



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 01:35 PM UTC

PDB ID : 2WHI / pdb_00002whi
Title : Crystal structure of Mycobacterium Tuberculosis Glutamine Synthetase in complex with a purine analogue inhibitor and L-methionine-S- sulfoximine phosphate.
Authors : Nilsson, M.T.; Krajewski, W.W.; Jones, T.A.; Mowbray, S.L.
Deposited on : 2009-05-05
Resolution : 2.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

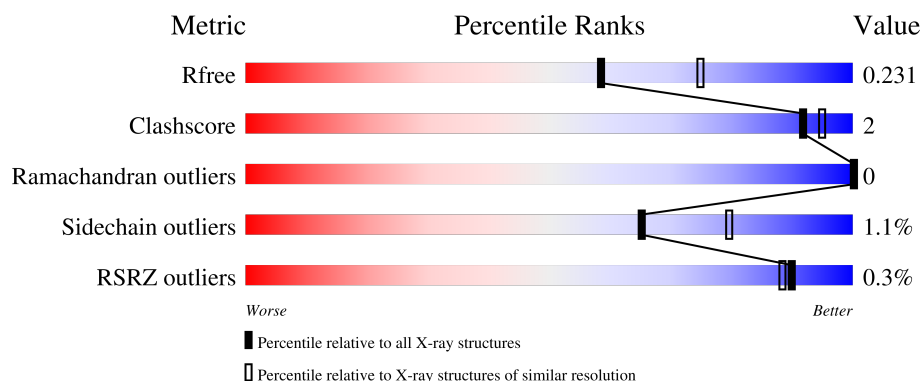
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

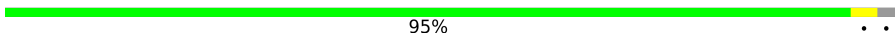
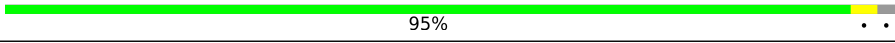
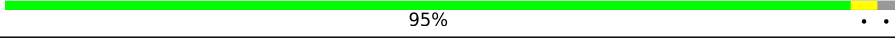
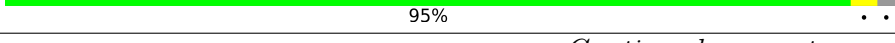
The reported resolution of this entry is 2.20 Å.

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.



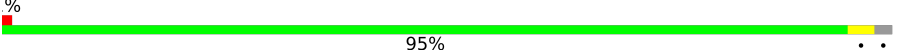
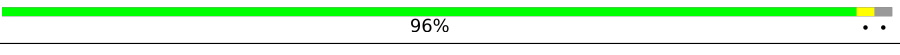
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	486	 95%
1	B	486	 95%
1	C	486	 95%
1	D	486	 95%

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Mol	Chain	Length	Quality of chain
1	E	486	 95%
1	F	486	 96%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
7	1PE	A	508	-	-	X	-
7	1PE	B	508	-	-	X	-
7	1PE	C	508	-	-	X	-
7	1PE	D	508	-	-	X	-
7	1PE	E	508	-	-	X	-
7	1PE	F	508	-	-	X	-

2 Entry composition [i](#)

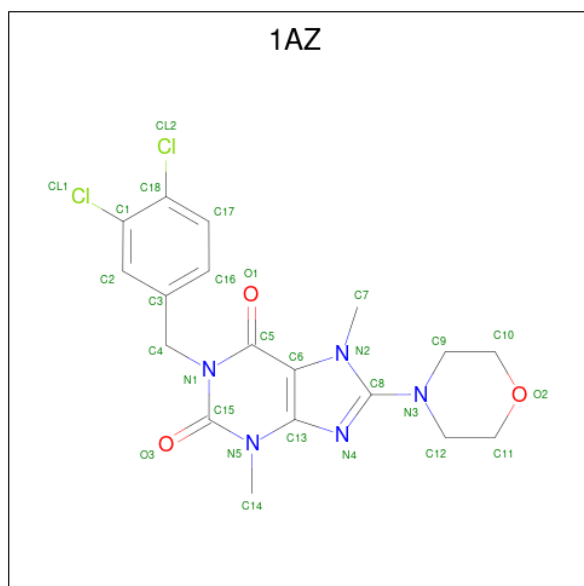
There are 8 unique types of molecules in this entry. The entry contains 24683 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 GLUTAMINE SYNTHETASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	476	Total	C	N	O	S	0	0	0
			3771	2402	632	725	12			
1	B	476	Total	C	N	O	S	0	0	0
			3771	2402	632	725	12			
1	C	476	Total	C	N	O	S	0	0	0
			3771	2402	632	725	12			
1	D	476	Total	C	N	O	S	0	0	0
			3771	2402	632	725	12			
1	E	476	Total	C	N	O	S	0	0	0
			3771	2402	632	725	12			
1	F	476	Total	C	N	O	S	0	0	0
			3771	2402	632	725	12			

- Molecule 2 is 1-(3,4-dichlorobenzyl)-3,7-dimethyl-8-morpholin-4-yl-3,7-dihydro-1H-purine-2,6-dione (CCD ID: 1AZ) (formula: C₁₈H₁₉Cl₂N₅O₃).

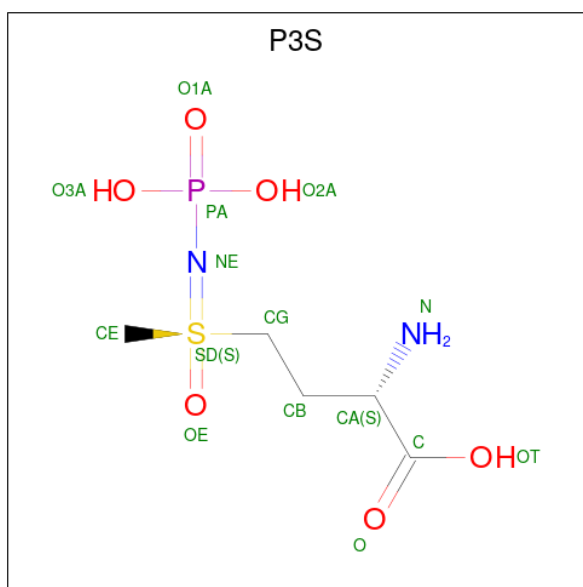


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	O	0	0
			28	18	2	5	3		
2	B	1	Total	C	Cl	N	O	0	0
			28	18	2	5	3		
2	C	1	Total	C	Cl	N	O	0	0
			28	18	2	5	3		
2	D	1	Total	C	Cl	N	O	0	0
			28	18	2	5	3		
2	E	1	Total	C	Cl	N	O	0	0
			28	18	2	5	3		
2	F	1	Total	C	Cl	N	O	0	0
			28	18	2	5	3		

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

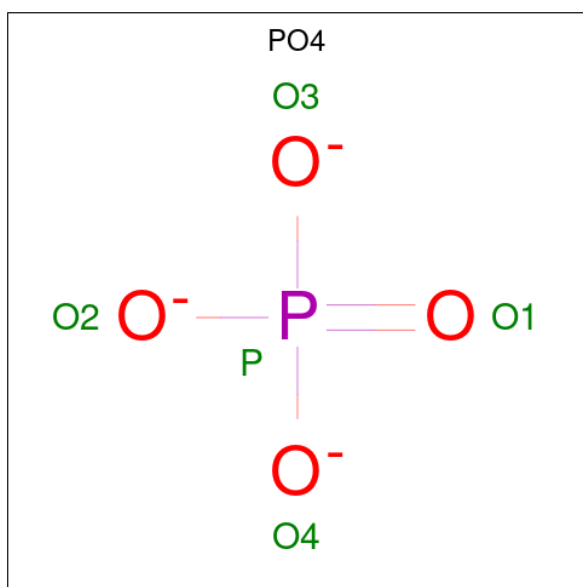
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total	Mg	0	0
			3	3		
3	B	3	Total	Mg	0	0
			3	3		
3	C	3	Total	Mg	0	0
			3	3		
3	D	3	Total	Mg	0	0
			3	3		
3	E	3	Total	Mg	0	0
			3	3		
3	F	3	Total	Mg	0	0
			3	3		

- Molecule 4 is L-METHIONINE-S-SULFOXIMINE PHOSPHATE (CCD ID: P3S) (formula: C₅H₁₃N₂O₆PS).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	S	0	0
			15	5	2	6	1	1		
4	B	1	Total	C	N	O	P	S	0	0
			15	5	2	6	1	1		
4	C	1	Total	C	N	O	P	S	0	0
			15	5	2	6	1	1		
4	D	1	Total	C	N	O	P	S	0	0
			15	5	2	6	1	1		
4	E	1	Total	C	N	O	P	S	0	0
			15	5	2	6	1	1		
4	F	1	Total	C	N	O	P	S	0	0
			15	5	2	6	1	1		

- Molecule 5 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).

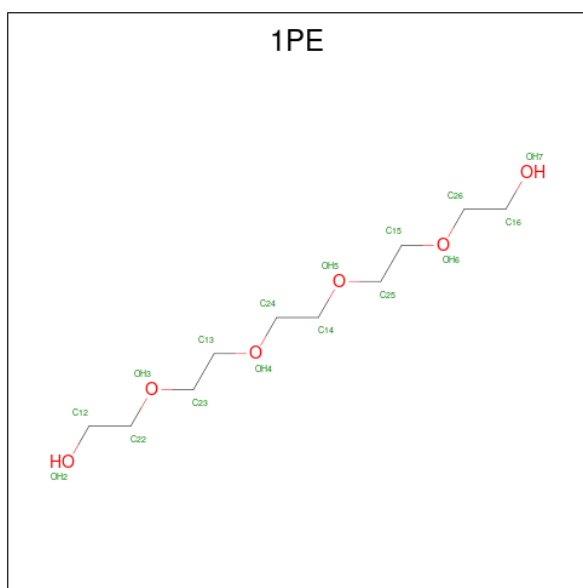


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	P	0	0
			5	4	1		
5	B	1	Total	O	P	0	0
			5	4	1		
5	C	1	Total	O	P	0	0
			5	4	1		
5	D	1	Total	O	P	0	0
			5	4	1		
5	E	1	Total	O	P	0	0
			5	4	1		
5	F	1	Total	O	P	0	0
			5	4	1		

- Molecule 6 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Cl	0	0
			1	1		
6	B	1	Total	Cl	0	0
			1	1		
6	C	1	Total	Cl	0	0
			1	1		
6	D	1	Total	Cl	0	0
			1	1		
6	E	1	Total	Cl	0	0
			1	1		
6	F	1	Total	Cl	0	0
			1	1		

- Molecule 7 is PENTAETHYLENE GLYCOL (CCD ID: 1PE) (formula: $C_{10}H_{22}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			16	10	6		
7	B	1	Total	C	O	0	0
			16	10	6		
7	C	1	Total	C	O	0	0
			16	10	6		
7	D	1	Total	C	O	0	0
			16	10	6		
7	E	1	Total	C	O	0	0
			16	10	6		
7	F	1	Total	C	O	0	0
			16	10	6		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	276	Total	O	0	0
			276	276		
8	B	276	Total	O	0	0
			276	276		
8	C	274	Total	O	0	0
			274	274		
8	D	279	Total	O	0	0
			279	279		
8	E	275	Total	O	0	0
			275	275		

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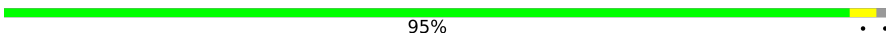
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	F	269	Total 269	O 269	0	0

3 Residue-property plots [i](#)

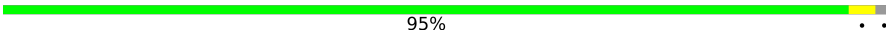
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: GLUTAMINE SYNTHETASE 1

Chain A: 

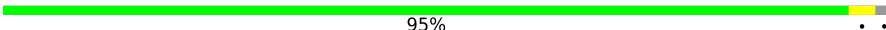


- Molecule 1: GLUTAMINE SYNTHETASE 1

Chain B: 

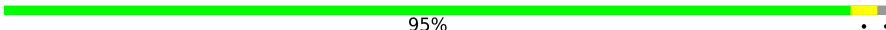


- Molecule 1: GLUTAMINE SYNTHETASE 1

Chain C: 

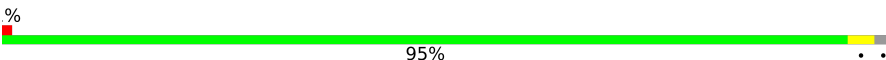


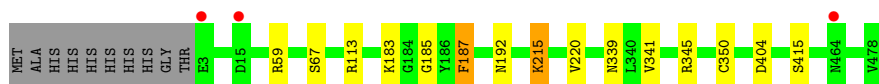
- Molecule 1: GLUTAMINE SYNTHETASE 1

Chain D: 

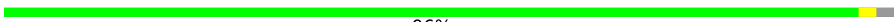


- Molecule 1: GLUTAMINE SYNTHETASE 1

Chain E: 



- Molecule 1: GLUTAMINE SYNTHETASE 1

Chain F:  96% ..



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	133.21Å 228.76Å 202.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.81 – 2.20 39.81 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.1 (39.81-2.20) 98.0 (39.81-2.20)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.96 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.211 , 0.231 0.212 , 0.231	Depositor DCC
R_{free} test set	7666 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	24.6	Xtriage
Anisotropy	0.462	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 33.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.036 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.044 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	24683	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.33% 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: CL, P3S, MG, PO4, 1AZ, 1PE

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	0.57	0/3877	0.81	4/5269 (0.1%)
1	B	0.57	0/3877	0.81	3/5269 (0.1%)
1	C	0.57	0/3877	0.80	0/5269
1	D	0.56	0/3877	0.80	1/5269 (0.0%)
1	E	0.57	0/3877	0.81	2/5269 (0.0%)
1	F	0.57	0/3877	0.80	2/5269 (0.0%)
All	All	0.57	0/23262	0.81	12/31614 (0.0%)

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	215	LYS	N-CA-C	5.89	117.20	108.60
1	E	215	LYS	N-CA-C	5.75	117.00	108.60
1	A	409	PRO	CA-C-N	5.73	127.00	119.84
1	A	409	PRO	C-N-CA	5.73	127.00	119.84
1	A	215	LYS	N-CA-C	5.72	116.94	108.60
1	B	215	LYS	N-CA-C	5.41	117.07	108.79
1	B	409	PRO	CA-C-N	5.36	126.53	119.84
1	B	409	PRO	C-N-CA	5.36	126.53	119.84
1	F	67	SER	N-CA-C	5.34	116.91	111.14
1	F	215	LYS	N-CA-C	5.27	116.29	108.60
1	E	67	SER	N-CA-C	5.21	116.76	111.14
1	A	67	SER	N-CA-C	5.09	116.64	111.14

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	3771	0	3597	11	0
1	B	3771	0	3597	11	0
1	C	3771	0	3597	12	0
1	D	3771	0	3597	12	0
1	E	3771	0	3597	12	0
1	F	3771	0	3597	8	0
2	A	28	0	19	0	0
2	B	28	0	19	0	0
2	C	28	0	19	0	0
2	D	28	0	19	0	0
2	E	28	0	19	0	0
2	F	28	0	19	0	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
3	C	3	0	0	0	0
3	D	3	0	0	0	0
3	E	3	0	0	0	0
3	F	3	0	0	0	0
4	A	15	0	10	0	0
4	B	15	0	10	0	0
4	C	15	0	10	0	0
4	D	15	0	10	0	0
4	E	15	0	10	0	0
4	F	15	0	10	0	0
5	A	5	0	0	0	0
5	B	5	0	0	0	0
5	C	5	0	0	0	0
5	D	5	0	0	0	0
5	E	5	0	0	0	0
5	F	5	0	0	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
6	E	1	0	0	0	0
6	F	1	0	0	0	0
7	A	16	0	22	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	16	0	22	7	0
7	C	16	0	22	8	0
7	D	16	0	22	8	0
7	E	16	0	22	7	0
7	F	16	0	22	8	0
8	A	276	0	0	1	0
8	B	276	0	0	1	0
8	C	274	0	0	1	0
8	D	279	0	0	1	0
8	E	275	0	0	2	0
8	F	269	0	0	1	0
All	All	24683	0	21888	70	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (70) 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:F:59:ARG:HH12	7:F:508:1PE:H121	1.22	1.01
1:B:59:ARG:HH12	7:B:508:1PE:H121	1.25	0.99
1:E:59:ARG:HH12	7:E:508:1PE:H121	1.26	0.99
1:C:59:ARG:HH12	7:C:508:1PE:H121	1.28	0.96
1:F:59:ARG:HH11	7:F:508:1PE:H131	1.31	0.95
1:C:59:ARG:HH11	7:C:508:1PE:H131	1.30	0.94
1:B:59:ARG:HH11	7:B:508:1PE:H131	1.31	0.94
1:D:59:ARG:HH12	7:D:508:1PE:H121	1.30	0.93
1:E:59:ARG:HH11	7:E:508:1PE:H131	1.30	0.93
1:D:59:ARG:HH11	7:D:508:1PE:H131	1.33	0.92
1:A:59:ARG:HH12	7:A:508:1PE:H121	1.34	0.91
1:A:59:ARG:HH11	7:A:508:1PE:H131	1.34	0.88
1:B:59:ARG:NH1	7:B:508:1PE:H131	1.91	0.85
1:A:59:ARG:NH1	7:A:508:1PE:H131	1.93	0.83
1:C:59:ARG:NH1	7:C:508:1PE:H131	1.93	0.83
1:D:59:ARG:NH1	7:D:508:1PE:H131	1.93	0.82
1:F:59:ARG:NH1	7:F:508:1PE:H131	1.96	0.81
1:E:59:ARG:NH1	7:E:508:1PE:H131	1.96	0.80
1:F:59:ARG:NH1	7:F:508:1PE:H121	1.99	0.76
1:E:59:ARG:NH1	7:E:508:1PE:H121	2.03	0.72
1:B:59:ARG:NH1	7:B:508:1PE:H121	2.04	0.69
1:D:59:ARG:NH1	7:D:508:1PE:H121	2.07	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:59:ARG:NH1	7:C:508:1PE:H121	2.05	0.66
1:E:59:ARG:HH12	7:E:508:1PE:C12	2.07	0.61
1:C:59:ARG:HH12	7:C:508:1PE:C12	2.10	0.59
1:D:59:ARG:HH12	7:D:508:1PE:C12	2.11	0.57
1:F:59:ARG:HH12	7:F:508:1PE:C12	2.04	0.57
1:A:59:ARG:NH1	7:A:508:1PE:H121	2.12	0.56
1:A:59:ARG:HH12	7:A:508:1PE:C12	2.14	0.52
1:E:415:SER:HB3	8:E:2229:HOH:O	2.09	0.52
7:E:508:1PE:H122	8:E:2275:HOH:O	2.11	0.51
1:D:59:ARG:HG2	7:D:508:1PE:H162	1.93	0.51
1:A:59:ARG:HG2	7:A:508:1PE:H162	1.93	0.50
7:A:508:1PE:H122	8:A:2276:HOH:O	2.11	0.50
1:B:59:ARG:HH12	7:B:508:1PE:C12	2.10	0.50
7:B:508:1PE:H122	8:B:2277:HOH:O	2.12	0.49
7:D:508:1PE:H122	8:D:2279:HOH:O	2.11	0.49
1:C:59:ARG:HG2	7:C:508:1PE:H162	1.95	0.48
1:B:59:ARG:HG2	7:B:508:1PE:H162	1.96	0.48
1:F:59:ARG:HG2	7:F:508:1PE:H162	1.96	0.47
7:F:508:1PE:H122	8:F:2269:HOH:O	2.15	0.47
1:D:183:LYS:HA	1:D:220:VAL:HG12	1.96	0.46
7:C:508:1PE:H122	8:C:2274:HOH:O	2.14	0.46
1:D:59:ARG:CG	7:D:508:1PE:H162	2.46	0.46
1:A:59:ARG:CG	7:A:508:1PE:H162	2.46	0.45
1:C:349:ALA:HA	1:C:405:LEU:HD12	1.99	0.45
1:D:68:ASP:HB2	1:E:345:ARG:HG3	1.99	0.45
1:A:183:LYS:HA	1:A:220:VAL:HG12	1.99	0.45
1:E:183:LYS:HA	1:E:220:VAL:HG12	1.99	0.45
1:F:59:ARG:CG	7:F:508:1PE:H162	2.48	0.44
1:F:183:LYS:HA	1:F:220:VAL:HG12	2.00	0.44
1:C:390:GLY:HA2	1:C:395:ILE:HD12	2.00	0.44
1:B:183:LYS:HA	1:B:220:VAL:HG12	2.00	0.43
1:C:119:LEU:HD11	1:C:125:ALA:HB3	2.00	0.43
1:B:390:GLY:HA2	1:B:395:ILE:HD12	2.00	0.43
1:B:263:MET:HA	1:B:264:PRO:HD3	1.93	0.43
1:C:183:LYS:HA	1:C:220:VAL:HG12	1.99	0.43
1:E:59:ARG:CG	7:E:508:1PE:H162	2.48	0.42
1:B:185:GLY:O	1:B:187:PHE:HA	2.19	0.42
1:A:68:ASP:HB2	1:B:345:ARG:HG3	2.02	0.42
1:E:339:ASN:O	1:E:350:CYS:HB2	2.20	0.42
1:E:404:ASP:OD1	1:E:404:ASP:C	2.63	0.42
1:A:390:GLY:HA2	1:A:395:ILE:HD12	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:59:ARG:CG	7:C:508:IPE:H162	2.49	0.41
1:D:339:ASN:O	1:D:350:CYS:HB2	2.21	0.41
1:D:390:GLY:HA2	1:D:395:ILE:HD12	2.02	0.41
1:A:185:GLY:O	1:A:187:PHE:HA	2.20	0.40
1:D:263:MET:HA	1:D:264:PRO:HD3	1.94	0.40
1:E:185:GLY:O	1:E:187:PHE:HA	2.22	0.40
1:C:317:LEU:HA	1:C:320:THR:OG1	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	474/486 (98%)	464 (98%)	10 (2%)	0	100	100
1	B	474/486 (98%)	466 (98%)	8 (2%)	0	100	100
1	C	474/486 (98%)	469 (99%)	5 (1%)	0	100	100
1	D	474/486 (98%)	466 (98%)	8 (2%)	0	100	100
1	E	474/486 (98%)	466 (98%)	8 (2%)	0	100	100
1	F	474/486 (98%)	467 (98%)	7 (2%)	0	100	100
All	All	2844/2916 (98%)	2798 (98%)	46 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	403/411 (98%)	399 (99%)	4 (1%)	68	81
1	B	403/411 (98%)	398 (99%)	5 (1%)	63	78
1	C	403/411 (98%)	399 (99%)	4 (1%)	68	81
1	D	403/411 (98%)	398 (99%)	5 (1%)	63	78
1	E	403/411 (98%)	398 (99%)	5 (1%)	63	78
1	F	403/411 (98%)	399 (99%)	4 (1%)	68	81
All	All	2418/2466 (98%)	2391 (99%)	27 (1%)	65	79

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	113	ARG
1	A	187	PHE
1	A	192	ASN
1	A	341	VAL
1	B	113	ARG
1	B	187	PHE
1	B	192	ASN
1	B	215	LYS
1	B	341	VAL
1	C	113	ARG
1	C	187	PHE
1	C	192	ASN
1	C	341	VAL
1	D	113	ARG
1	D	187	PHE
1	D	192	ASN
1	D	215	LYS
1	D	341	VAL
1	E	113	ARG
1	E	187	PHE
1	E	192	ASN
1	E	215	LYS
1	E	341	VAL
1	F	113	ARG
1	F	187	PHE
1	F	192	ASN
1	F	341	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	62	GLN
1	A	256	ASN
1	A	271	ASN
1	A	321	ASN
1	A	398	GLN
1	B	256	ASN
1	B	271	ASN
1	B	321	ASN
1	B	398	GLN
1	B	422	GLN
1	C	62	GLN
1	C	65	HIS
1	C	256	ASN
1	C	271	ASN
1	C	321	ASN
1	C	398	GLN
1	C	422	GLN
1	D	62	GLN
1	D	251	ASN
1	D	256	ASN
1	D	271	ASN
1	D	321	ASN
1	D	398	GLN
1	D	422	GLN
1	E	62	GLN
1	E	271	ASN
1	E	321	ASN
1	E	398	GLN
1	E	422	GLN
1	F	62	GLN
1	F	256	ASN
1	F	271	ASN
1	F	321	ASN
1	F	422	GLN

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](#)

Of 48 ligands modelled in this entry, 24 are monoatomic - leaving 24 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	1AZ	D	501	-	31,31,31	1.51	6 (19%)	45,46,46	2.31	15 (33%)
5	PO4	E	506	3	4,4,4	0.98	0	6,6,6	0.59	0
2	1AZ	A	501	-	31,31,31	1.58	5 (16%)	45,46,46	2.28	17 (37%)
7	1PE	E	508	-	15,15,15	0.63	0	14,14,14	0.28	0
4	P3S	E	505	3	11,14,14	1.75	3 (27%)	9,21,21	0.93	0
2	1AZ	C	501	-	31,31,31	1.49	6 (19%)	45,46,46	2.29	15 (33%)
5	PO4	F	506	3	4,4,4	0.99	0	6,6,6	0.71	0
2	1AZ	F	501	-	31,31,31	1.54	5 (16%)	45,46,46	2.31	16 (35%)
4	P3S	A	505	3	11,14,14	1.67	2 (18%)	9,21,21	1.10	0
5	PO4	D	506	3	4,4,4	0.97	0	6,6,6	0.74	0
7	1PE	A	508	-	15,15,15	0.61	0	14,14,14	0.38	0
7	1PE	C	508	-	15,15,15	0.65	0	14,14,14	0.35	0
7	1PE	D	508	-	15,15,15	0.63	0	14,14,14	0.36	0
7	1PE	F	508	-	15,15,15	0.62	0	14,14,14	0.35	0
4	P3S	B	505	3	11,14,14	1.68	2 (18%)	9,21,21	0.87	0
5	PO4	B	506	3	4,4,4	0.71	0	6,6,6	0.66	0
2	1AZ	E	501	-	31,31,31	1.54	6 (19%)	45,46,46	2.34	15 (33%)
5	PO4	C	506	3	4,4,4	0.85	0	6,6,6	0.78	0
4	P3S	D	505	3	11,14,14	1.69	2 (18%)	9,21,21	0.97	0
5	PO4	A	506	3	4,4,4	0.81	0	6,6,6	0.74	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	P3S	F	505	3	11,14,14	1.64	3 (27%)	9,21,21	0.84	0
7	1PE	B	508	-	15,15,15	0.62	0	14,14,14	0.33	0
2	1AZ	B	501	-	31,31,31	1.50	6 (19%)	45,46,46	2.33	17 (37%)
4	P3S	C	505	3	11,14,14	1.81	2 (18%)	9,21,21	0.94	0

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	1AZ	D	501	-	-	1/8/16/16	0/4/4/4
7	1PE	F	508	-	-	7/13/13/13	-
2	1AZ	E	501	-	-	1/8/16/16	0/4/4/4
4	P3S	E	505	3	-	4/9/16/16	-
2	1AZ	C	501	-	-	1/8/16/16	0/4/4/4
4	P3S	D	505	3	-	4/9/16/16	-
2	1AZ	F	501	-	-	1/8/16/16	0/4/4/4
4	P3S	A	505	3	-	4/9/16/16	-
4	P3S	F	505	3	-	4/9/16/16	-
4	P3S	C	505	3	-	4/9/16/16	-
7	1PE	B	508	-	-	7/13/13/13	-
2	1AZ	B	501	-	-	1/8/16/16	0/4/4/4
7	1PE	A	508	-	-	7/13/13/13	-
7	1PE	E	508	-	-	6/13/13/13	-
4	P3S	B	505	3	-	4/9/16/16	-
2	1AZ	A	501	-	-	1/8/16/16	0/4/4/4
7	1PE	C	508	-	-	6/13/13/13	-
7	1PE	D	508	-	-	8/13/13/13	-

All (48) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	1AZ	C8-N3	4.39	1.50	1.37
2	C	501	1AZ	C8-N3	4.20	1.49	1.37
2	B	501	1AZ	C8-N3	4.16	1.49	1.37
2	F	501	1AZ	C8-N3	4.15	1.49	1.37
2	E	501	1AZ	C8-N3	4.11	1.49	1.37
2	D	501	1AZ	C8-N3	4.07	1.49	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	505	P3S	PA-O1A	4.02	1.52	1.46
4	E	505	P3S	PA-O1A	3.47	1.52	1.46
4	D	505	P3S	PA-O1A	3.46	1.52	1.46
2	E	501	1AZ	C18-CL2	3.18	1.81	1.73
2	D	501	1AZ	C18-CL2	3.09	1.80	1.73
4	A	505	P3S	PA-NE	3.07	1.69	1.58
2	F	501	1AZ	C5-N1	-3.07	1.34	1.40
4	C	505	P3S	PA-NE	3.05	1.69	1.58
4	B	505	P3S	PA-O1A	3.00	1.51	1.46
2	B	501	1AZ	C5-N1	-3.00	1.35	1.40
2	A	501	1AZ	C5-N1	-2.96	1.35	1.40
4	B	505	P3S	PA-NE	2.92	1.69	1.58
2	A	501	1AZ	C18-CL2	2.86	1.80	1.73
4	D	505	P3S	PA-NE	2.84	1.68	1.58
4	E	505	P3S	PA-NE	2.82	1.68	1.58
4	F	505	P3S	PA-O1A	2.82	1.51	1.46
2	C	501	1AZ	C5-N1	-2.76	1.35	1.40
2	F	501	1AZ	C6-N2	-2.74	1.34	1.39
2	F	501	1AZ	C18-CL2	2.74	1.80	1.73
2	D	501	1AZ	C5-N1	-2.67	1.35	1.40
2	C	501	1AZ	C1-CL1	2.66	1.79	1.73
2	A	501	1AZ	C6-N2	-2.65	1.35	1.39
2	E	501	1AZ	C6-N2	-2.62	1.35	1.39
2	F	501	1AZ	C1-CL1	2.60	1.79	1.73
4	A	505	P3S	PA-O1A	2.60	1.50	1.46
4	F	505	P3S	PA-NE	2.58	1.68	1.58
2	E	501	1AZ	C5-N1	-2.56	1.35	1.40
2	B	501	1AZ	C18-CL2	2.53	1.79	1.73
2	D	501	1AZ	C6-N2	-2.52	1.35	1.39
2	A	501	1AZ	C1-CL1	2.51	1.79	1.73
2	C	501	1AZ	C6-N2	-2.47	1.35	1.39
2	B	501	1AZ	C6-N2	-2.39	1.35	1.39
2	D	501	1AZ	C1-CL1	2.34	1.79	1.73
2	E	501	1AZ	C1-CL1	2.34	1.79	1.73
2	C	501	1AZ	C18-CL2	2.32	1.79	1.73
2	B	501	1AZ	C1-CL1	2.30	1.79	1.73
2	D	501	1AZ	C15-N5	-2.19	1.34	1.39
2	C	501	1AZ	C15-N5	-2.12	1.34	1.39
4	F	505	P3S	PA-O2A	-2.04	1.50	1.54
2	E	501	1AZ	C15-N1	2.04	1.42	1.38
2	B	501	1AZ	C15-N5	-2.02	1.35	1.39
4	E	505	P3S	PA-O3A	-2.00	1.50	1.54

All (95) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	501	1AZ	C8-N4-C13	5.66	108.71	102.71
2	E	501	1AZ	C8-N4-C13	5.57	108.62	102.71
2	D	501	1AZ	C8-N4-C13	5.55	108.60	102.71
2	B	501	1AZ	C8-N4-C13	5.54	108.58	102.71
2	A	501	1AZ	C8-N4-C13	5.53	108.57	102.71
2	C	501	1AZ	C8-N4-C13	5.48	108.52	102.71
2	E	501	1AZ	C5-N1-C15	-5.18	119.24	125.62
2	F	501	1AZ	N2-C8-N4	-4.96	108.45	114.64
2	D	501	1AZ	C6-C13-N4	-4.91	106.75	112.77
2	B	501	1AZ	C5-N1-C15	-4.91	119.58	125.62
2	C	501	1AZ	C6-C13-N4	-4.90	106.77	112.77
2	A	501	1AZ	N2-C8-N4	-4.89	108.55	114.64
2	F	501	1AZ	C6-C13-N4	-4.88	106.79	112.77
2	E	501	1AZ	C6-C13-N4	-4.84	106.83	112.77
2	B	501	1AZ	N2-C8-N4	-4.84	108.60	114.64
2	D	501	1AZ	N2-C8-N4	-4.77	108.70	114.64
2	D	501	1AZ	C5-N1-C15	-4.74	119.78	125.62
2	B	501	1AZ	C6-C13-N4	-4.72	106.98	112.77
2	E	501	1AZ	N2-C8-N4	-4.71	108.77	114.64
2	A	501	1AZ	C6-C13-N4	-4.71	107.00	112.77
2	C	501	1AZ	N2-C8-N4	-4.65	108.84	114.64
2	A	501	1AZ	C5-N1-C15	-4.53	120.04	125.62
2	C	501	1AZ	C5-N1-C15	-4.48	120.10	125.62
2	F	501	1AZ	C5-N1-C15	-4.43	120.16	125.62
2	F	501	1AZ	N5-C13-N4	4.15	132.37	125.59
2	C	501	1AZ	N5-C13-N4	4.15	132.37	125.59
2	E	501	1AZ	N5-C13-N4	4.13	132.33	125.59
2	E	501	1AZ	N3-C8-N2	4.12	125.65	121.42
2	D	501	1AZ	N5-C13-N4	4.12	132.32	125.59
2	C	501	1AZ	N3-C8-N2	4.06	125.59	121.42
2	A	501	1AZ	N5-C13-N4	4.05	132.21	125.59
2	B	501	1AZ	N5-C13-N4	4.05	132.20	125.59
2	F	501	1AZ	N3-C8-N2	4.04	125.57	121.42
2	B	501	1AZ	C6-C5-N1	4.02	119.80	112.23
2	D	501	1AZ	C6-C5-N1	3.93	119.61	112.23
2	E	501	1AZ	C6-C5-N1	3.91	119.58	112.23
2	B	501	1AZ	N3-C8-N2	3.89	125.42	121.42
2	F	501	1AZ	C6-C5-N1	3.84	119.46	112.23
2	A	501	1AZ	N3-C8-N2	3.81	125.33	121.42
2	A	501	1AZ	C6-C5-N1	3.79	119.36	112.23
2	D	501	1AZ	N3-C8-N2	3.72	125.24	121.42
2	C	501	1AZ	C6-C5-N1	3.67	119.14	112.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	501	1AZ	N1-C15-N5	3.45	120.98	116.72
2	C	501	1AZ	N1-C15-N5	3.26	120.74	116.72
2	D	501	1AZ	O1-C5-C6	-3.26	119.70	126.38
2	D	501	1AZ	C5-C6-C13	-3.25	118.82	122.92
2	B	501	1AZ	C5-C6-C13	-3.22	118.87	122.92
2	C	501	1AZ	C5-C6-C13	-3.10	119.01	122.92
2	F	501	1AZ	C5-C6-C13	-3.08	119.04	122.92
2	E	501	1AZ	O1-C5-C6	-3.07	120.09	126.38
2	B	501	1AZ	N1-C15-N5	3.04	120.46	116.72
2	E	501	1AZ	C5-C6-C13	-3.03	119.10	122.92
2	C	501	1AZ	O1-C5-C6	-3.03	120.17	126.38
2	D	501	1AZ	N1-C15-N5	3.02	120.44	116.72
2	A	501	1AZ	O1-C5-C6	-2.98	120.27	126.38
2	B	501	1AZ	O1-C5-C6	-2.94	120.35	126.38
2	F	501	1AZ	O1-C5-C6	-2.91	120.41	126.38
2	A	501	1AZ	C5-C6-C13	-2.91	119.26	122.92
2	A	501	1AZ	C10-C9-N3	-2.81	103.90	109.82
2	E	501	1AZ	C11-C12-N3	-2.80	103.93	109.82
2	F	501	1AZ	N1-C15-N5	2.78	120.14	116.72
2	A	501	1AZ	N1-C15-N5	2.77	120.14	116.72
2	C	501	1AZ	C10-C9-N3	-2.76	104.00	109.82
2	B	501	1AZ	C4-N1-C5	2.64	121.44	117.72
2	B	501	1AZ	C10-C9-N3	-2.63	104.27	109.82
2	E	501	1AZ	C4-N1-C5	2.62	121.42	117.72
2	F	501	1AZ	C11-C12-N3	-2.62	104.30	109.82
2	F	501	1AZ	C10-C9-N3	-2.59	104.36	109.82
2	D	501	1AZ	C4-N1-C5	2.55	121.32	117.72
2	C	501	1AZ	C11-C12-N3	-2.54	104.47	109.82
2	A	501	1AZ	C1-C2-C3	-2.51	118.84	120.46
2	D	501	1AZ	C10-C9-N3	-2.51	104.53	109.82
2	D	501	1AZ	C11-C12-N3	-2.47	104.63	109.82
2	A	501	1AZ	C11-C12-N3	-2.46	104.64	109.82
2	C	501	1AZ	O3-C15-N1	-2.40	118.75	121.98
2	E	501	1AZ	C10-C9-N3	-2.36	104.86	109.82
2	C	501	1AZ	C4-N1-C5	2.35	121.03	117.72
2	B	501	1AZ	C1-C2-C3	-2.33	118.96	120.46
2	B	501	1AZ	C11-C12-N3	-2.32	104.92	109.82
2	A	501	1AZ	C4-N1-C5	2.30	120.96	117.72
2	B	501	1AZ	O3-C15-N1	-2.27	118.93	121.98
2	E	501	1AZ	C1-C2-C3	-2.25	119.00	120.46
2	A	501	1AZ	O3-C15-N1	-2.23	118.98	121.98
2	B	501	1AZ	C5-C6-N2	2.21	133.84	131.26

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	501	1AZ	C1-C2-C3	-2.13	119.09	120.46
2	F	501	1AZ	C5-C6-N2	2.11	133.72	131.26
2	C	501	1AZ	C9-N3-C8	-2.11	111.43	119.07
2	D	501	1AZ	C9-N3-C8	-2.09	111.48	119.07
2	A	501	1AZ	O2-C11-C12	-2.08	107.29	111.77
2	B	501	1AZ	C9-N3-C8	-2.07	111.57	119.07
2	E	501	1AZ	C9-N3-C8	-2.06	111.61	119.07
2	F	501	1AZ	C9-N3-C8	-2.06	111.62	119.07
2	F	501	1AZ	C12-N3-C8	-2.04	111.69	119.07
2	F	501	1AZ	C4-N1-C5	2.04	120.59	117.72
2	A	501	1AZ	C9-N3-C8	-2.02	111.73	119.07

There are no chirality outliers.

All (71) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	501	1AZ	N4-C8-N3-C9
2	D	501	1AZ	N4-C8-N3-C9
2	E	501	1AZ	N4-C8-N3-C9
2	F	501	1AZ	N4-C8-N3-C9
7	B	508	1PE	C24-C14-OH5-C25
7	F	508	1PE	C24-C14-OH5-C25
7	A	508	1PE	C24-C14-OH5-C25
7	D	508	1PE	C24-C14-OH5-C25
7	E	508	1PE	C24-C14-OH5-C25
7	C	508	1PE	C24-C14-OH5-C25
4	A	505	P3S	OT-C-CA-CB
4	B	505	P3S	OT-C-CA-CB
4	D	505	P3S	OT-C-CA-CB
4	E	505	P3S	OT-C-CA-CB
4	F	505	P3S	OT-C-CA-CB
7	A	508	1PE	OH2-C12-C22-OH3
4	E	505	P3S	OT-C-CA-N
4	F	505	P3S	OT-C-CA-N
7	B	508	1PE	OH2-C12-C22-OH3
7	B	508	1PE	OH7-C16-C26-OH6
7	C	508	1PE	OH2-C12-C22-OH3
7	D	508	1PE	OH2-C12-C22-OH3
7	D	508	1PE	OH7-C16-C26-OH6
7	E	508	1PE	OH2-C12-C22-OH3
7	E	508	1PE	OH7-C16-C26-OH6
7	F	508	1PE	OH2-C12-C22-OH3

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Mol	Chain	Res	Type	Atoms
7	F	508	1PE	OH7-C16-C26-OH6
4	C	505	P3S	OT-C-CA-N
7	A	508	1PE	OH7-C16-C26-OH6
7	C	508	1PE	OH7-C16-C26-OH6
4	C	505	P3S	OT-C-CA-CB
4	A	505	P3S	OT-C-CA-N
4	D	505	P3S	OT-C-CA-N
4	B	505	P3S	OT-C-CA-N
4	B	505	P3S	O-C-CA-CB
4	D	505	P3S	O-C-CA-CB
4	F	505	P3S	O-C-CA-CB
4	A	505	P3S	O-C-CA-CB
4	E	505	P3S	O-C-CA-CB
4	C	505	P3S	O-C-CA-CB
4	A	505	P3S	O-C-CA-N
4	B	505	P3S	O-C-CA-N
4	C	505	P3S	O-C-CA-N
4	D	505	P3S	O-C-CA-N
4	E	505	P3S	O-C-CA-N
4	F	505	P3S	O-C-CA-N
7	A	508	1PE	C13-C23-OH3-C22
7	D	508	1PE	C13-C23-OH3-C22
7	B	508	1PE	C13-C23-OH3-C22
7	C	508	1PE	C13-C23-OH3-C22
7	F	508	1PE	C13-C23-OH3-C22
7	E	508	1PE	C13-C23-OH3-C22
7	D	508	1PE	OH5-C14-C24-OH4
7	F	508	1PE	OH5-C14-C24-OH4
7	E	508	1PE	C16-C26-OH6-C15
7	A	508	1PE	C16-C26-OH6-C15
7	B	508	1PE	C16-C26-OH6-C15
7	A	508	1PE	OH5-C14-C24-OH4
7	D	508	1PE	C16-C26-OH6-C15
7	C	508	1PE	C16-C26-OH6-C15
7	F	508	1PE	C16-C26-OH6-C15
7	B	508	1PE	OH5-C14-C24-OH4
7	E	508	1PE	OH5-C14-C24-OH4
7	C	508	1PE	OH5-C14-C24-OH4
2	A	501	1AZ	N4-C8-N3-C9
2	C	501	1AZ	N4-C8-N3-C9
7	D	508	1PE	C12-C22-OH3-C23
7	A	508	1PE	OH4-C13-C23-OH3

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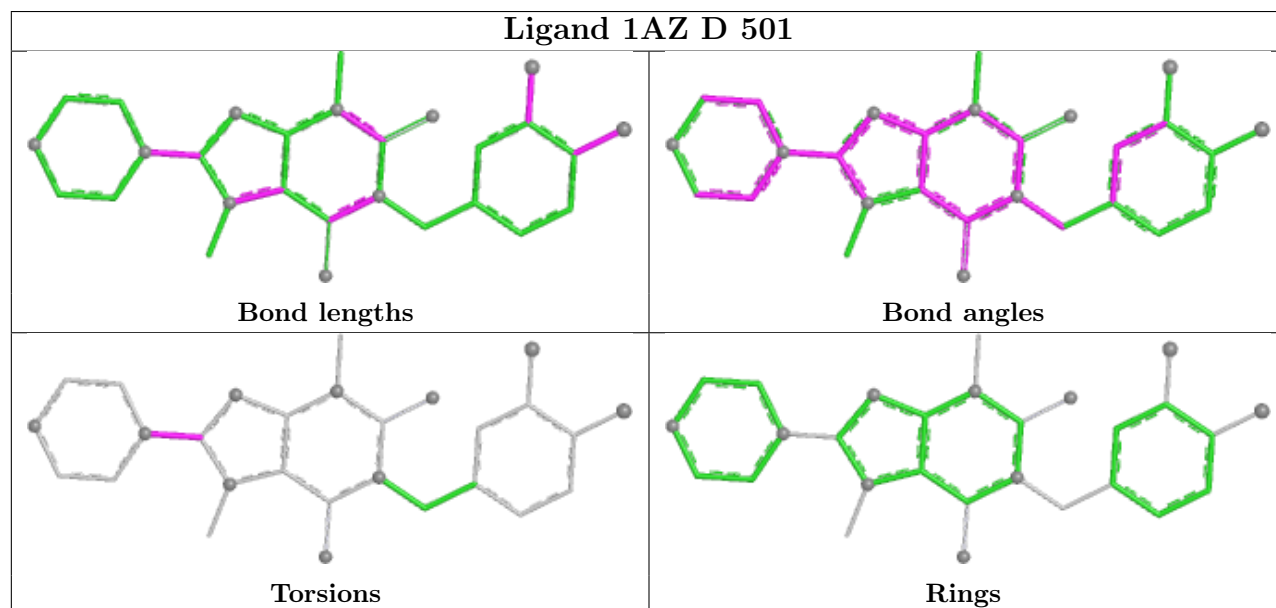
Mol	Chain	Res	Type	Atoms
7	B	508	1PE	OH4-C13-C23-OH3
7	D	508	1PE	OH4-C13-C23-OH3
7	F	508	1PE	OH4-C13-C23-OH3

There are no ring outliers.

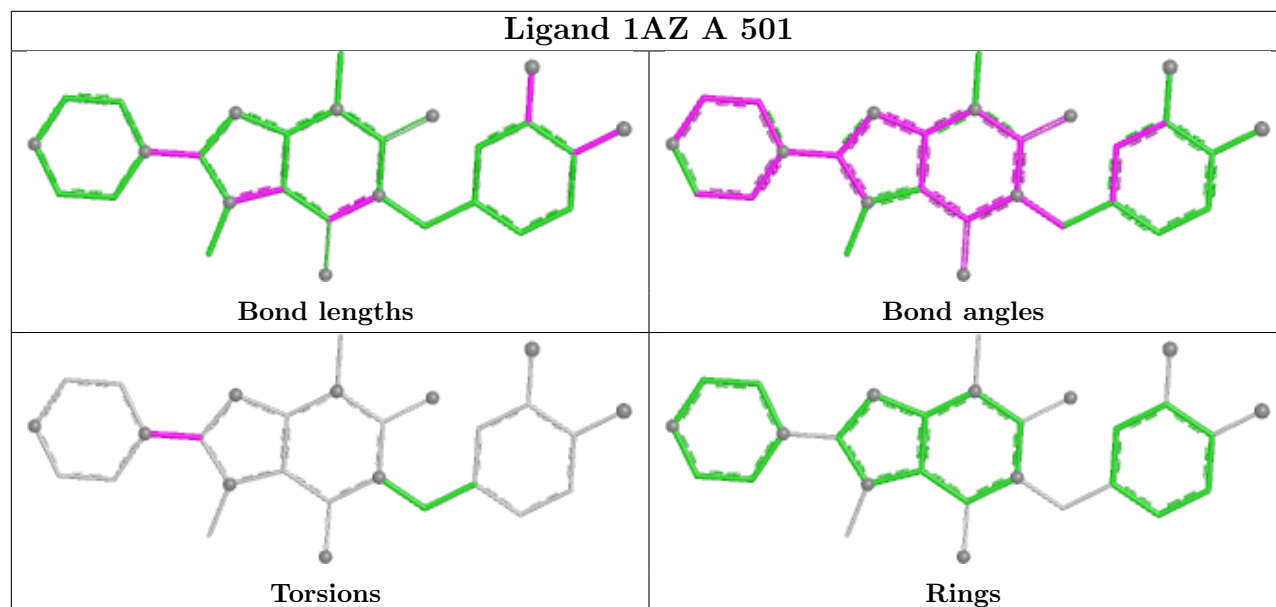
6 monomers are involved in 46 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	E	508	1PE	7	0
7	A	508	1PE	8	0
7	C	508	1PE	8	0
7	D	508	1PE	8	0
7	F	508	1PE	8	0
7	B	508	1PE	7	0

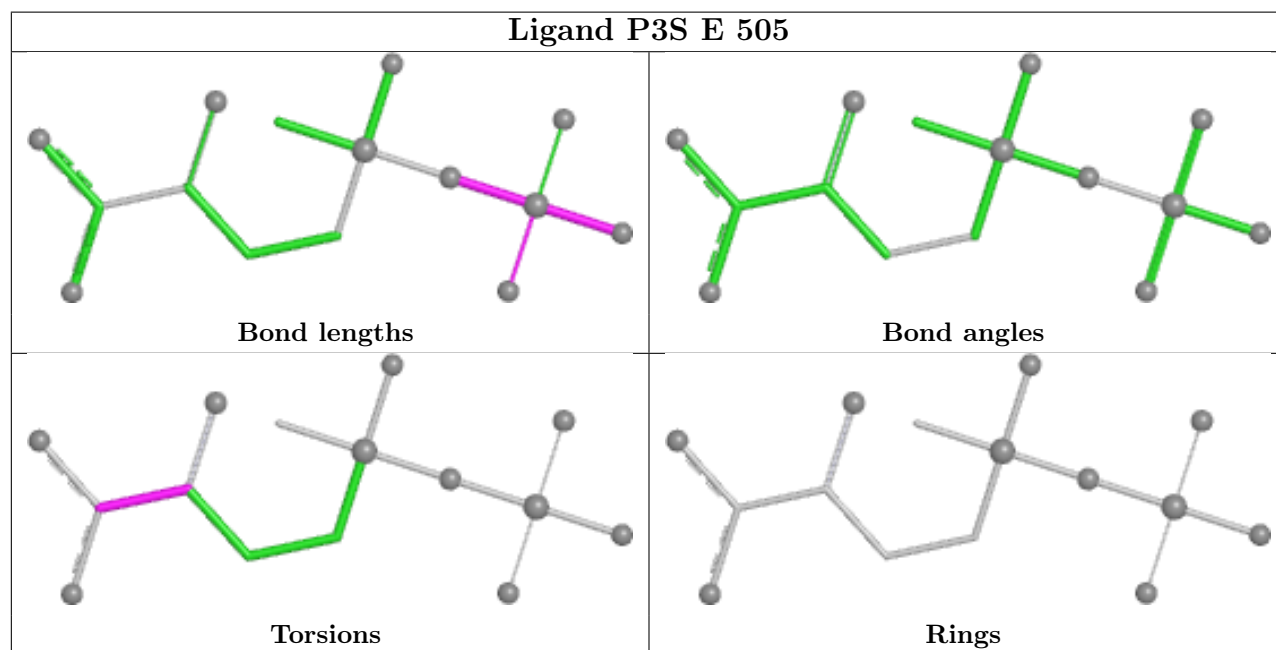
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



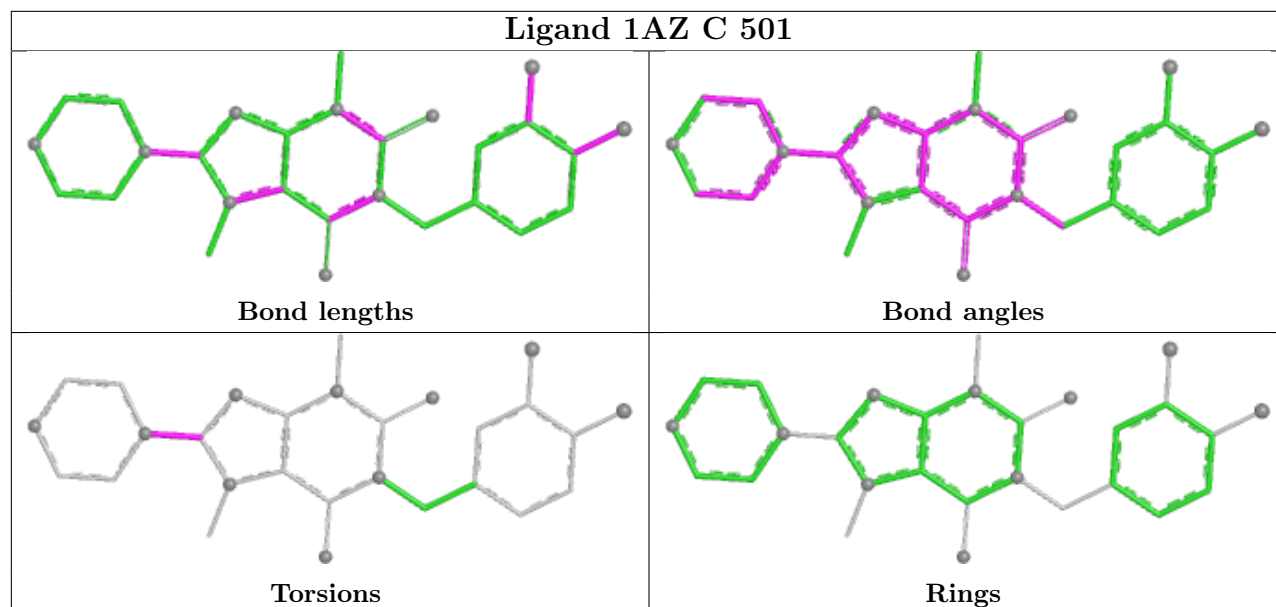
Ligand 1AZ A 501



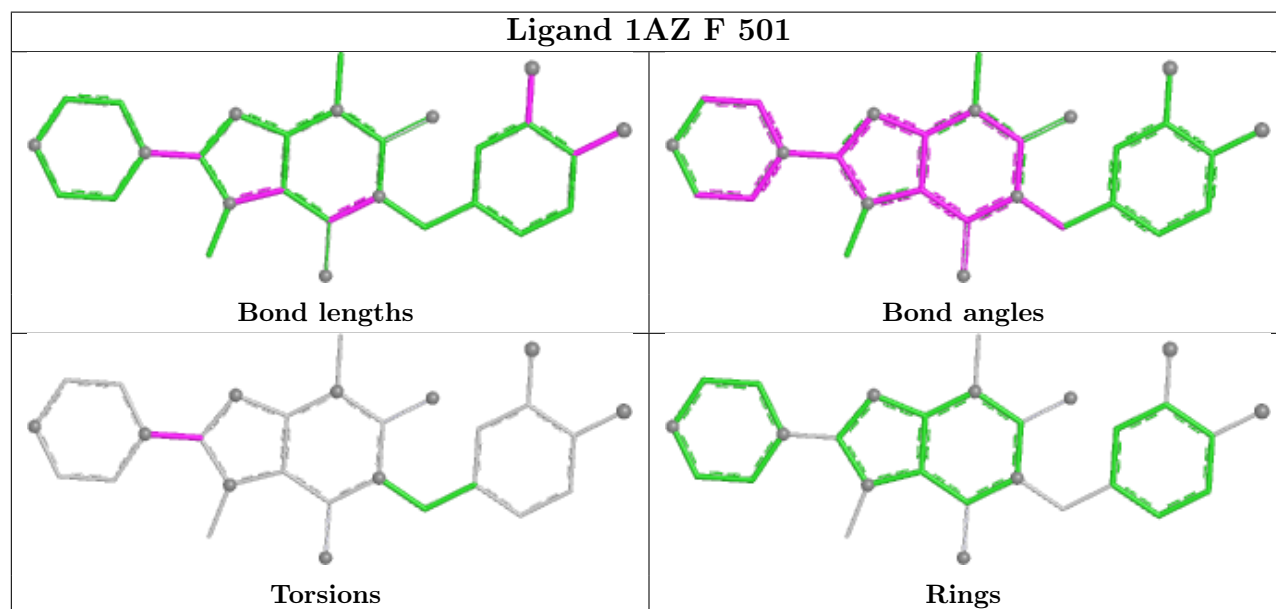
Ligand P3S E 505



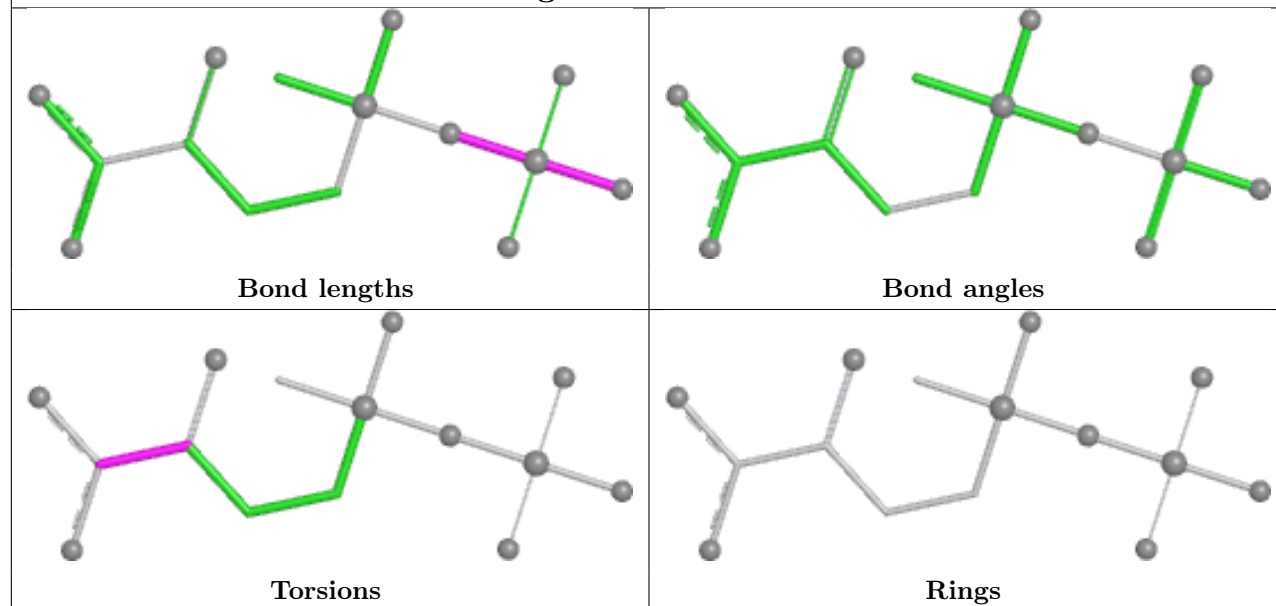
Ligand 1AZ C 501



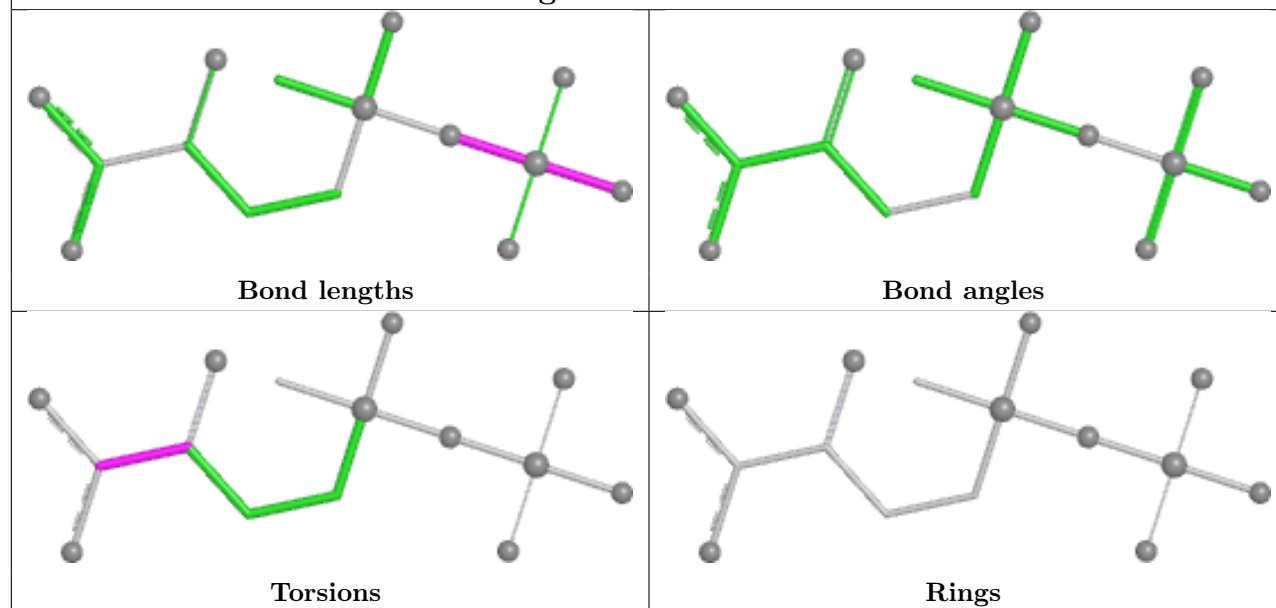
Ligand 1AZ F 501



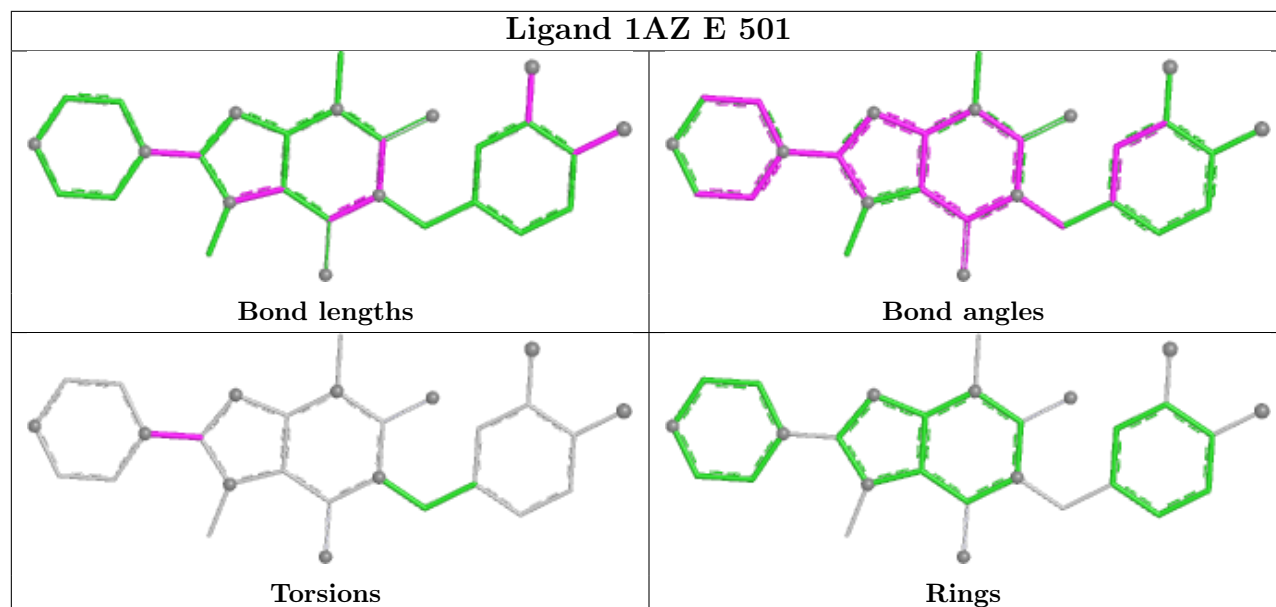
Ligand P3S A 505



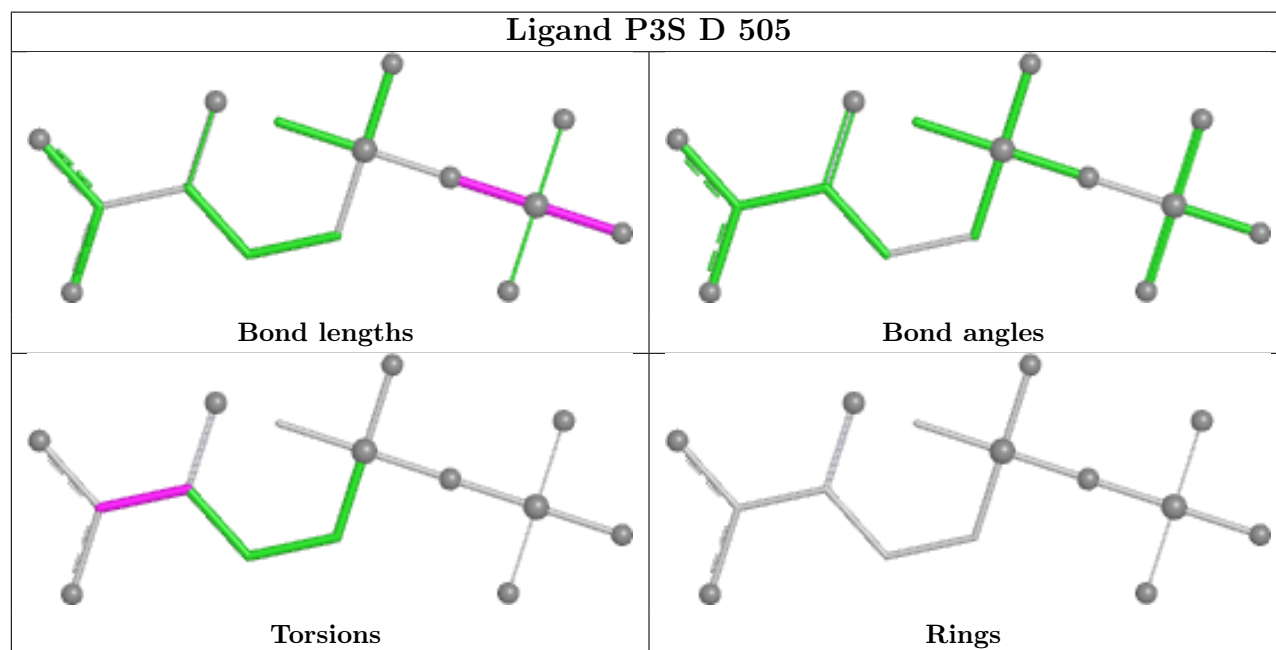
Ligand P3S B 505



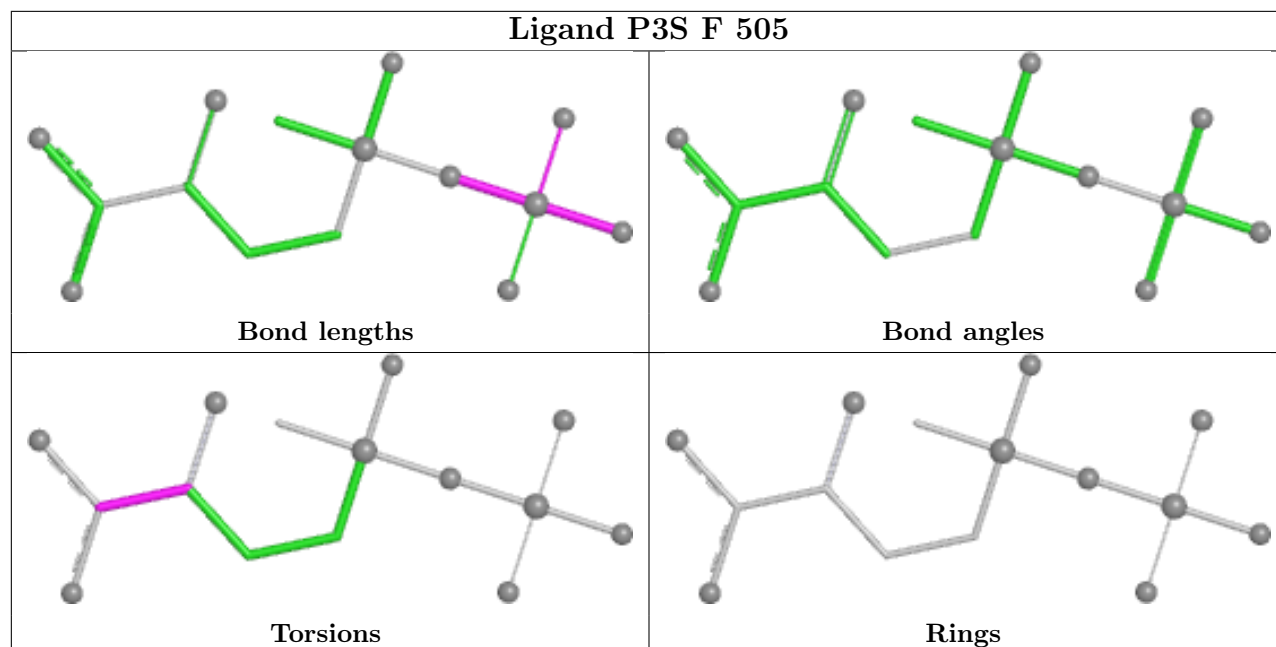
Ligand 1AZ E 501



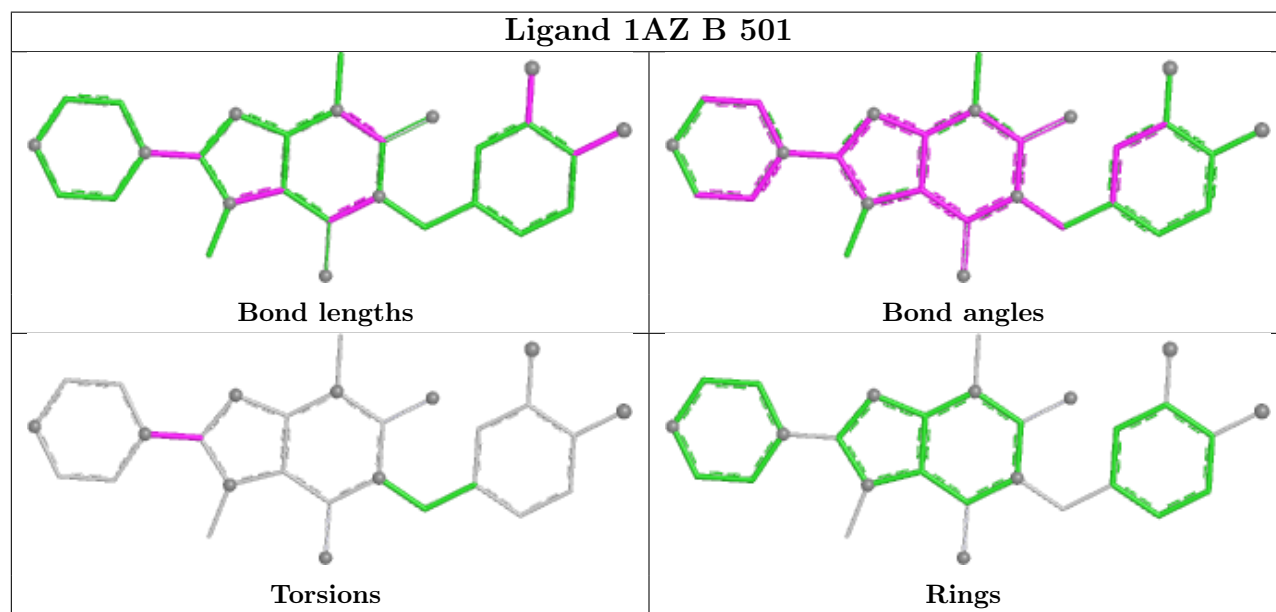
Ligand P3S D 505

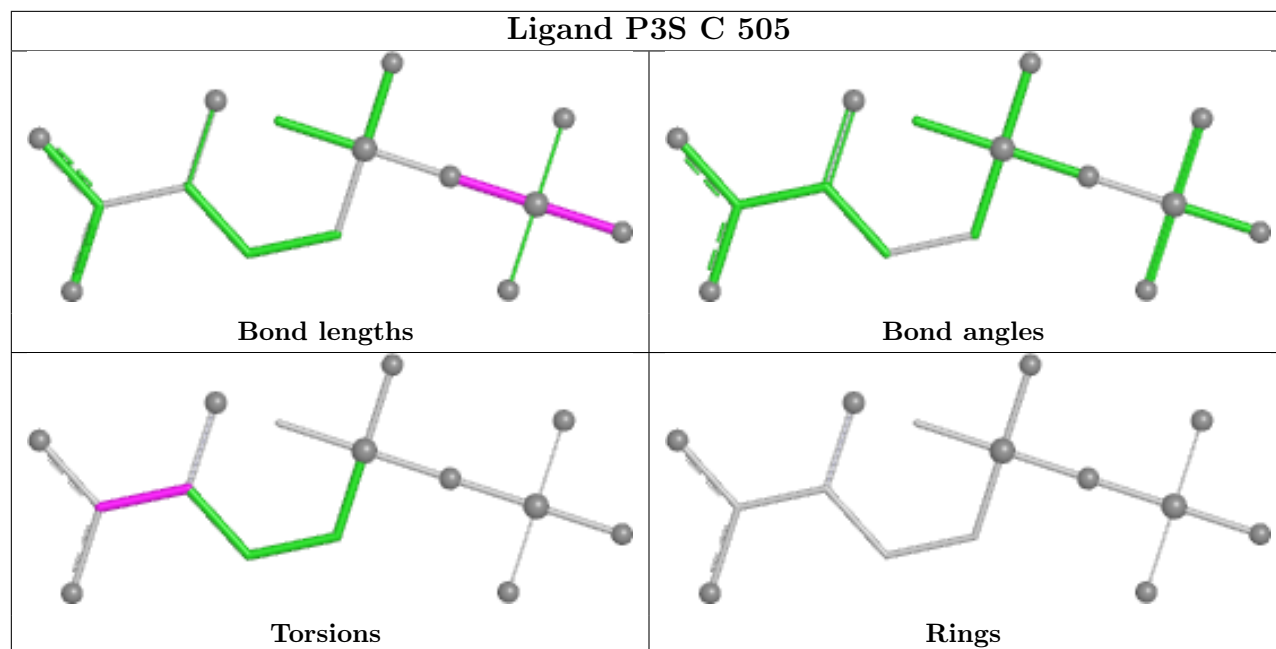


Ligand P3S F 505



Ligand 1AZ B 501





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	476/486 (97%)	-0.01	1 (0%) 91 90	18, 26, 39, 57	0
1	B	476/486 (97%)	-0.02	2 (0%) 88 87	18, 26, 39, 57	0
1	C	476/486 (97%)	-0.03	1 (0%) 91 90	18, 26, 39, 57	0
1	D	476/486 (97%)	-0.07	0 100 100	18, 26, 39, 57	0
1	E	476/486 (97%)	-0.06	3 (0%) 85 83	18, 26, 37, 57	0
1	F	476/486 (97%)	-0.02	2 (0%) 88 87	18, 26, 38, 57	0
All	All	2856/2916 (97%)	-0.04	9 (0%) 90 88	18, 26, 39, 57	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	4	LYS	2.8
1	B	3	GLU	2.8
1	F	3	GLU	2.2
1	E	15	ASP	2.2
1	E	3	GLU	2.2
1	F	435	GLU	2.1
1	A	399	ALA	2.1
1	C	3	GLU	2.1
1	E	464	ASN	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 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
7	1PE	C	508	16/16	0.72	0.15	31,32,37,38	0
7	1PE	E	508	16/16	0.72	0.14	30,32,37,38	0
7	1PE	B	508	16/16	0.76	0.15	30,32,37,38	0
7	1PE	F	508	16/16	0.76	0.14	30,32,37,38	0
7	1PE	D	508	16/16	0.78	0.14	30,32,37,38	0
7	1PE	A	508	16/16	0.81	0.13	30,32,37,38	0
5	PO4	B	506	5/5	0.88	0.13	37,37,39,39	0
2	1AZ	E	501	28/28	0.89	0.11	37,38,40,41	0
5	PO4	C	506	5/5	0.89	0.19	37,37,39,39	0
2	1AZ	A	501	28/28	0.90	0.11	37,38,40,41	0
2	1AZ	B	501	28/28	0.90	0.10	37,38,40,41	0
2	1AZ	D	501	28/28	0.90	0.11	37,38,40,41	0
5	PO4	A	506	5/5	0.91	0.13	37,37,39,39	0
2	1AZ	F	501	28/28	0.92	0.10	37,38,40,41	0
2	1AZ	C	501	28/28	0.92	0.09	37,38,40,41	0
5	PO4	D	506	5/5	0.92	0.12	37,37,39,39	0
5	PO4	F	506	5/5	0.94	0.09	37,37,39,39	0
3	MG	A	503	1/1	0.95	0.08	27,27,27,27	0
4	P3S	C	505	15/15	0.96	0.08	24,24,25,25	0
4	P3S	E	505	15/15	0.96	0.07	24,24,24,25	0
3	MG	A	502	1/1	0.96	0.04	25,25,25,25	0
3	MG	A	504	1/1	0.96	0.05	25,25,25,25	0
3	MG	B	502	1/1	0.96	0.04	25,25,25,25	0
4	P3S	A	505	15/15	0.96	0.07	24,24,25,25	0
5	PO4	E	506	5/5	0.96	0.09	37,37,39,39	0
4	P3S	B	505	15/15	0.97	0.06	24,24,25,25	0
3	MG	E	504	1/1	0.97	0.07	24,24,24,24	0
3	MG	F	502	1/1	0.97	0.07	25,25,25,25	0
3	MG	F	503	1/1	0.97	0.04	26,26,26,26	0
3	MG	B	503	1/1	0.97	0.04	27,27,27,27	0
3	MG	E	502	1/1	0.98	0.09	24,24,24,24	0
6	CL	A	507	1/1	0.98	0.04	28,28,28,28	0
6	CL	B	507	1/1	0.98	0.03	28,28,28,28	0
6	CL	C	507	1/1	0.98	0.07	28,28,28,28	0
6	CL	D	507	1/1	0.98	0.05	28,28,28,28	0
4	P3S	F	505	15/15	0.98	0.06	24,24,25,25	0
3	MG	F	504	1/1	0.98	0.04	24,24,24,24	0

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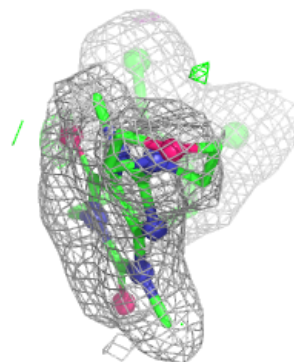
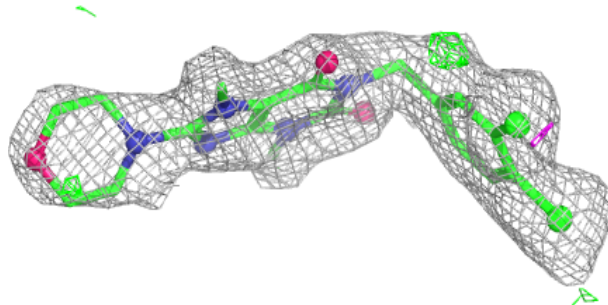
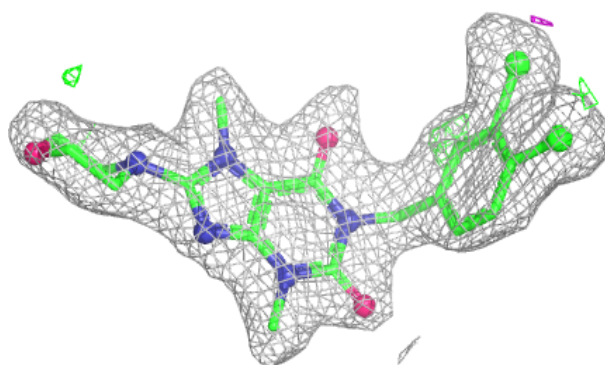
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	MG	E	503	1/1	0.98	0.03	27,27,27,27	0
3	MG	B	504	1/1	0.98	0.03	25,25,25,25	0
3	MG	C	502	1/1	0.98	0.03	25,25,25,25	0
4	P3S	D	505	15/15	0.98	0.06	24,24,25,25	0
3	MG	D	503	1/1	0.99	0.03	27,27,27,27	0
3	MG	D	504	1/1	0.99	0.03	25,25,25,25	0
3	MG	C	503	1/1	0.99	0.05	27,27,27,27	0
3	MG	D	502	1/1	0.99	0.04	25,25,25,25	0
6	CL	E	507	1/1	0.99	0.03	28,28,28,28	0
6	CL	F	507	1/1	0.99	0.02	28,28,28,28	0
3	MG	C	504	1/1	1.00	0.02	24,24,24,24	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.

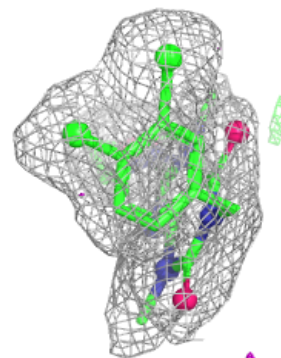
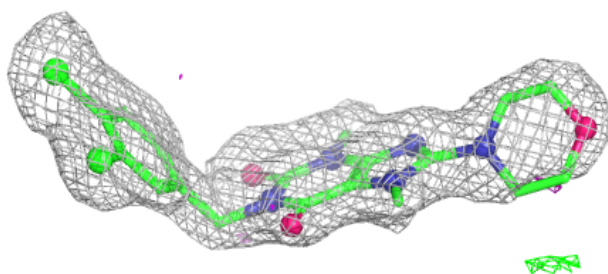
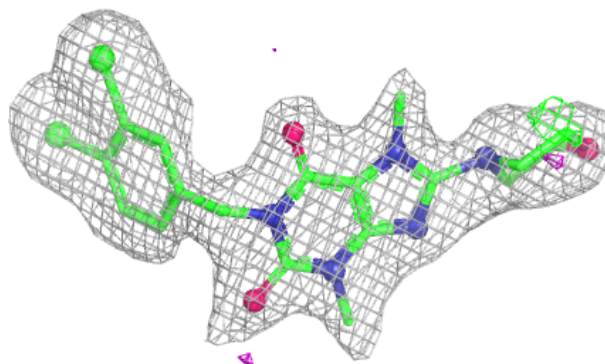
Electron density around 1AZ E 501:

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

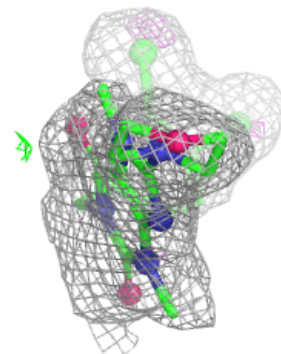
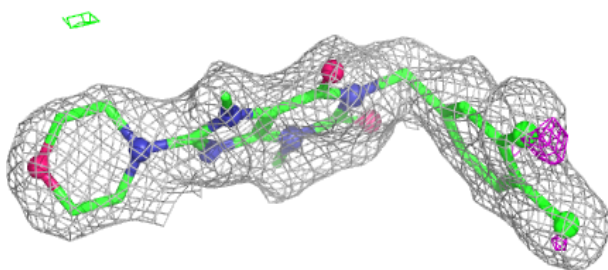
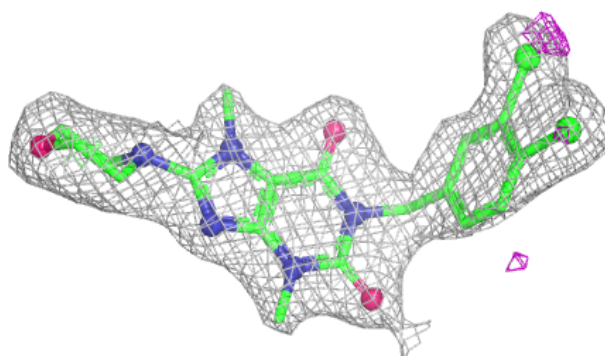


Electron density around 1AZ A 501:

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

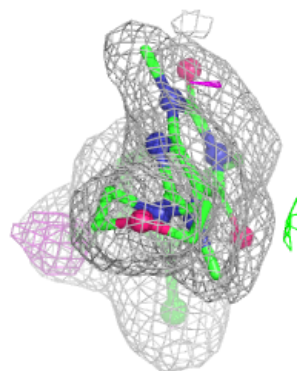
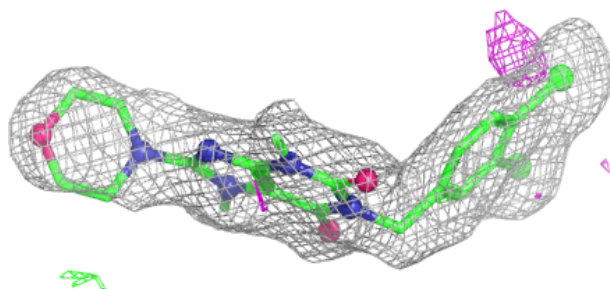
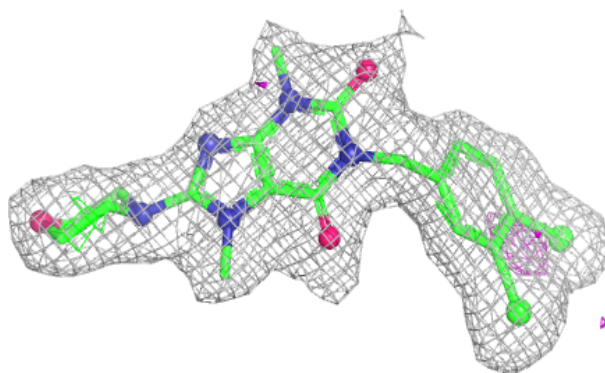
**Electron density around 1AZ B 501:**

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

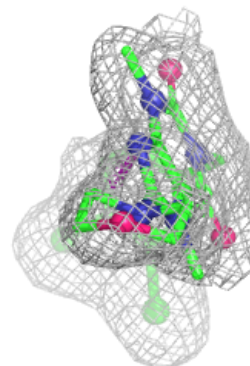
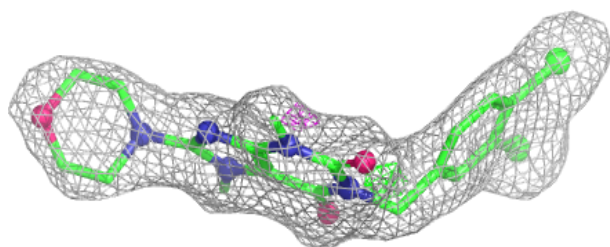
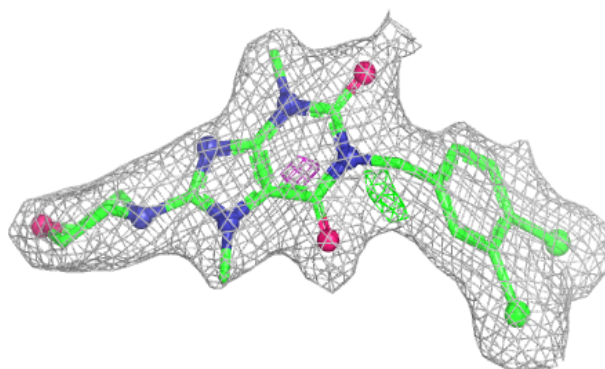


Electron density around 1AZ D 501:

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and green (positive)

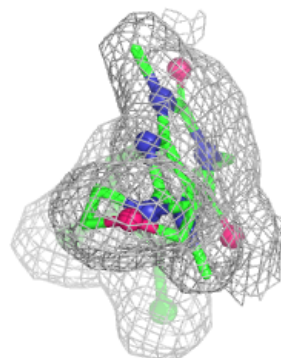
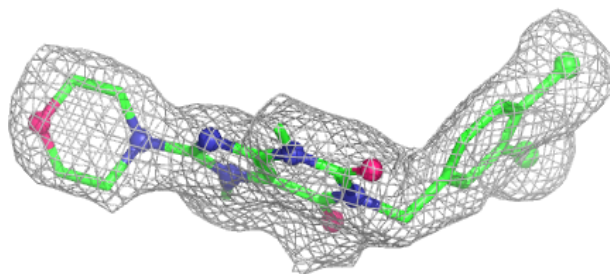
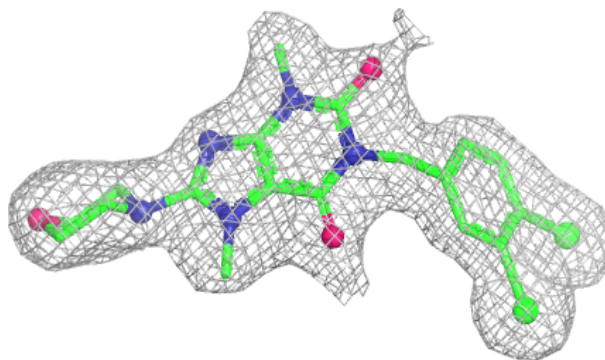
**Electron density around 1AZ F 501:**

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

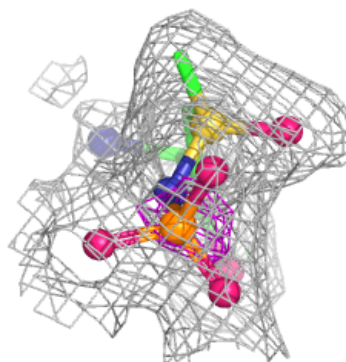
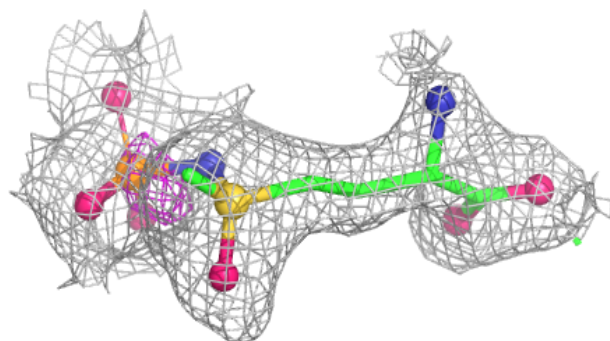
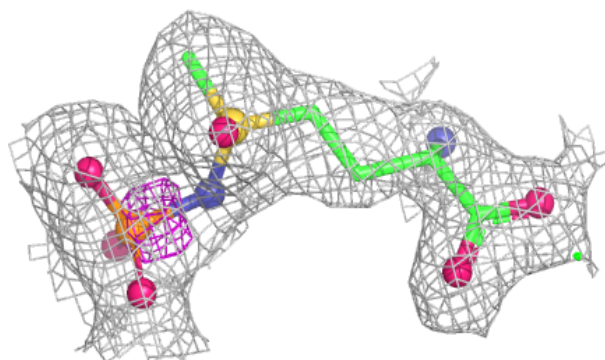


Electron density around 1AZ C 501:

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

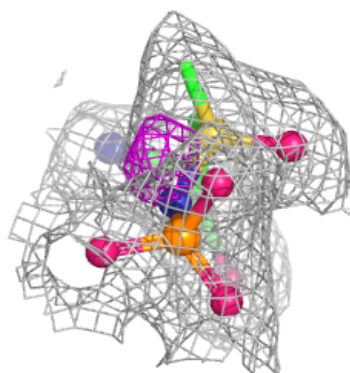
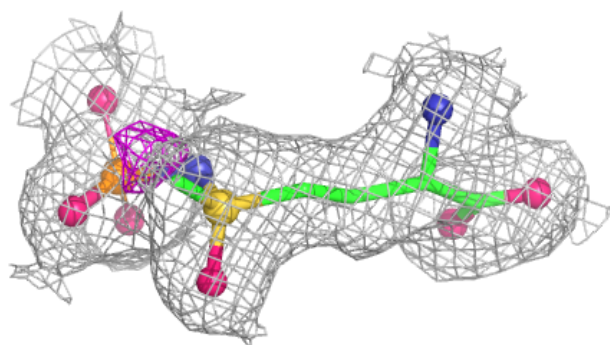
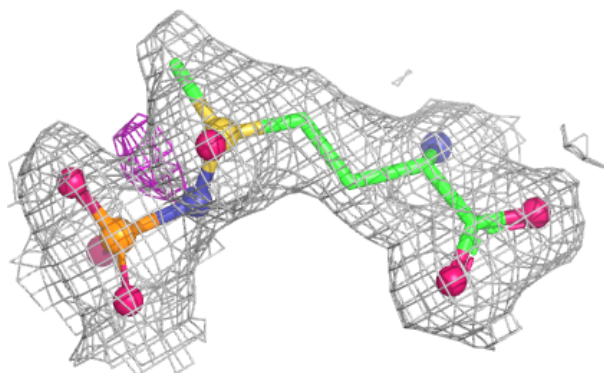
**Electron density around P3S C 505:**

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

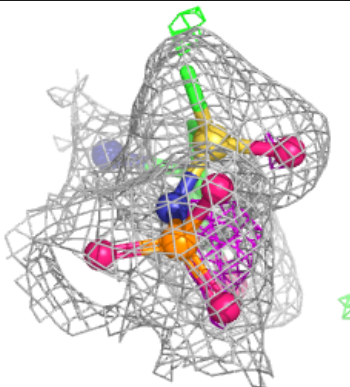
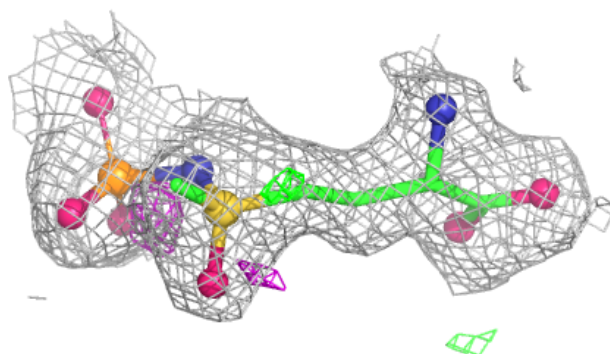
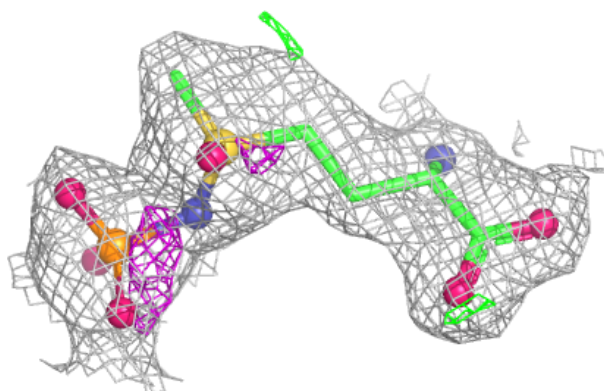


Electron density around P3S E 505:

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

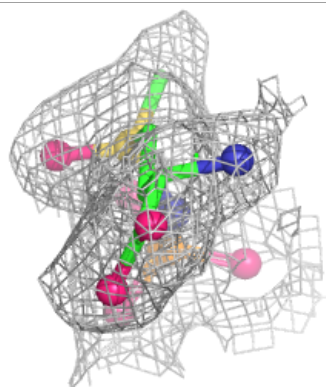
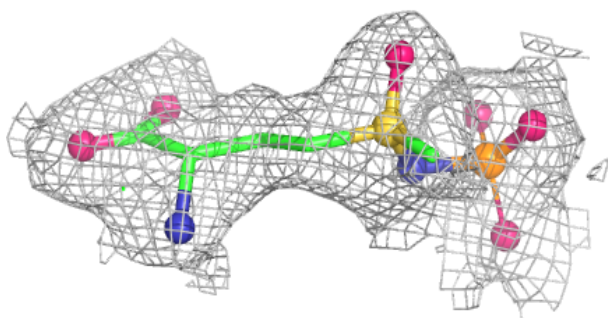
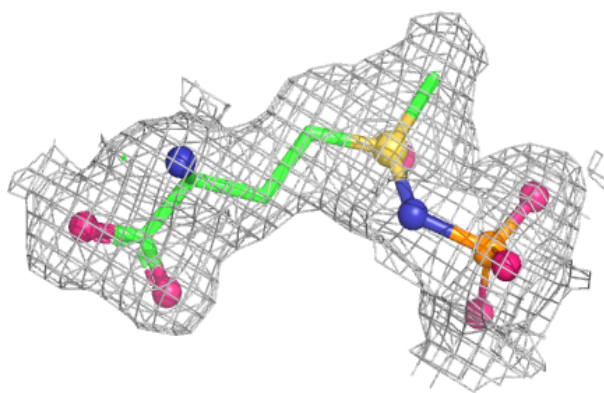
**Electron density around P3S A 505:**

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

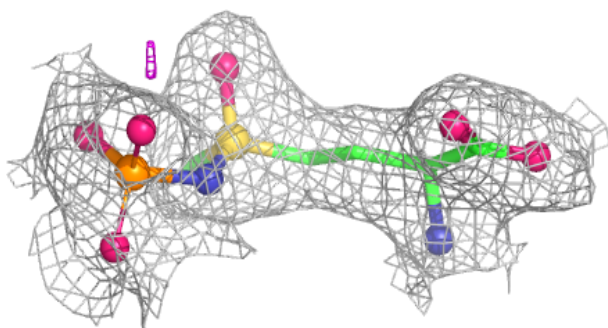
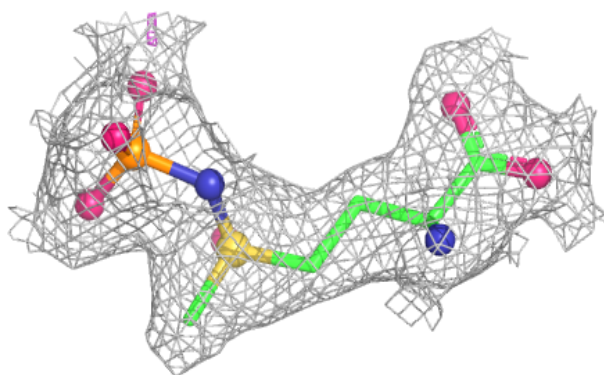


Electron density around P3S B 505:

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

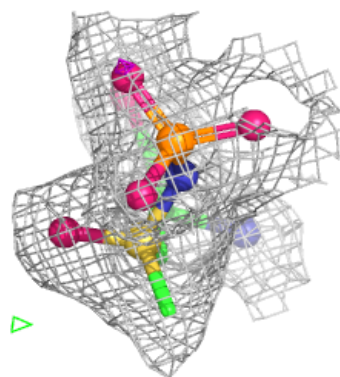
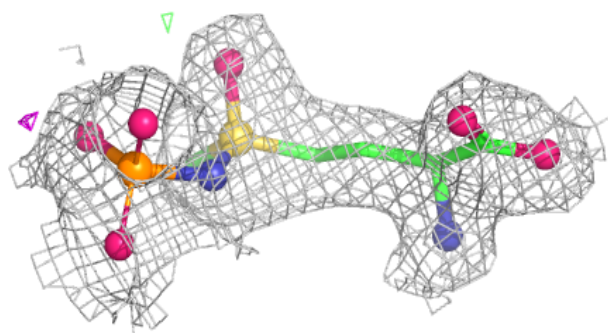
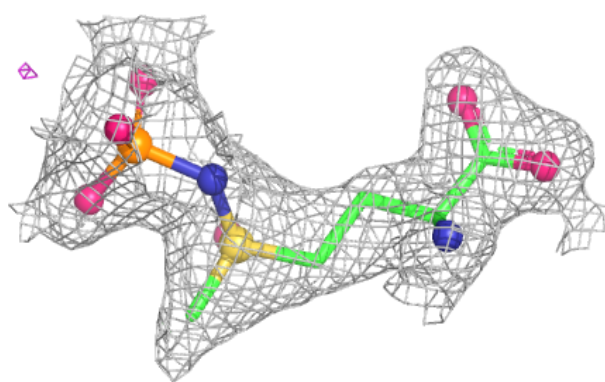
**Electron density around P3S F 505:**

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



Electron density around P3S D 505:

$2mF_o-DF_c$ (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.