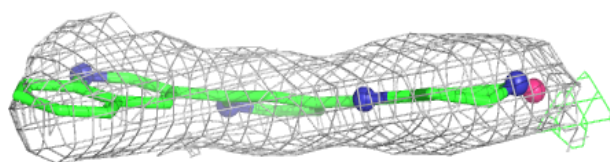
**Electron density around P4O B 1:**

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

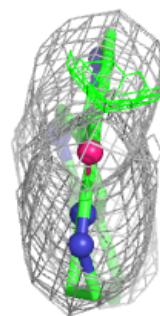
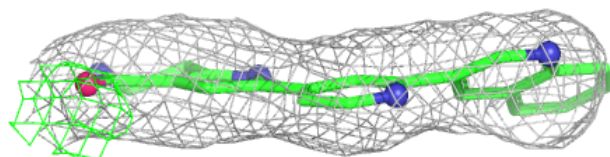
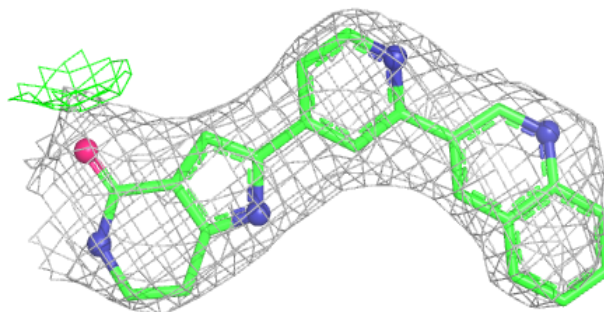


Electron density around P4O H 1:

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

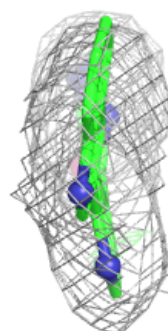
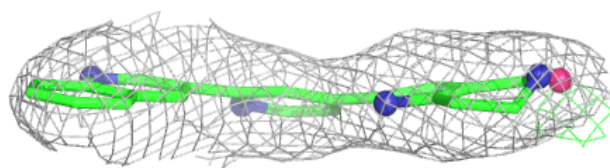
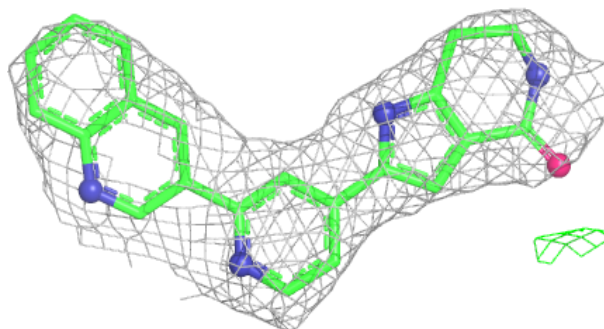
**Electron density around P4O I 1:**

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

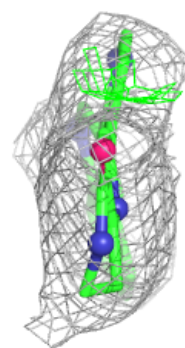
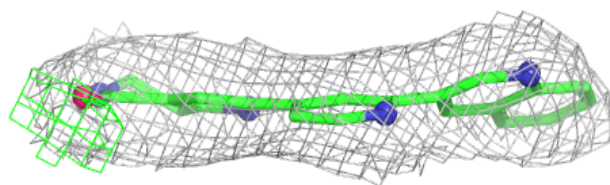
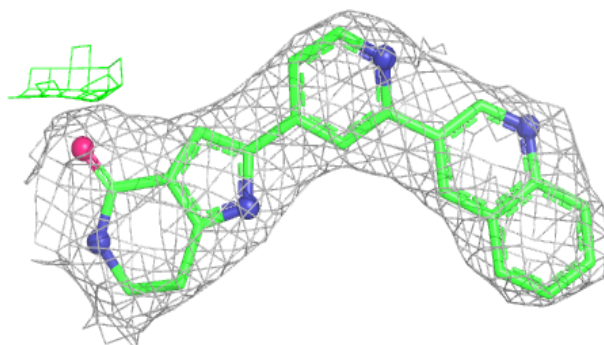


Electron density around P4O E 1:

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

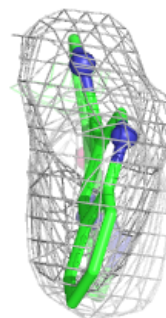
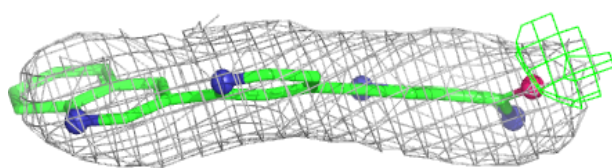
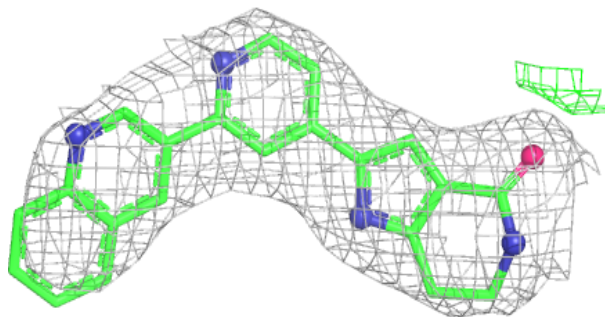
**Electron density around P4O A 1:**

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

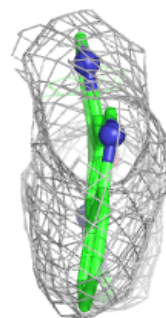
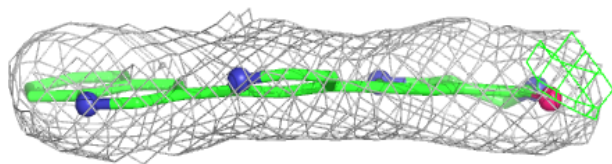
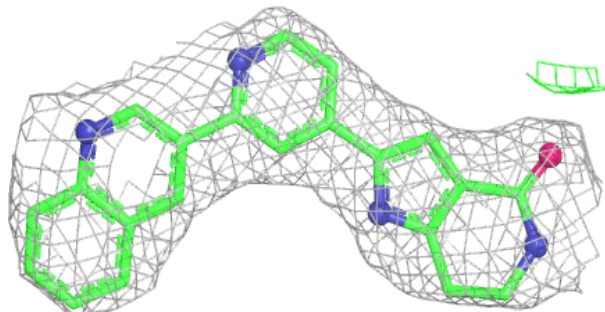


Electron density around P4O C 1:

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

**Electron density around P4O D 1:**

$2mF_o-DF_c$ (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.