



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 29, 2026 – 04:26 PM UTC

PDB ID : 4Y95 / pdb_00004y95
Title : Crystal structure of the kinase domain of Bruton's tyrosine kinase with mutations in the activation loop
Authors : Wang, Q.; Rosen, C.E.; Kuriyan, J.
Deposited on : 2015-02-16
Resolution : 1.60 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

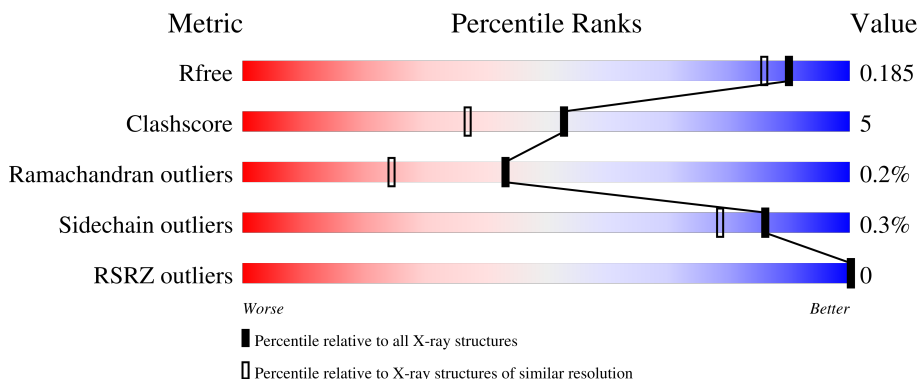
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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	4673 (1.60-1.60)
Clashscore	190562	4931 (1.60-1.60)
Ramachandran outliers	187476	4831 (1.60-1.60)
Sidechain outliers	187428	4830 (1.60-1.60)
RSRZ outliers	180081	4672 (1.60-1.60)

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	266	90% 10%
1	B	266	90% 10%
1	C	266	90% 9%
1	D	266	91% 9%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 18889 atoms, of which 8799 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 Non-specific protein-tyrosine kinase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	266	Total	C	H	N	O	S	0	11	0
			4358	1420	2151	354	411	22			
1	B	266	Total	C	H	N	O	S	0	14	0
			4405	1429	2180	360	414	22			
1	C	266	Total	C	H	N	O	S	0	12	0
			4360	1415	2154	354	414	23			
1	D	265	Total	C	H	N	O	S	0	9	0
			4324	1405	2138	353	407	21			

There are 40 discrepancies between the modelled and reference sequences:

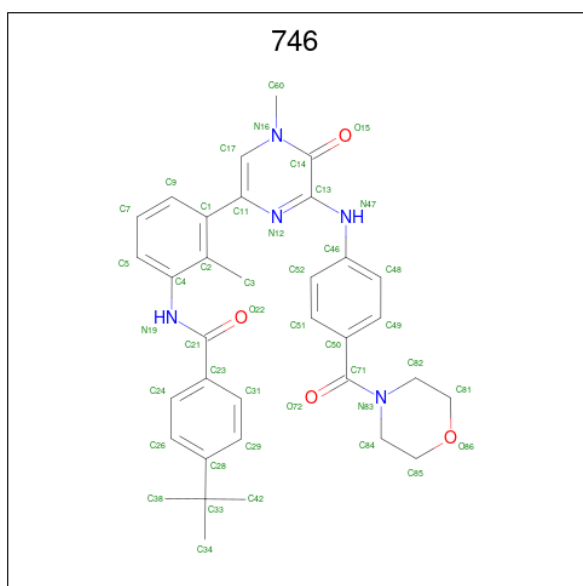
Chain	Residue	Modelled	Actual	Comment	Reference
A	394	ALA	-	expression tag	UNP Q3ZC95
A	542	MET	LEU	engineered mutation	UNP Q3ZC95
A	543	THR	SER	engineered mutation	UNP Q3ZC95
A	545	PHE	TYR	engineered mutation	UNP Q3ZC95
A	555	THR	VAL	engineered mutation	UNP Q3ZC95
A	557	THR	SER	engineered mutation	UNP Q3ZC95
A	562	LYS	ARG	engineered mutation	UNP Q3ZC95
A	564	ALA	SER	engineered mutation	UNP Q3ZC95
A	565	SER	PRO	engineered mutation	UNP Q3ZC95
A	617	PRO	TYR	engineered mutation	UNP Q3ZC95
B	394	ALA	-	expression tag	UNP Q3ZC95
B	542	MET	LEU	engineered mutation	UNP Q3ZC95
B	543	THR	SER	engineered mutation	UNP Q3ZC95
B	545	PHE	TYR	engineered mutation	UNP Q3ZC95
B	555	THR	VAL	engineered mutation	UNP Q3ZC95
B	557	THR	SER	engineered mutation	UNP Q3ZC95
B	562	LYS	ARG	engineered mutation	UNP Q3ZC95
B	564	ALA	SER	engineered mutation	UNP Q3ZC95
B	565	SER	PRO	engineered mutation	UNP Q3ZC95
B	617	PRO	TYR	engineered mutation	UNP Q3ZC95
C	394	ALA	-	expression tag	UNP Q3ZC95

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Chain	Residue	Modelled	Actual	Comment	Reference
C	542	MET	LEU	engineered mutation	UNP Q3ZC95
C	543	THR	SER	engineered mutation	UNP Q3ZC95
C	545	PHE	TYR	engineered mutation	UNP Q3ZC95
C	555	THR	VAL	engineered mutation	UNP Q3ZC95
C	557	THR	SER	engineered mutation	UNP Q3ZC95
C	562	LYS	ARG	engineered mutation	UNP Q3ZC95
C	564	ALA	SER	engineered mutation	UNP Q3ZC95
C	565	SER	PRO	engineered mutation	UNP Q3ZC95
C	617	PRO	TYR	engineered mutation	UNP Q3ZC95
D	394	ALA	-	expression tag	UNP Q3ZC95
D	542	MET	LEU	engineered mutation	UNP Q3ZC95
D	543	THR	SER	engineered mutation	UNP Q3ZC95
D	545	PHE	TYR	engineered mutation	UNP Q3ZC95
D	555	THR	VAL	engineered mutation	UNP Q3ZC95
D	557	THR	SER	engineered mutation	UNP Q3ZC95
D	562	LYS	ARG	engineered mutation	UNP Q3ZC95
D	564	ALA	SER	engineered mutation	UNP Q3ZC95
D	565	SER	PRO	engineered mutation	UNP Q3ZC95
D	617	PRO	TYR	engineered mutation	UNP Q3ZC95

- Molecule 2 is 4-tert-butyl-N-[2-methyl-3-(4-methyl-6-{[4-(morpholin-4-ylcarbonyl)phenyl]amino}-5-oxo-4,5-dihydropyrazin-2-yl)phenyl]benzamide (CCD ID: 746) (formula: C₃₄H₃₇N₅O₄).



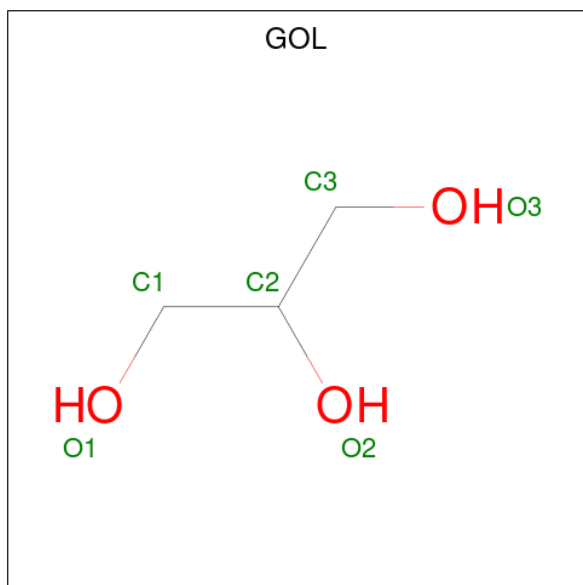
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			43	34	5	4		

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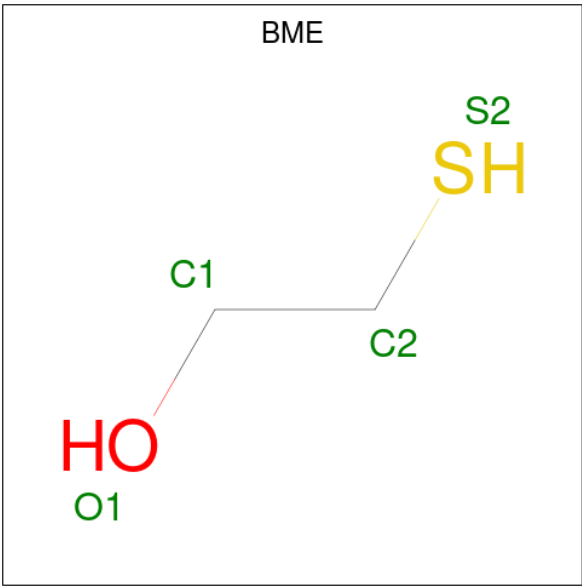
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	N	O	0	0
			43	34	5	4		
2	C	1	Total	C	N	O	0	0
			43	34	5	4		
2	D	1	Total	C	N	O	0	0
			43	34	5	4		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



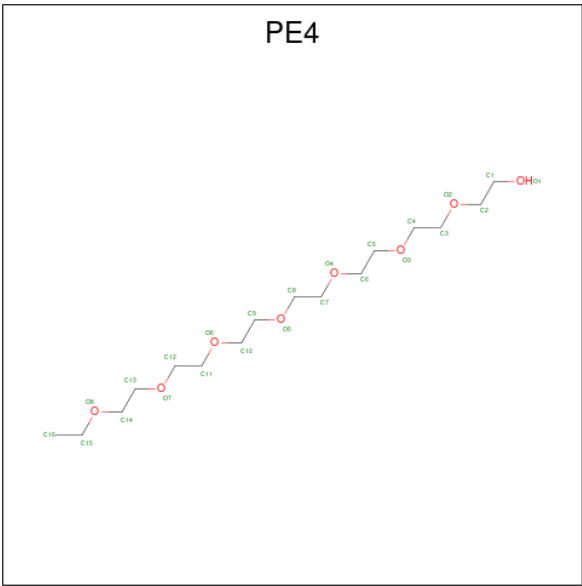
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	0
			14	3	8	3		
3	B	1	Total	C	H	O	0	0
			14	3	8	3		
3	B	1	Total	C	H	O	0	0
			14	3	8	3		
3	C	1	Total	C	H	O	0	1
			28	6	16	6		
3	D	1	Total	C	H	O	0	0
			14	3	8	3		
3	D	1	Total	C	H	O	0	0
			14	3	8	3		
3	D	1	Total	C	H	O	0	0
			14	3	8	3		
3	D	1	Total	C	H	O	0	0
			14	3	8	3		

- Molecule 4 is BETA-MERCAPTOETHANOL (CCD ID: BME) (formula: C₂H₆OS).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total 20	C 4	H 12	O 2	S 2	0	1
4	B	1	Total 20	C 4	H 12	O 2	S 2	0	1
4	C	1	Total 20	C 4	H 12	O 2	S 2	0	1

- Molecule 5 is 2-{2-[2-(2-{2-[2-(2-ETHOXY-ETHOXY)-ETHOXY]-ETHOXY}-ETHOXY)-ETHOXY]-ETHOXY}-ETHANOL (CCD ID: PE4) (formula: C₁₆H₃₄O₈).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	H	O	0	0
			58	16	34	8		
5	C	1	Total	C	H	O	0	0
			58	16	34	8		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	240	Total	O	0	0
			240	240		
6	B	237	Total	O	0	0
			237	237		
6	C	250	Total	O	0	0
			250	250		
6	D	241	Total	O	0	0
			241	241		

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: Non-specific protein-tyrosine kinase

Chain A:  90% 10%



- Molecule 1: Non-specific protein-tyrosine kinase

Chain B:  90% 10%



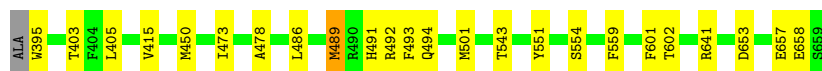
- Molecule 1: Non-specific protein-tyrosine kinase

Chain C:  90% 9%



- Molecule 1: Non-specific protein-tyrosine kinase

Chain D:  91% 9%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	50.93Å 79.07Å 79.18Å 90.73° 89.90° 89.99°	Depositor
Resolution (Å)	39.59 – 1.60 39.59 – 1.60	Depositor EDS
% Data completeness (in resolution range)	96.4 (39.59-1.60) 93.9 (39.59-1.60)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.20 (at 1.60Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.155 , 0.184 0.156 , 0.185	Depositor DCC
R_{free} test set	2009 reflections (1.27%)	wwPDB-VP
Wilson B-factor (Å ²)	17.4	Xtriage
Anisotropy	0.227	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.43 , 43.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.045 for h,l,-k 0.045 for h,-l,k 0.468 for h,-k,-l 0.026 for -h,k,-l 0.026 for -h,-k,l 0.019 for -h,l,k 0.020 for -h,-l,-k	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	18889	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.88% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: BME, PE4, 746, GOL

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	0.65	1/2291 (0.0%)	0.84	5/3092 (0.2%)
1	B	0.57	0/2317	0.85	7/3125 (0.2%)
1	C	0.62	2/2290 (0.1%)	0.83	6/3087 (0.2%)
1	D	0.63	0/2263	0.86	7/3053 (0.2%)
All	All	0.62	3/9161 (0.0%)	0.85	25/12357 (0.2%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	439	GLU	C-O	-7.06	1.15	1.24
1	C	440	ASP	C-O	-5.61	1.17	1.24
1	A	431	MET	C-N	-5.07	1.27	1.33

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	395	TRP	N-CA-C	-8.10	102.42	111.82
1	B	616	LEU	N-CA-C	7.92	118.70	109.60
1	C	439	GLU	N-CA-C	7.12	119.12	111.36
1	D	601	PHE	N-CA-C	6.84	120.61	110.48
1	B	494	GLN	N-CA-C	-6.30	101.15	110.48

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2207	2151	2172	16	0
1	B	2225	2180	2198	21	3
1	C	2206	2154	2178	19	3
1	D	2186	2138	2149	19	0
2	A	43	0	37	3	0
2	B	43	0	37	6	0
2	C	43	0	37	3	0
2	D	43	0	37	2	0
3	A	6	8	8	1	0
3	B	12	16	16	0	0
3	C	12	16	16	0	0
3	D	24	32	32	1	0
4	A	8	12	12	1	0
4	B	8	12	12	0	0
4	C	8	12	12	1	0
5	B	24	34	34	8	0
5	C	24	34	34	6	0
6	A	240	0	0	6	1
6	B	237	0	0	4	2
6	C	250	0	0	3	3
6	D	241	0	0	4	2
All	All	10090	8799	9021	90	7

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.

The worst 5 of 90 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:D:486:LEU:O	1:D:489:MET:O	1.86	0.92
1:B:433:LYS:HZ1	5:B:705:PE4:H81	1.31	0.92
1:D:491:HIS:ND1	6:D:801:HOH:O	2.10	0.82
1:C:625:ARG:HH22	1:C:657:GLU:HG3	1.55	0.71
1:B:433:LYS:HZ1	5:B:705:PE4:H101	1.56	0.69

The worst 5 of 7 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)
6:B:854:HOH:O	6:C:1161:HOH:O[1_645]	1.91	0.29
6:A:849:HOH:O	6:C:1159:HOH:O[1_556]	1.97	0.23
6:B:850:HOH:O	6:D:871:HOH:O[1_556]	1.98	0.22
1:B:659:SER:OG	1:C:595:LYS:NZ[1_645]	2.06	0.14
6:C:1164:HOH:O	6:D:856:HOH:O[1_465]	2.07	0.13

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	275/266 (103%)	268 (98%)	7 (2%)	0	100	100
1	B	278/266 (104%)	271 (98%)	6 (2%)	1 (0%)	30	14
1	C	276/266 (104%)	268 (97%)	7 (2%)	1 (0%)	30	14
1	D	272/266 (102%)	265 (97%)	7 (3%)	0	100	100
All	All	1101/1064 (104%)	1072 (97%)	27 (2%)	2 (0%)	43	24

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	490	ARG
1	C	490	ARG

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	244/238 (102%)	242 (99%)	2 (1%)	73	59
1	B	247/238 (104%)	247 (100%)	0	100	100
1	C	245/238 (103%)	245 (100%)	0	100	100
1	D	242/238 (102%)	241 (100%)	1 (0%)	84	75
All	All	978/952 (103%)	975 (100%)	3 (0%)	86	78

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	395	TRP
1	A	405	LEU
1	D	494	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	603	ASN
1	C	491	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

21 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
5	PE4	B	705	-	23,23,23	0.73	0	22,22,22	1.54	6 (27%)
3	GOL	D	705	-	5,5,5	0.35	0	5,5,5	0.26	0
3	GOL	D	702	-	5,5,5	0.51	0	5,5,5	0.62	0
3	GOL	B	702	-	5,5,5	0.35	0	5,5,5	0.18	0
3	GOL	A	702	-	5,5,5	0.38	0	5,5,5	1.10	1 (20%)
4	BME	B	704[B]	-	3,3,3	0.25	0	2,2,2	0.30	0
3	GOL	D	703	-	5,5,5	0.70	0	5,5,5	1.78	3 (60%)
3	GOL	B	703	-	5,5,5	0.35	0	5,5,5	0.46	0
4	BME	B	704[A]	-	3,3,3	0.26	0	2,2,2	0.26	0
3	GOL	D	704	-	5,5,5	0.37	0	5,5,5	0.40	0
2	746	B	701	-	47,47,47	2.35	11 (23%)	60,68,68	1.41	10 (16%)
4	BME	A	703[B]	-	3,3,3	0.24	0	2,2,2	0.28	0
2	746	A	701	-	47,47,47	2.40	9 (19%)	60,68,68	1.33	10 (16%)
4	BME	A	703[A]	-	3,3,3	0.22	0	2,2,2	0.48	0
3	GOL	C	1002[B]	-	5,5,5	0.33	0	5,5,5	0.90	0
2	746	D	701	-	47,47,47	2.34	10 (21%)	60,68,68	1.28	7 (11%)
3	GOL	C	1002[A]	-	5,5,5	0.30	0	5,5,5	0.35	0
5	PE4	C	1004	-	23,23,23	0.58	0	22,22,22	0.66	0
2	746	C	1001	-	47,47,47	2.29	12 (25%)	60,68,68	1.44	11 (18%)
4	BME	C	1003[B]	-	3,3,3	0.29	0	2,2,2	0.10	0
4	BME	C	1003[A]	-	3,3,3	0.27	0	2,2,2	0.10	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
5	PE4	B	705	-	-	8/21/21/21	-
3	GOL	D	705	-	-	1/4/4/4	-
3	GOL	D	702	-	-	1/4/4/4	-
3	GOL	B	702	-	-	0/4/4/4	-
3	GOL	A	702	-	-	2/4/4/4	-
4	BME	B	704[B]	-	-	0/1/1/1	-
3	GOL	D	703	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	B	703	-	-	2/4/4/4	-
4	BME	B	704[A]	-	-	0/1/1/1	-
3	GOL	D	704	-	-	0/4/4/4	-
2	746	B	701	-	-	2/29/38/38	0/5/5/5
4	BME	A	703[B]	-	-	0/1/1/1	-
2	746	A	701	-	-	2/29/38/38	0/5/5/5
4	BME	A	703[A]	-	-	0/1/1/1	-
3	GOL	C	1002[B]	-	-	2/4/4/4	-
2	746	D	701	-	-	2/29/38/38	0/5/5/5
3	GOL	C	1002[A]	-	-	0/4/4/4	-
5	PE4	C	1004	-	-	9/21/21/21	-
2	746	C	1001	-	-	2/29/38/38	0/5/5/5
4	BME	C	1003[B]	-	-	0/1/1/1	-
4	BME	C	1003[A]	-	-	1/1/1/1	-

The worst 5 of 42 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	701	746	C17-C11	11.53	1.49	1.36
2	D	701	746	C17-C11	11.24	1.49	1.36
2	B	701	746	C17-C11	10.66	1.48	1.36
2	C	1001	746	C17-C11	10.18	1.48	1.36
2	C	1001	746	C71-N83	5.68	1.46	1.34

The worst 5 of 48 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	701	746	C60-N16-C14	4.16	122.83	117.14
2	C	1001	746	C81-C82-N83	4.09	118.42	109.82
2	B	701	746	C81-C82-N83	3.91	118.05	109.82
2	C	1001	746	C85-C84-N83	3.47	117.11	109.82
2	C	1001	746	C60-N16-C14	3.35	121.73	117.14

There are no chirality outliers.

5 of 36 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	702	GOL	O1-C1-C2-C3
3	D	703	GOL	C1-C2-C3-O3
3	D	703	GOL	O2-C2-C3-O3

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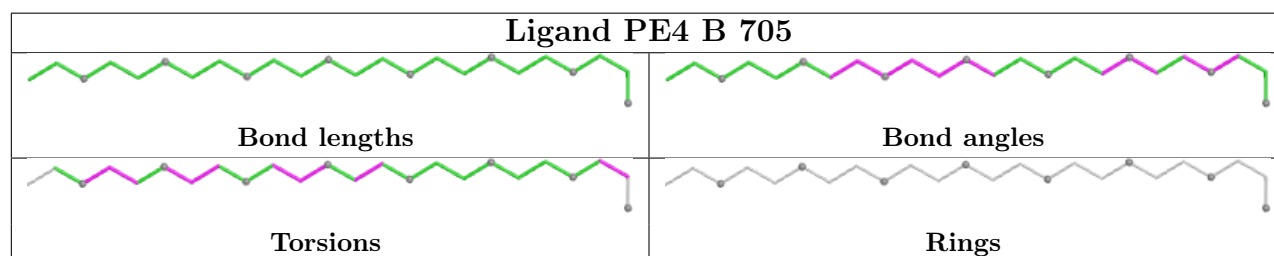
Mol	Chain	Res	Type	Atoms
5	B	705	PE4	C10-C9-O5-C8
5	C	1004	PE4	C13-C14-O8-C15

There are no ring outliers.

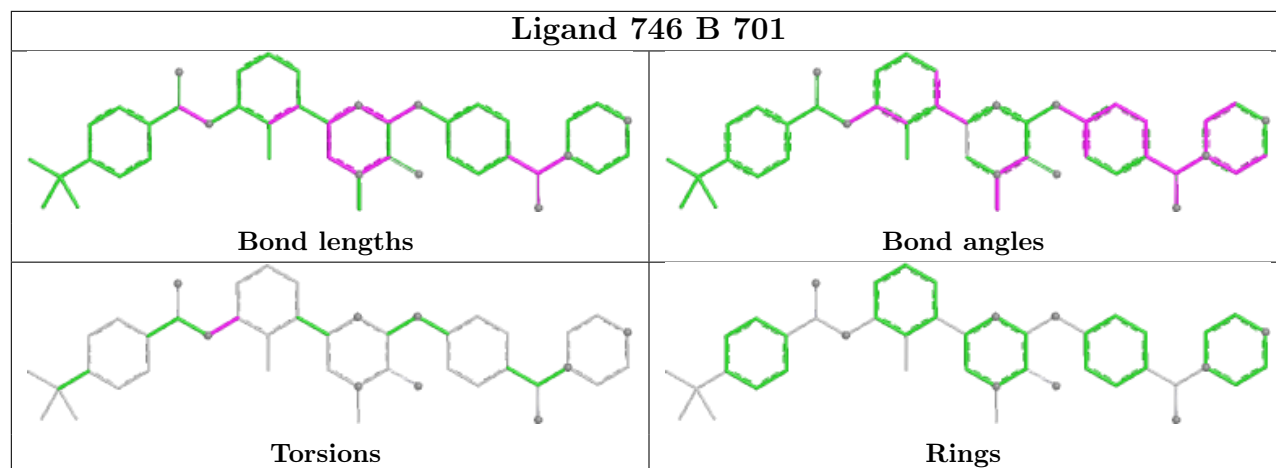
10 monomers are involved in 32 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	705	PE4	8	0
3	D	702	GOL	1	0
3	A	702	GOL	1	0
2	B	701	746	6	0
4	A	703[B]	BME	1	0
2	A	701	746	3	0
2	D	701	746	2	0
5	C	1004	PE4	6	0
2	C	1001	746	3	0
4	C	1003[B]	BME	1	0

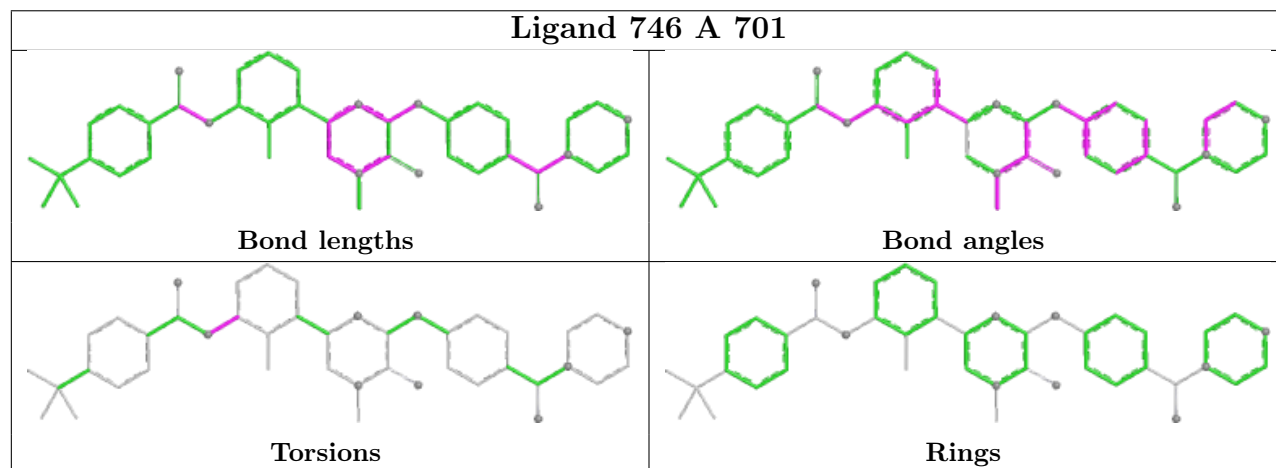
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



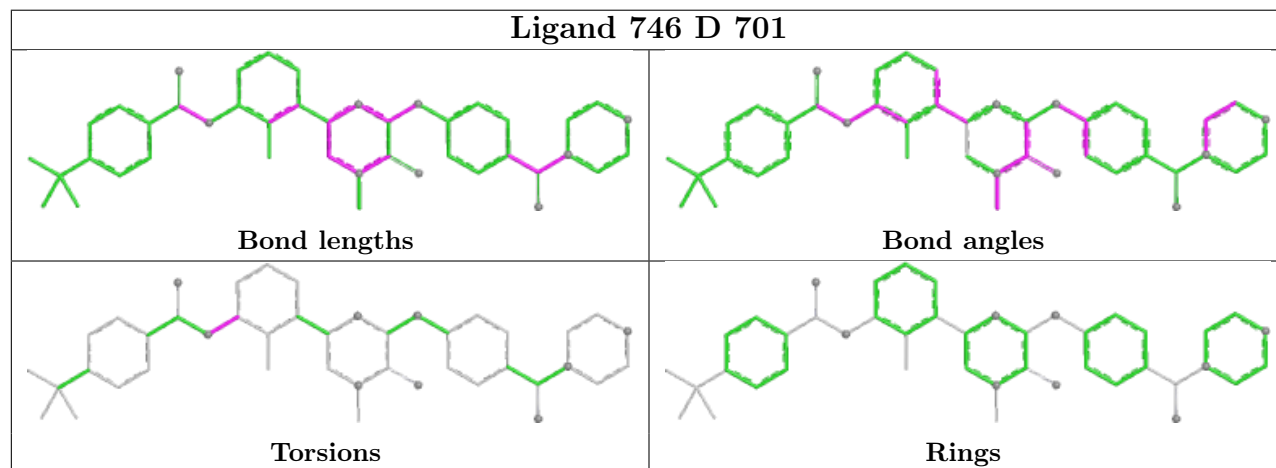
Ligand 746 B 701



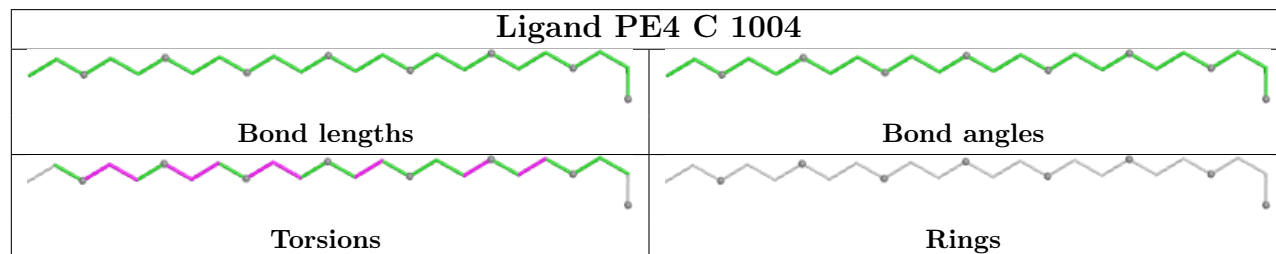
Ligand 746 A 701

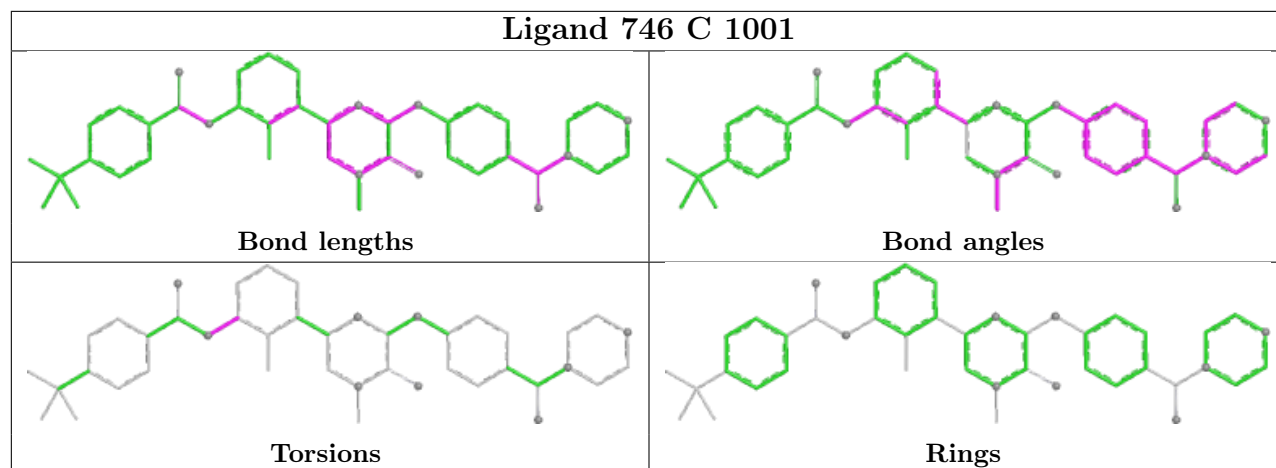


Ligand 746 D 701



Ligand PE4 C 1004





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	266/266 (100%)	-1.10	0 100 100	9, 21, 46, 83	11 (4%)
1	B	266/266 (100%)	-1.06	0 100 100	10, 21, 44, 78	14 (5%)
1	C	266/266 (100%)	-1.07	0 100 100	9, 22, 45, 78	12 (4%)
1	D	265/266 (99%)	-1.07	0 100 100	9, 21, 47, 72	9 (3%)
All	All	1063/1064 (99%)	-1.07	0 100 100	9, 21, 47, 83	46 (4%)

There are no RSRZ outliers to report.

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 [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
3	GOL	D	702	6/6	0.97	0.07	25,33,45,54	0
4	BME	A	703[A]	4/4	0.97	0.08	22,27,32,38	10
4	BME	A	703[B]	4/4	0.97	0.08	23,28,31,35	10
5	PE4	C	1004	24/24	0.97	0.07	30,48,73,73	0

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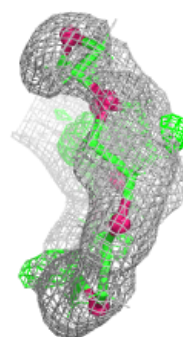
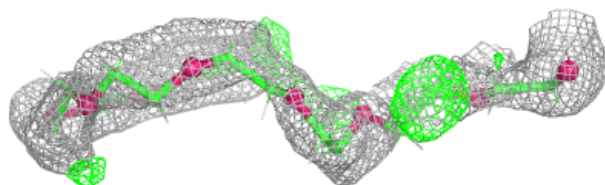
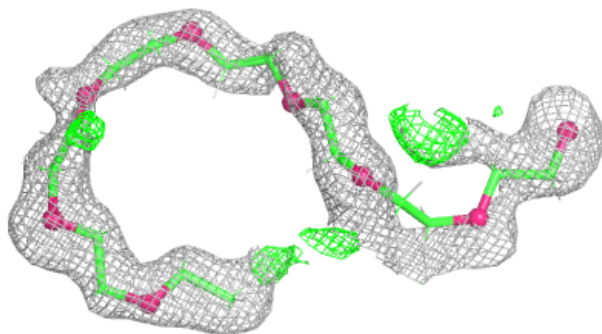
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	GOL	D	705	6/6	0.98	0.05	24,38,49,56	0
4	BME	B	704[A]	4/4	0.98	0.06	26,31,33,39	10
4	BME	B	704[B]	4/4	0.98	0.06	25,30,42,51	10
5	PE4	B	705	24/24	0.98	0.06	30,50,64,68	0
3	GOL	B	702	6/6	0.98	0.05	26,36,45,50	0
2	746	B	701	43/43	0.99	0.04	11,14,44,61	0
3	GOL	D	703	6/6	0.99	0.05	17,40,58,58	0
3	GOL	D	704	6/6	0.99	0.04	20,29,47,57	0
2	746	C	1001	43/43	0.99	0.04	11,14,42,61	0
2	746	D	701	43/43	0.99	0.04	12,16,41,49	0
3	GOL	A	702	6/6	0.99	0.04	15,26,52,52	0
2	746	A	701	43/43	0.99	0.04	11,16,39,49	0
3	GOL	B	703	6/6	0.99	0.04	19,26,35,40	0
4	BME	C	1003[A]	4/4	0.99	0.06	23,28,32,39	10
4	BME	C	1003[B]	4/4	0.99	0.06	15,27,37,45	10
3	GOL	C	1002[A]	6/6	0.99	0.04	17,22,35,43	14
3	GOL	C	1002[B]	6/6	0.99	0.04	17,23,31,31	14

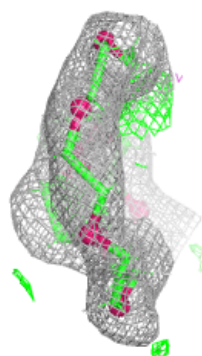
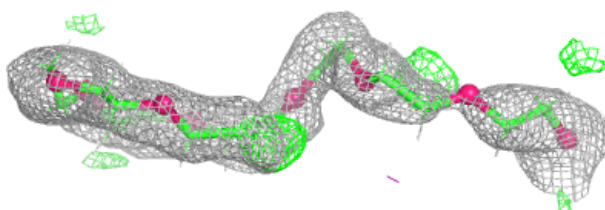
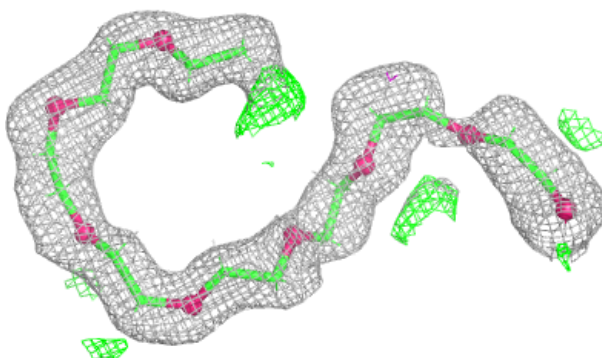
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around PE4 C 1004:

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

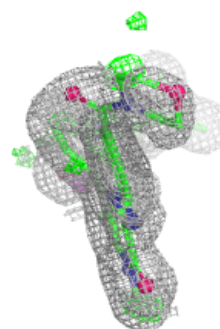
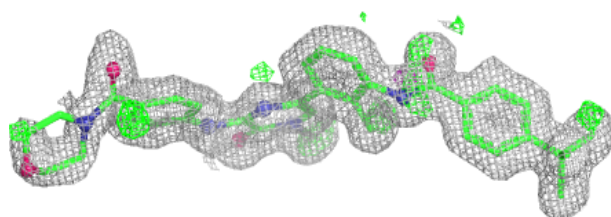
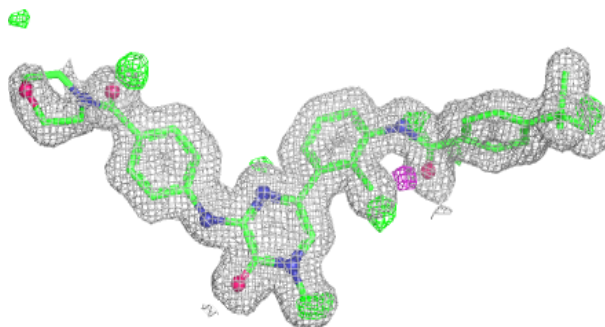
**Electron density around PE4 B 705:**

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

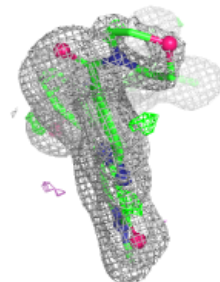
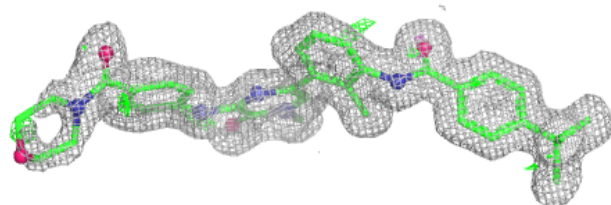
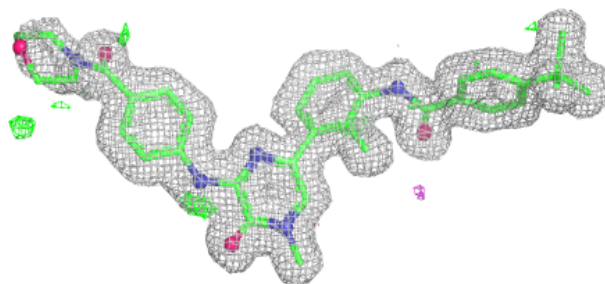


Electron density around 746 B 701:

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

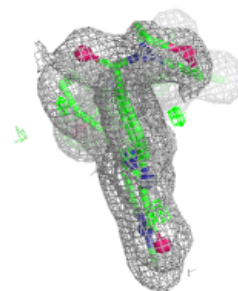
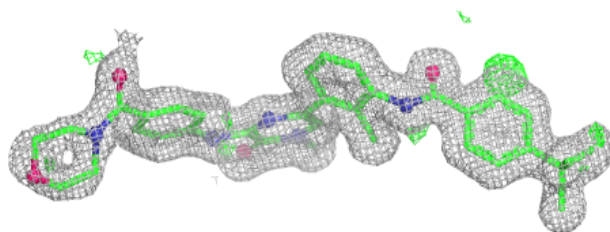
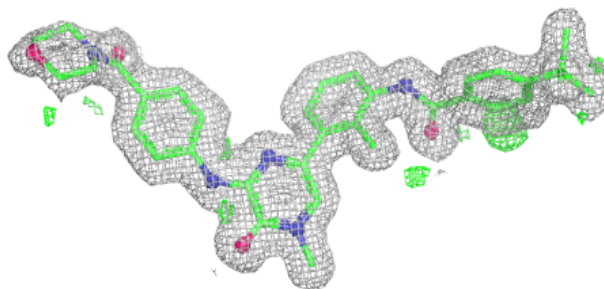
**Electron density around 746 C 1001:**

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

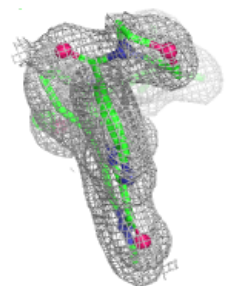
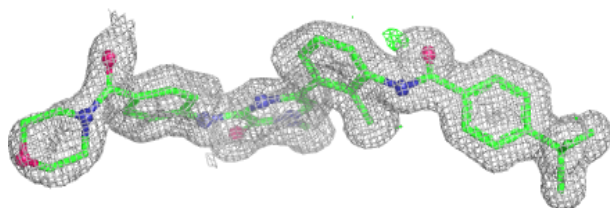
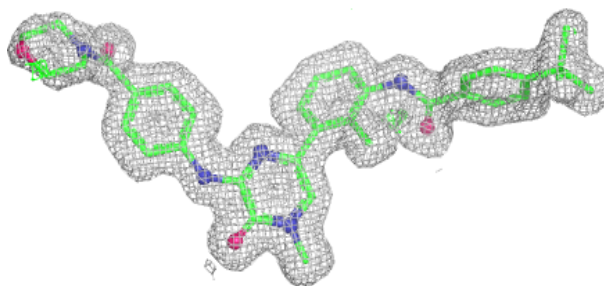


Electron density around 746 D 701:

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

**Electron density around 746 A 701:**

$2mF_o-DF_c$ (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.