Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 03:41 am BST

PDB ID	:	4Y5D
Title	:	CRYSTAL STRUCTURE OF ALiS2-STREPTAVIDIN COMPLEX
Authors	:	Sugiyama, S.; Terai, T.; Kohno, M.; Ishida, H.; Nagano, T.
Deposited on	:	2015-02-11
Resolution	:	1.20 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 following versions of software and data (see references ⓘ) were used in the production of this report:

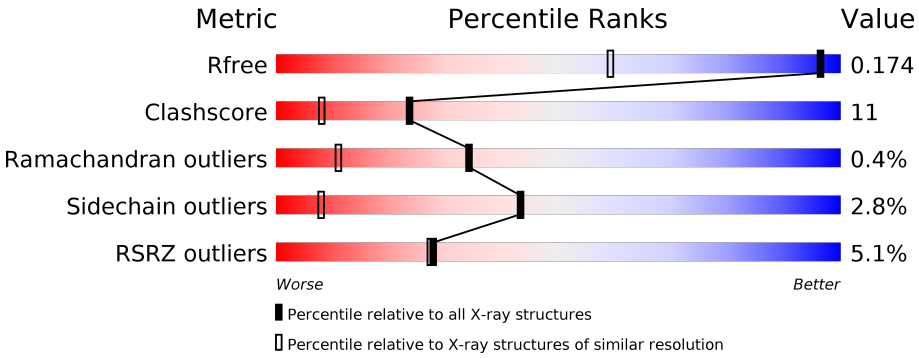
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

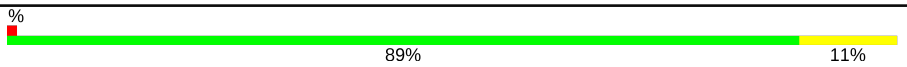
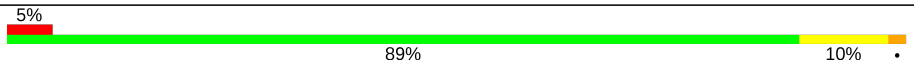
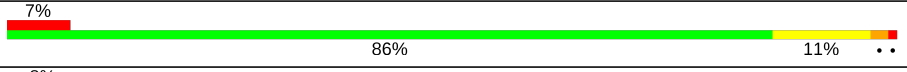
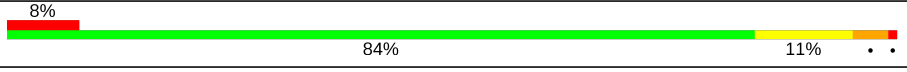
The reported resolution of this entry is 1.20 Å.

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}	130704	1223 (1.22-1.18)
Clashscore	141614	1286 (1.22-1.18)
Ramachandran outliers	138981	1240 (1.22-1.18)
Sidechain outliers	138945	1239 (1.22-1.18)
RSRZ outliers	127900	1200 (1.22-1.18)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	122	
1	B	122	
1	C	122	
1	D	122	

2 Entry composition

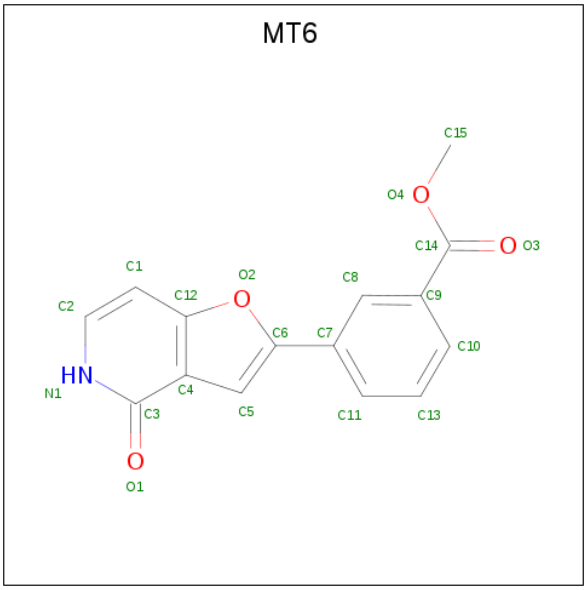
There are 6 unique types of molecules in this entry. The entry contains 4380 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Streptavidin.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	122	Total	C	N	O	0	5	0
			952	593	167	192			
1	B	122	Total	C	N	O	0	6	0
			954	593	164	197			
1	C	122	Total	C	N	O	0	9	0
			975	608	167	200			
1	D	122	Total	C	N	O	0	6	0
			955	596	165	194			

- Molecule 2 is methyl 3-(4-oxo-4,5-dihydrofuro[3,2-c]pyridin-2-yl)benzoate (three-letter code: MT6) (formula: $C_{15}H_{11}NO_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			20	15	1	4		
2	B	1	Total	C	N	O	0	0
			20	15	1	4		

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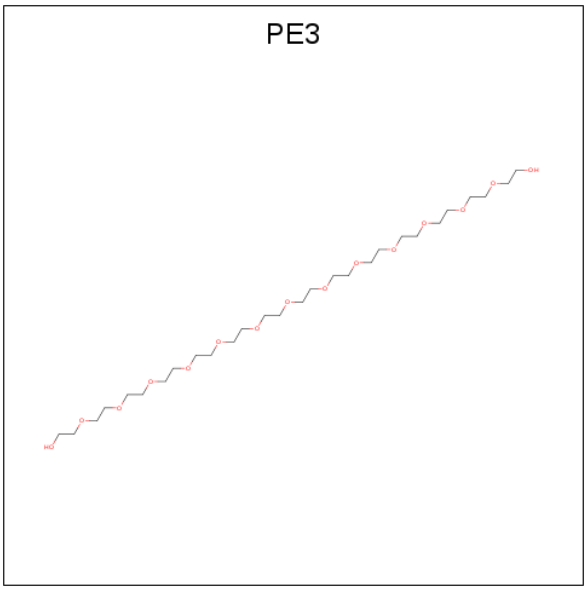
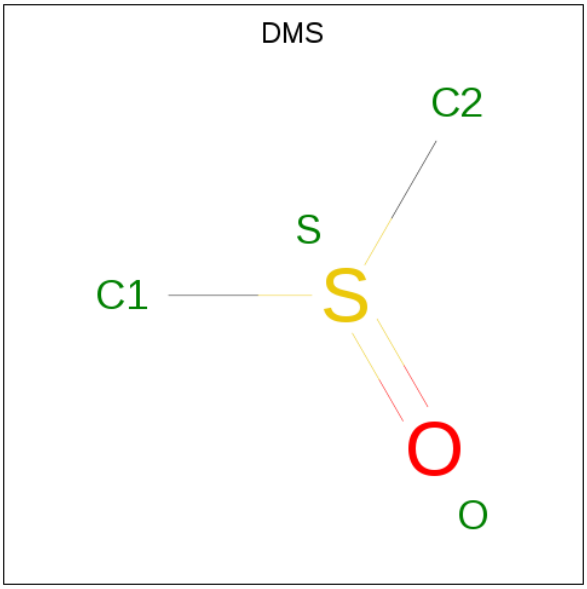
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	D	1	Total	C	N	O	0	0
			20	15	1	4		

- Molecule 3 is 3,6,9,12,15,18,21,24,27,30,33,36,39-TRIDECAOXAHENTETRACONTANE-1 ,41-DIOL (three-letter code: PE3) (formula: $C_{28}H_{58}O_{15}$).



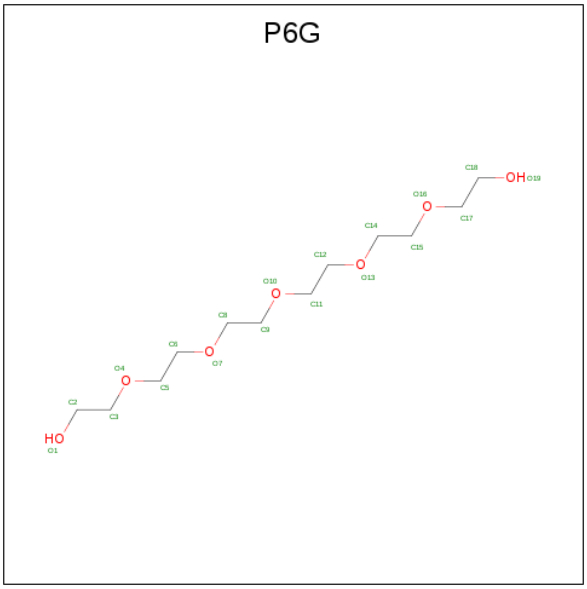
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			28	18	10		

- Molecule 4 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C_2H_6OS).



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

- Molecule 5 is HEXAETHYLENE GLYCOL (three-letter code: P6G) (formula: $C_{12}H_{26}O_7$).



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

- Molecule 6 is water.

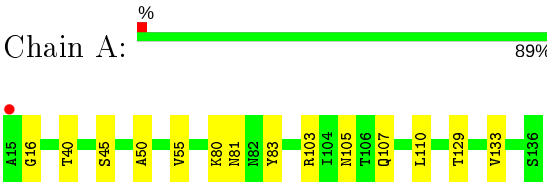
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	136	Total O 143 143	0	6
6	B	99	Total O 104 104	0	5
6	C	82	Total O 89 89	0	5
6	D	96	Total O 102 102	0	5

3 Residue-property plots (i)

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

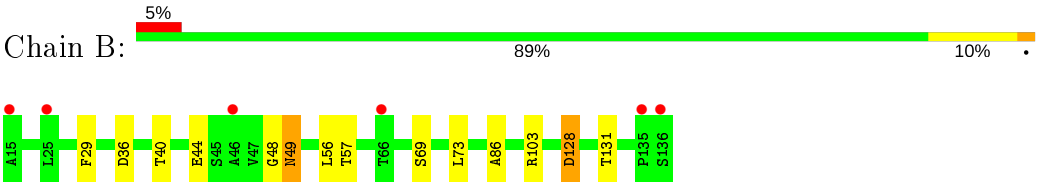
- Molecule 1: Streptavidin

Chain A:



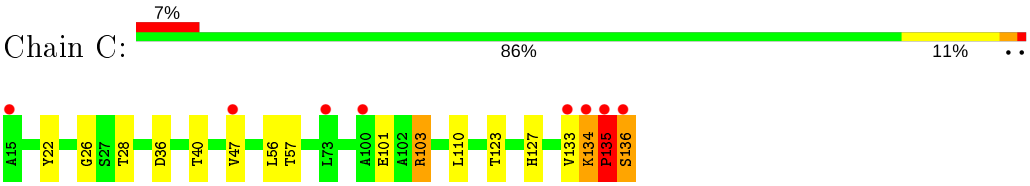
- Molecule 1: Streptavidin

Chain B:



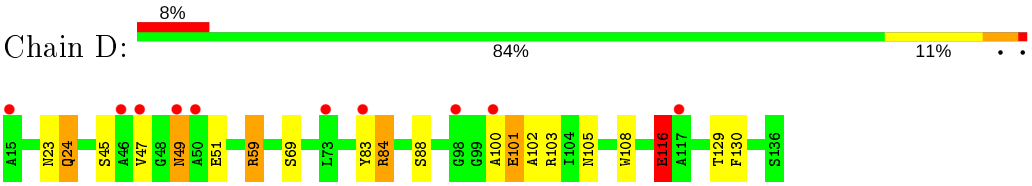
- Molecule 1: Streptavidin

Chain C:



- Molecule 1: Streptavidin

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	57.93Å 83.77Å 45.95Å 90.00° 98.75° 90.00°	Depositor
Resolution (Å)	50.00 – 1.20 30.79 – 1.20	Depositor EDS
% Data completeness (in resolution range)	98.0 (50.00-1.20) 98.1 (30.79-1.20)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.82 (at 1.20Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.138 , 0.174 0.140 , 0.174	Depositor DCC
R_{free} test set	6649 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å^2)	10.9	Xtriage
Anisotropy	0.385	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 54.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	4380	wwPDB-VP
Average B, all atoms (Å^2)	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.57% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: DMS, MT6, P6G, PE3

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	1.06	1/975 (0.1%)	1.06	0/1333
1	B	1.11	2/977 (0.2%)	1.09	4/1337 (0.3%)
1	C	1.11	3/998 (0.3%)	1.10	4/1366 (0.3%)
1	D	1.02	2/978 (0.2%)	1.08	2/1338 (0.1%)
All	All	1.08	8/3928 (0.2%)	1.08	10/5374 (0.2%)

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	C	0	1
1	D	0	1
All	All	0	2

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	135	PRO	N-CD	5.74	1.55	1.47
1	A	83	TYR	CG-CD1	5.61	1.46	1.39
1	B	29	PHE	CG-CD2	-5.60	1.30	1.38
1	C	22	TYR	CD2-CE2	5.59	1.47	1.39
1	D	116	GLU	CD-OE1	5.47	1.31	1.25
1	B	69	SER	CB-OG	-5.12	1.35	1.42
1	D	69	SER	CB-OG	-5.01	1.35	1.42
1	C	134	LYS	C-N	5.01	1.43	1.34

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	135	PRO	CA-N-CD	-6.60	102.26	111.50
1	C	103	ARG	NE-CZ-NH1	5.56	123.08	120.30
1	D	59	ARG	NE-CZ-NH2	-5.45	117.57	120.30
1	B	73[A]	LEU	CB-CG-CD1	5.29	120.00	111.00
1	B	73[B]	LEU	CB-CG-CD1	5.29	120.00	111.00
1	D	84	ARG	NE-CZ-NH2	-5.22	117.69	120.30
1	C	36	ASP	CB-CG-OD1	5.12	122.91	118.30
1	C	22	TYR	CD1-CE1-CZ	-5.07	115.24	119.80
1	B	128[A]	ASP	CB-CG-OD2	-5.05	113.76	118.30
1	B	128[B]	ASP	CB-CG-OD2	-5.05	113.76	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	134	LYS	Peptide
1	D	45	SER	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	952	0	894	22	0
1	B	954	0	885	10	0
1	C	975	0	913	28	0
1	D	955	0	896	22	0
2	A	20	0	11	6	0
2	B	20	0	11	2	0
2	D	20	0	11	2	0
3	A	28	0	37	16	0
4	C	4	0	6	0	0
5	C	14	0	18	1	0
6	A	143	0	0	6	0
6	B	104	0	0	4	0
6	C	89	0	0	2	0
6	D	102	0	0	2	0
All	All	4380	0	3682	86	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 11.

All (86) 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:80:LYS:HZ1	3:A:201:PE3:H362	1.08	1.14
1:A:80:LYS:HZ2	3:A:201:PE3:H302	1.16	1.08
1:B:40[B]:THR:HG22	6:B:370[B]:HOH:O	1.74	0.85
1:A:40:THR:HG22	6:A:368[A]:HOH:O	1.74	0.84
1:A:80:LYS:NZ	3:A:201:PE3:H362	1.92	0.84
1:C:103:ARG:HG2	1:C:103:ARG:HH11	1.39	0.84
1:C:133:VAL:HB	1:C:136:SER:HB2	1.60	0.83
1:C:40[B]:THR:HG23	6:C:302:HOH:O	1.77	0.82
1:D:100:ALA:N	1:D:101:GLU:HA	1.94	0.82
1:C:133:VAL:CB	1:C:136:SER:HB2	2.09	0.82
1:D:101:GLU:HG2	1:D:102:ALA:H	1.45	0.81
1:A:103:ARG:HH11	1:A:129[A]:THR:HG21	1.50	0.76
1:C:56[B]:LEU:O	1:C:57[B]:THR:HG22	1.85	0.76
1:A:45:SER:OG	2:A:200:MT6:H2	1.85	0.76
1:D:103:ARG:HH11	1:D:129[A]:THR:HG21	1.52	0.74
1:C:57[B]:THR:HG22	6:C:302:HOH:O	1.92	0.69
1:D:101:GLU:CG	1:D:102:ALA:H	2.04	0.69
3:A:201:PE3:H332	6:B:367:HOH:O	1.94	0.68
1:A:107[B]:GLN:HE22	1:C:127:HIS:HD2	1.43	0.67
1:B:49:ASN:H	1:B:49:ASN:HD22	1.40	0.67
1:C:57[B]:THR:HG21	6:D:347:HOH:O	1.93	0.67
1:A:80:LYS:NZ	3:A:201:PE3:H331	2.10	0.66
1:C:133:VAL:HG21	1:C:136:SER:CB	2.25	0.66
1:C:101:GLU:OE2	1:C:103:ARG:NH2	2.29	0.66
1:C:28[A]:THR:OG1	1:C:47:VAL:HG22	1.96	0.65
1:A:81:ASN:HA	3:A:201:PE3:H271	1.77	0.65
1:A:103:ARG:HH11	1:A:129[A]:THR:CG2	2.10	0.64
3:A:201:PE3:H272	6:A:384:HOH:O	1.96	0.64
6:A:369:HOH:O	1:B:57[B]:THR:HG21	1.97	0.64
1:B:103:ARG:HD3	1:B:131:THR:HG22	1.80	0.64
1:D:47:VAL:HB	1:D:49:ASN:HD22	1.64	0.63
1:A:105:ASN:OD1	1:A:129[A]:THR:HG23	1.99	0.63
1:D:24:GLN:H	1:D:24:GLN:NE2	1.96	0.62
1:C:133:VAL:CG2	1:C:136:SER:HB2	2.29	0.62
1:C:103:ARG:CG	1:C:103:ARG:HH11	2.13	0.61
1:D:103:ARG:HH11	1:D:129[A]:THR:CG2	2.15	0.59
1:D:105:ASN:OD1	1:D:129[A]:THR:HG23	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:56[B]:LEU:O	1:C:57[B]:THR:CG2	2.50	0.59
1:C:133:VAL:HG21	1:C:136:SER:HB2	1.86	0.58
1:A:50:ALA:HB2	2:A:200:MT6:H9	1.85	0.58
1:B:86:ALA:CB	2:B:200:MT6:O3	2.52	0.58
3:A:201:PE3:H242	6:A:328:HOH:O	2.04	0.57
1:B:36[B]:ASP:CG	6:B:384:HOH:O	2.42	0.56
1:B:40[B]:THR:CG2	6:B:370[B]:HOH:O	2.40	0.56
1:A:80:LYS:NZ	3:A:201:PE3:H391	2.22	0.55
2:A:200:MT6:H5	6:A:433:HOH:O	2.06	0.55
1:C:133:VAL:CG2	1:C:136:SER:H	2.20	0.55
1:D:51:GLU:HG3	1:D:83:TYR:CG	2.42	0.54
1:D:47:VAL:HB	1:D:49:ASN:ND2	2.22	0.53
1:D:101:GLU:HG2	1:D:102:ALA:N	2.18	0.52
1:C:133:VAL:CG2	1:C:136:SER:N	2.73	0.52
1:B:44:GLU:OE1	1:B:48:GLY:HA2	2.09	0.52
1:A:110[B]:LEU:HD21	2:A:200:MT6:H1	1.90	0.51
1:D:101:GLU:CG	1:D:102:ALA:N	2.73	0.51
1:A:80:LYS:HZ2	3:A:201:PE3:H331	1.74	0.51
1:D:24:GLN:HE21	1:D:24:GLN:H	1.59	0.51
1:D:88[A]:SER:OG	2:D:200:MT6:H7	2.12	0.50
1:A:110[B]:LEU:CD2	2:A:200:MT6:H1	2.41	0.50
1:D:108:TRP:CE2	2:D:200:MT6:H4	2.48	0.49
1:A:80:LYS:HZ2	3:A:201:PE3:C30	2.06	0.48
1:C:103:ARG:NH1	1:C:103:ARG:CG	2.72	0.48
1:D:47:VAL:HG12	6:D:323:HOH:O	2.13	0.48
1:C:57[B]:THR:HG23	1:D:59:ARG:HD3	1.96	0.47
1:A:80:LYS:NZ	3:A:201:PE3:H302	2.04	0.47
1:C:133:VAL:HG23	1:C:136:SER:H	1.79	0.47
1:D:51:GLU:HB3	1:D:84:ARG:CZ	2.45	0.46
1:D:116:GLU:CD	1:D:116:GLU:H	2.18	0.46
1:A:55:VAL:HG23	3:A:201:PE3:H241	1.97	0.45
1:C:101:GLU:HG2	1:C:103:ARG:HH22	1.81	0.45
1:D:51:GLU:HG3	1:D:83:TYR:CD1	2.52	0.45
1:A:103:ARG:HD3	1:A:129[A]:THR:CG2	2.47	0.44
1:A:80:LYS:HZ1	3:A:201:PE3:H391	1.82	0.44
3:A:201:PE3:H272	3:A:201:PE3:H241	1.70	0.43
1:C:133:VAL:HG23	1:C:136:SER:N	2.34	0.42
5:C:202:P6G:H31	5:C:202:P6G:H62	1.48	0.42
1:A:80:LYS:HZ1	3:A:201:PE3:H331	1.83	0.42
1:C:133:VAL:HG21	1:C:136:SER:N	2.34	0.42
1:C:103:ARG:NH1	1:C:103:ARG:HG2	2.16	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:57[A]:THR:HG22	1:D:59:ARG:HG2	2.01	0.41
1:C:26:GLY:O	1:C:47:VAL:HG23	2.20	0.41
1:C:56[B]:LEU:C	1:C:57[B]:THR:CG2	2.88	0.41
1:C:110[B]:LEU:O	1:C:123:THR:HA	2.21	0.41
1:B:86:ALA:HB3	2:B:200:MT6:O3	2.21	0.41
1:B:103:ARG:CD	1:B:131:THR:HG22	2.49	0.41
2:A:200:MT6:C15	6:A:433:HOH:O	2.66	0.40
1:D:23:ASN:HB3	1:D:130:PHE:CE2	2.56	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	125/122 (102%)	121 (97%)	3 (2%)	1 (1%)	19 3
1	B	126/122 (103%)	124 (98%)	2 (2%)	0	100 100
1	C	129/122 (106%)	123 (95%)	5 (4%)	1 (1%)	19 3
1	D	126/122 (103%)	122 (97%)	4 (3%)	0	100 100
All	All	506/488 (104%)	490 (97%)	14 (3%)	2 (0%)	34 11

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	135	PRO
1	A	16	GLY

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	95/90 (106%)	94 (99%)	1 (1%)	73 41
1	B	96/90 (107%)	92 (96%)	4 (4%)	30 3
1	C	99/90 (110%)	97 (98%)	2 (2%)	55 17
1	D	96/90 (107%)	92 (96%)	4 (4%)	30 3
All	All	386/360 (107%)	375 (97%)	11 (3%)	43 8

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	133	VAL
1	B	49	ASN
1	B	56	LEU
1	B	128[A]	ASP
1	B	128[B]	ASP
1	C	135	PRO
1	C	136	SER
1	D	24	GLN
1	D	49	ASN
1	D	101	GLU
1	D	116	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	24	GLN
1	B	49	ASN
1	B	82	ASN
1	B	127	HIS
1	C	82	ASN
1	D	24	GLN
1	D	49	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 carbohydrates in this entry.

5.6 Ligand geometry (i)

7 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	P6G	C	203	-	6,6,18	0.44	0	5,5,17	0.82	0
2	MT6	A	200	-	16,22,22	3.41	8 (50%)	19,31,31	3.74	8 (42%)
4	DMS	C	201	-	3,3,3	0.47	0	3,3,3	0.29	0
3	PE3	A	201	-	27,27,42	1.15	2 (7%)	26,26,41	1.36	5 (19%)
2	MT6	D	200	-	16,22,22	2.49	6 (37%)	19,31,31	3.15	6 (31%)
2	MT6	B	200	-	16,22,22	3.21	7 (43%)	19,31,31	4.90	12 (63%)
5	P6G	C	202	-	6,6,18	0.40	0	5,5,17	0.45	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	P6G	C	203	-	-	0/4/4/16	-
2	MT6	A	200	-	-	4/8/10/10	0/3/3/3
3	PE3	A	201	-	-	12/25/25/40	-
2	MT6	D	200	-	-	0/8/10/10	0/3/3/3
2	MT6	B	200	-	-	4/8/10/10	0/3/3/3
5	P6G	C	202	-	-	3/4/4/16	-

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	200	MT6	C1-C2	8.31	1.48	1.36
2	B	200	MT6	C1-C2	8.02	1.48	1.36
2	A	200	MT6	C8-C7	-6.86	1.27	1.39
2	B	200	MT6	O4-C14	6.26	1.47	1.33
2	B	200	MT6	O1-C3	5.29	1.37	1.24
2	D	200	MT6	O4-C14	5.18	1.44	1.33
2	A	200	MT6	C2-N1	5.03	1.45	1.34
2	D	200	MT6	C2-N1	4.49	1.44	1.34
2	D	200	MT6	C1-C2	4.31	1.42	1.36
2	B	200	MT6	C4-C12	3.57	1.51	1.43
2	D	200	MT6	O1-C3	3.48	1.33	1.24
2	A	200	MT6	O1-C3	2.96	1.32	1.24
2	D	200	MT6	C4-C12	2.68	1.49	1.43
2	A	200	MT6	O4-C15	2.62	1.51	1.45
2	A	200	MT6	C11-C7	-2.55	1.33	1.39
3	A	201	PE3	O28-C29	2.52	1.53	1.42
2	A	200	MT6	C3-N1	2.49	1.37	1.33
2	B	200	MT6	C7-C6	2.42	1.50	1.46
3	A	201	PE3	O43-C42	2.42	1.54	1.42
2	D	200	MT6	C9-C14	-2.15	1.44	1.50
2	A	200	MT6	C7-C6	-2.09	1.42	1.46
2	B	200	MT6	C9-C14	-2.05	1.45	1.50
2	B	200	MT6	C2-N1	2.02	1.38	1.34

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	200	MT6	C2-C1-C12	-16.25	105.44	119.31
2	A	200	MT6	C2-C1-C12	-12.82	108.37	119.31
2	D	200	MT6	C2-C1-C12	-10.38	110.45	119.31
2	B	200	MT6	C1-C2-N1	8.39	132.08	123.81
2	B	200	MT6	O4-C14-C9	6.49	122.18	112.34
2	D	200	MT6	O4-C14-C9	4.85	119.69	112.34
2	A	200	MT6	C13-C10-C9	-4.81	114.66	120.34
2	A	200	MT6	C10-C9-C8	4.73	124.84	119.24
2	B	200	MT6	C10-C9-C8	3.87	123.82	119.24
2	D	200	MT6	C2-N1-C3	3.82	125.56	116.43
2	B	200	MT6	C15-O4-C14	3.65	122.86	115.83
2	B	200	MT6	C8-C9-C14	-3.40	113.50	120.10
2	D	200	MT6	C7-C8-C9	-3.26	117.56	121.09
2	A	200	MT6	C5-C6-C7	3.24	136.74	129.68
2	A	200	MT6	C13-C11-C7	3.03	124.38	120.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	201	PE3	O22-C21-C20	2.97	123.81	110.39
2	B	200	MT6	C13-C10-C9	-2.75	117.08	120.34
2	D	200	MT6	C11-C7-C8	2.63	121.88	118.16
2	B	200	MT6	C3-C4-C12	2.57	120.41	117.53
2	B	200	MT6	O3-C14-C9	-2.56	113.69	122.09
2	A	200	MT6	O4-C14-O3	-2.52	118.53	123.45
3	A	201	PE3	O43-C42-C41	2.49	126.23	111.81
2	A	200	MT6	C1-C2-N1	2.41	126.19	123.81
2	A	200	MT6	C15-O4-C14	2.35	120.36	115.83
2	B	200	MT6	C7-C8-C9	-2.25	118.65	121.09
3	A	201	PE3	O28-C27-C26	2.21	120.37	110.39
3	A	201	PE3	O19-C18-C17	2.17	119.58	110.07
2	B	200	MT6	C5-C6-C7	-2.16	124.98	129.68
2	D	200	MT6	C8-C7-C6	-2.13	117.73	120.42
3	A	201	PE3	O40-C39-C38	2.11	119.92	110.39
2	B	200	MT6	C2-N1-C3	2.00	121.22	116.43

There are no chirality outliers.

All (23) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	202	P6G	C6-C5-O4-C3
2	B	200	MT6	O4-C14-C9-C10
2	B	200	MT6	O4-C14-C9-C8
2	B	200	MT6	O3-C14-C9-C8
2	B	200	MT6	O3-C14-C9-C10
3	A	201	PE3	C24-C23-O22-C21
3	A	201	PE3	O40-C41-C42-O43
2	A	200	MT6	C9-C14-O4-C15
2	A	200	MT6	O3-C14-O4-C15
5	C	202	P6G	O4-C5-C6-O7
3	A	201	PE3	O25-C26-C27-O28
3	A	201	PE3	O22-C23-C24-O25
3	A	201	PE3	C42-C41-O40-C39
3	A	201	PE3	C38-C39-O40-C41
3	A	201	PE3	C21-C20-O19-C18
3	A	201	PE3	C26-C27-O28-C29
2	A	200	MT6	O4-C14-C9-C8
2	A	200	MT6	O4-C14-C9-C10
3	A	201	PE3	C30-C29-O28-C27
3	A	201	PE3	O19-C20-C21-O22
3	A	201	PE3	O37-C38-C39-O40

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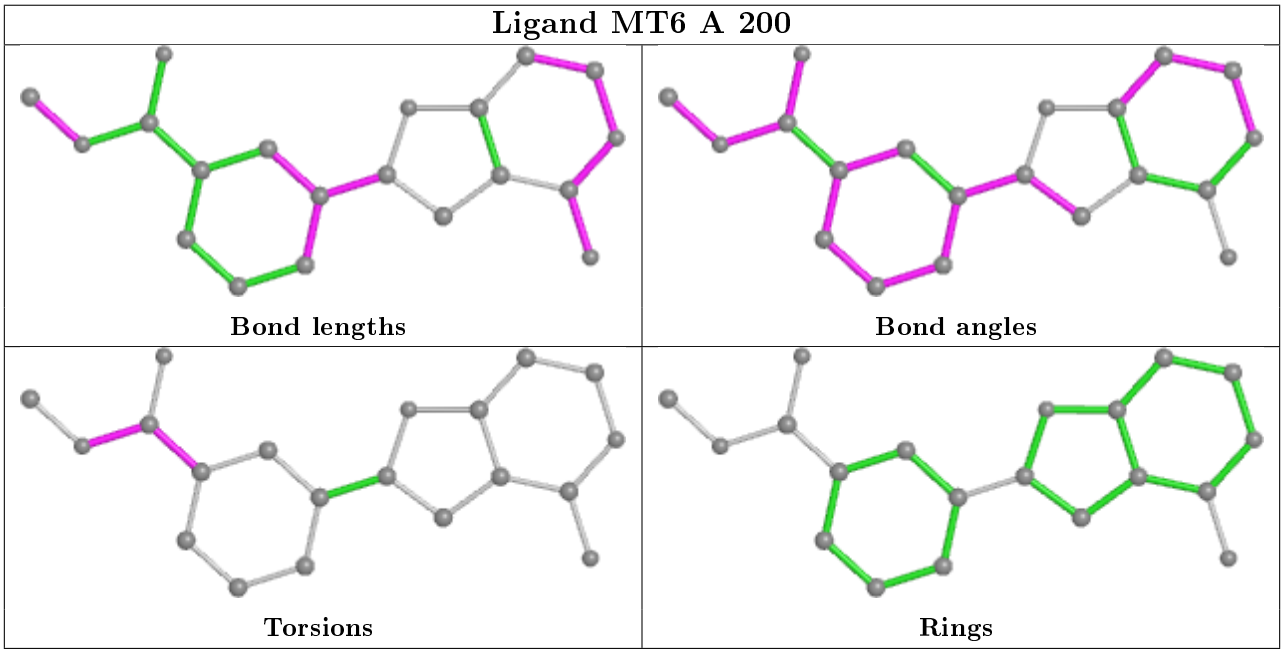
Mol	Chain	Res	Type	Atoms
5	C	202	P6G	O1-C2-C3-O4
3	A	201	PE3	O31-C32-C33-O34

There are no ring outliers.

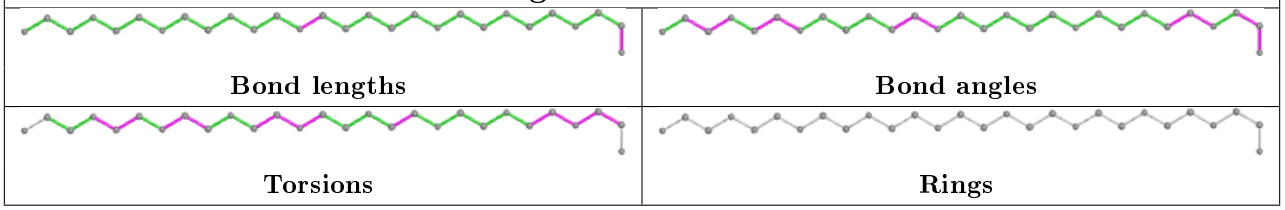
5 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	200	MT6	6	0
3	A	201	PE3	16	0
2	D	200	MT6	2	0
2	B	200	MT6	2	0
5	C	202	P6G	1	0

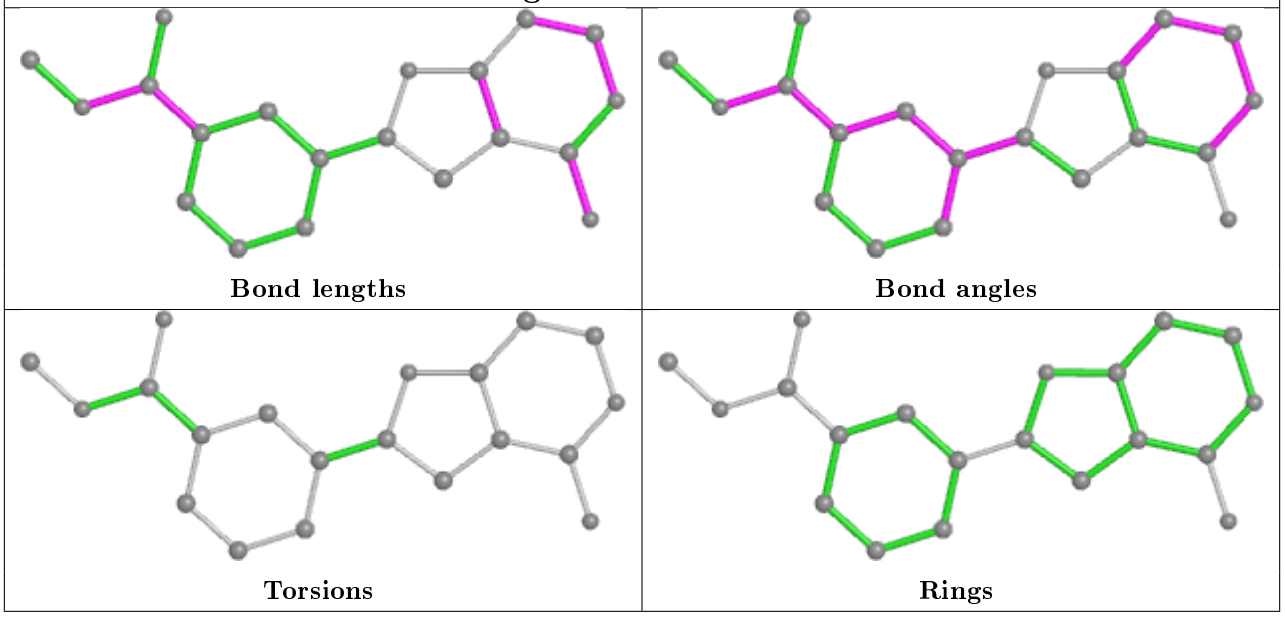
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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



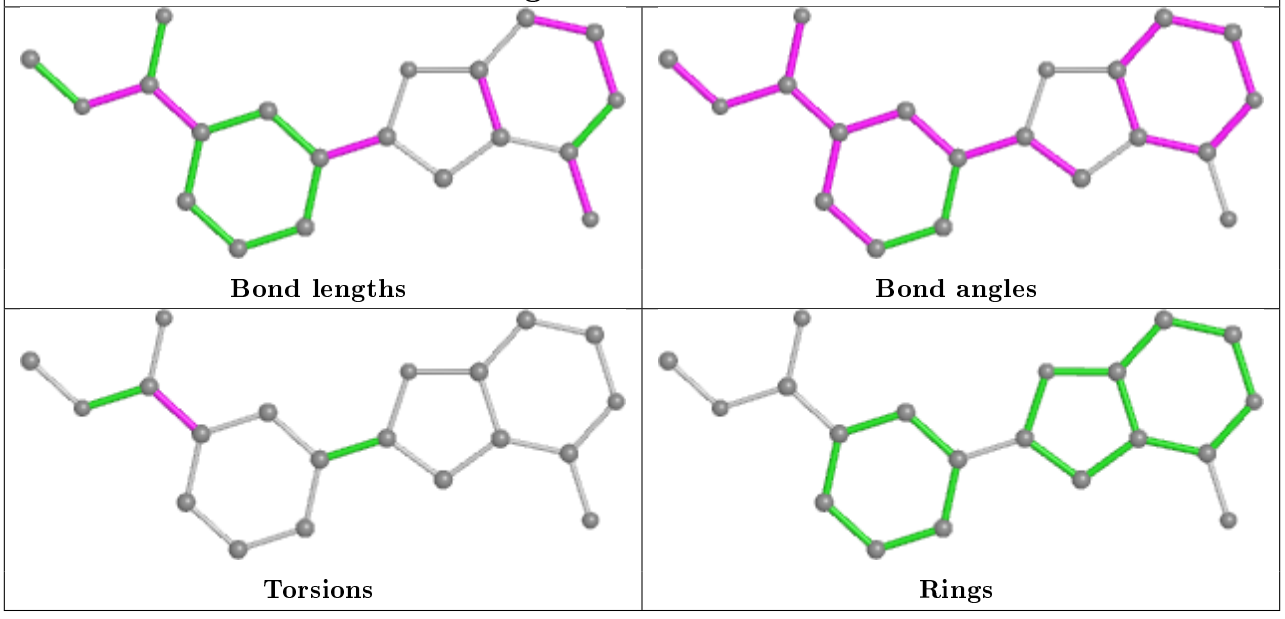
Ligand PE3 A 201

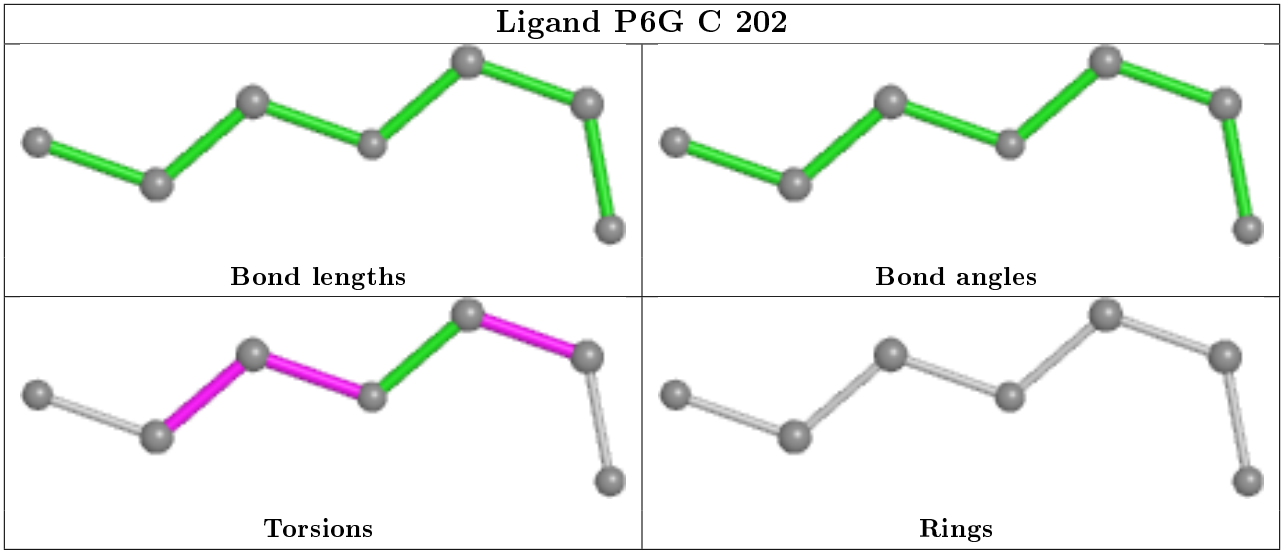


Ligand MT6 D 200



Ligand MT6 B 200





5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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	122/122 (100%)	-0.18	1 (0%)	86	86	8, 13, 27, 43	6 (4%)
1	B	122/122 (100%)	0.02	6 (4%)	29	29	9, 14, 32, 44	12 (9%)
1	C	122/122 (100%)	0.11	8 (6%)	18	17	7, 13, 35, 56	9 (7%)
1	D	122/122 (100%)	0.26	10 (8%)	11	11	8, 15, 42, 64	9 (7%)
All	All	488/488 (100%)	0.05	25 (5%)	28	27	7, 14, 35, 64	36 (7%)

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	15	ALA	11.9
1	D	15	ALA	9.7
1	C	15	ALA	9.0
1	D	47	VAL	6.9
1	C	135	PRO	6.2
1	D	100	ALA	6.0
1	B	135	PRO	5.6
1	C	133	VAL	3.9
1	B	136	SER	3.7
1	B	46	ALA	3.6
1	C	47	VAL	3.4
1	D	117	ALA	3.2
1	C	134	LYS	3.1
1	D	83	TYR	3.1
1	D	98	GLY	2.9
1	D	50	ALA	2.7
1	D	46	ALA	2.5
1	B	66	THR	2.3
1	D	49	ASN	2.3
1	B	25	LEU	2.3
1	C	100	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	73[A]	LEU	2.2
1	B	15	ALA	2.1
1	C	73[A]	LEU	2.0
1	C	136	SER	2.0

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

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

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

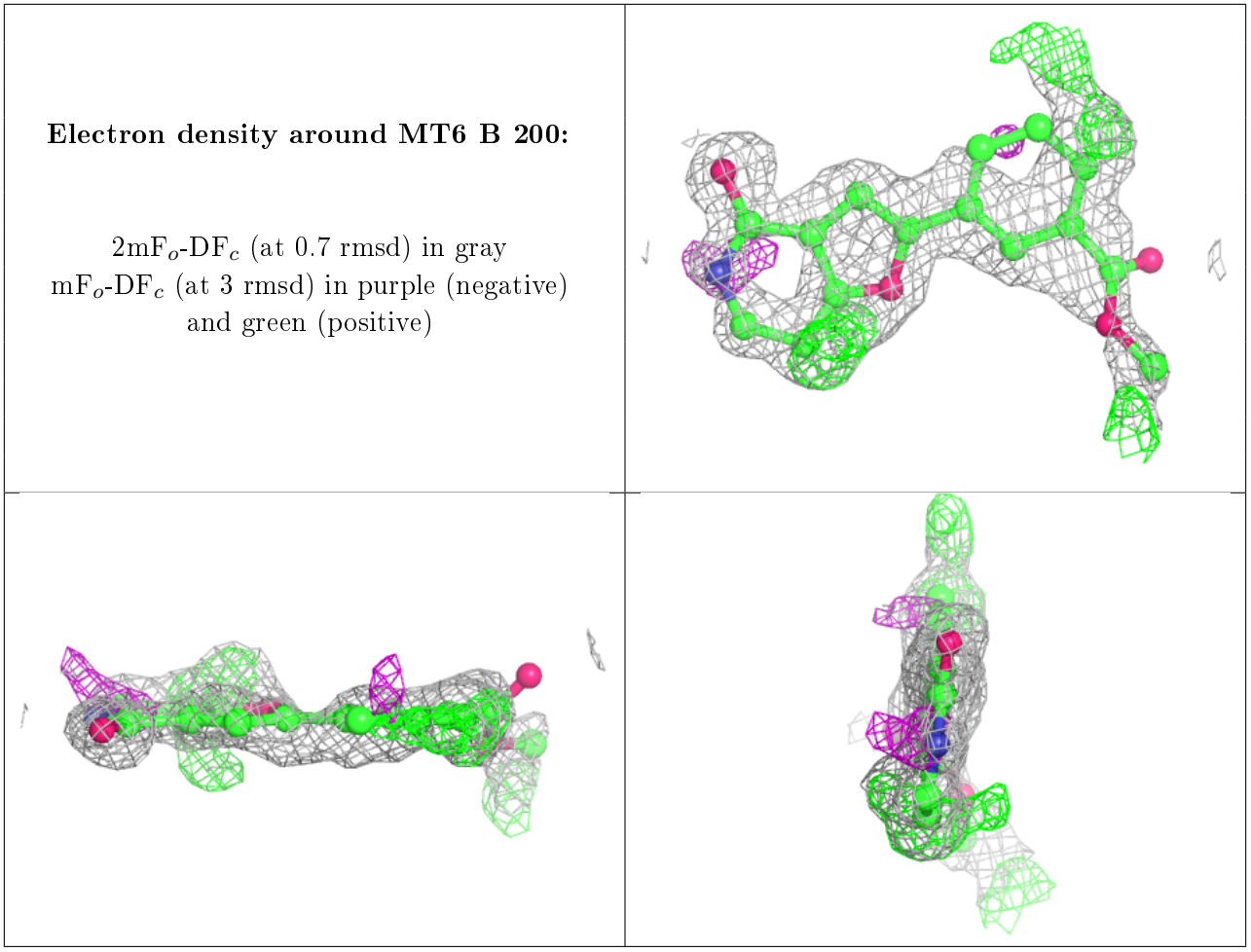
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
5	P6G	C	203	7/19	0.76	0.22	21,26,33,33	7
2	MT6	B	200	20/20	0.77	0.20	8,35,62,64	20
2	MT6	D	200	20/20	0.87	0.13	12,26,42,52	0
3	PE3	A	201	28/43	0.88	0.14	11,23,40,49	0
5	P6G	C	202	7/19	0.88	0.25	22,25,31,32	7
2	MT6	A	200	20/20	0.92	0.12	12,19,29,32	20
4	DMS	C	201	4/4	0.98	0.06	14,16,17,18	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.

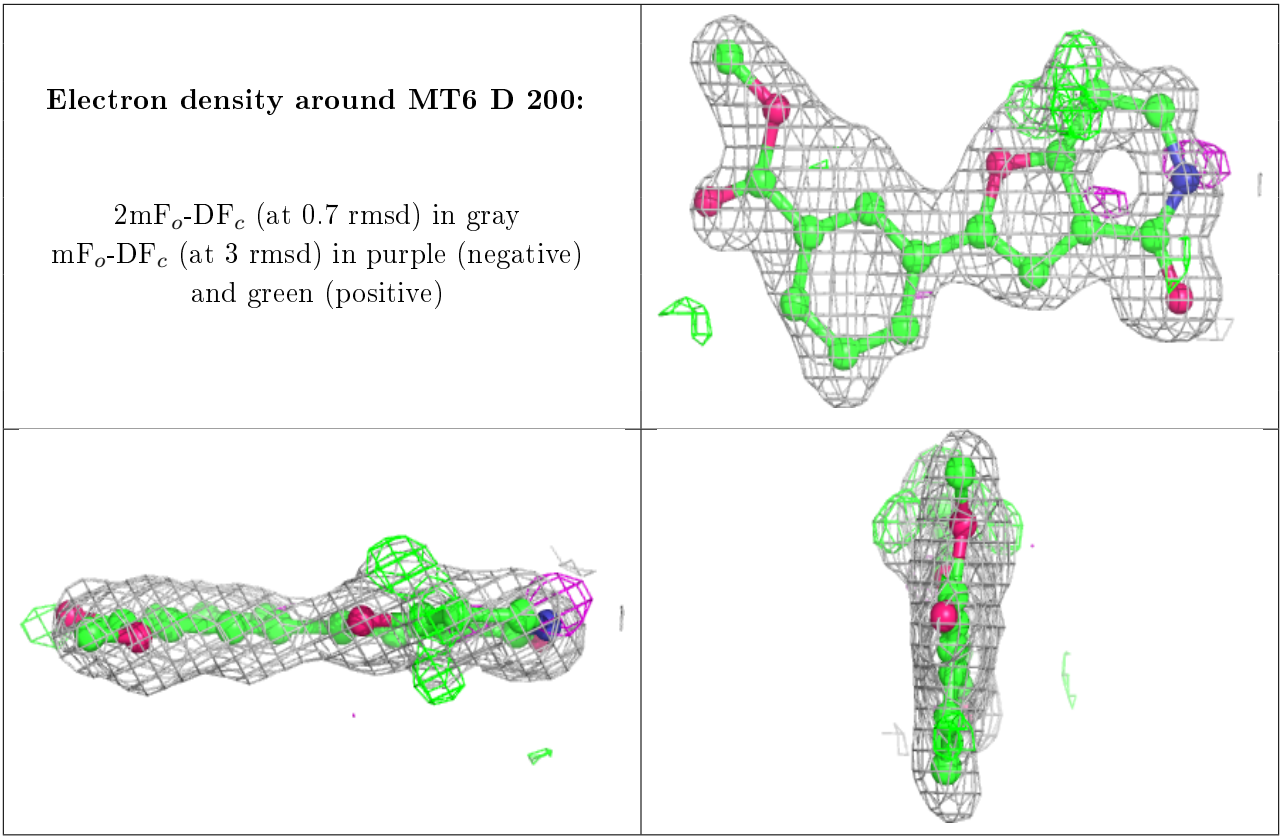
Electron density around MT6 B 200:

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



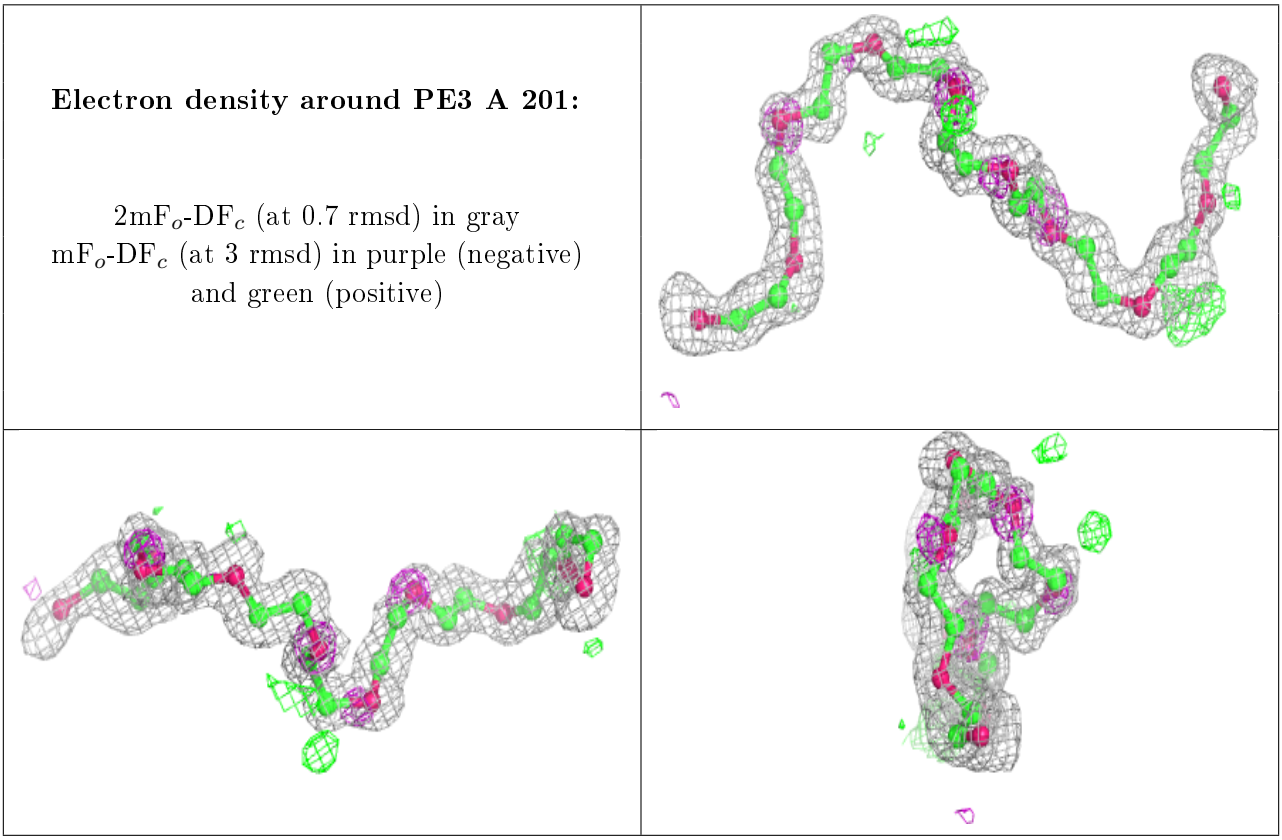
Electron density around MT6 D 200:

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



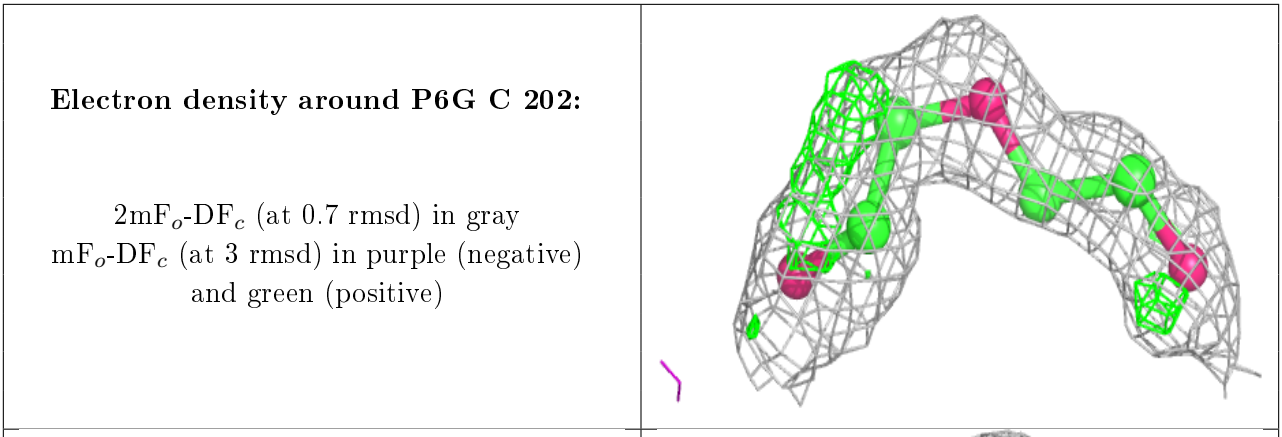
Electron density around PE3 A 201:

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



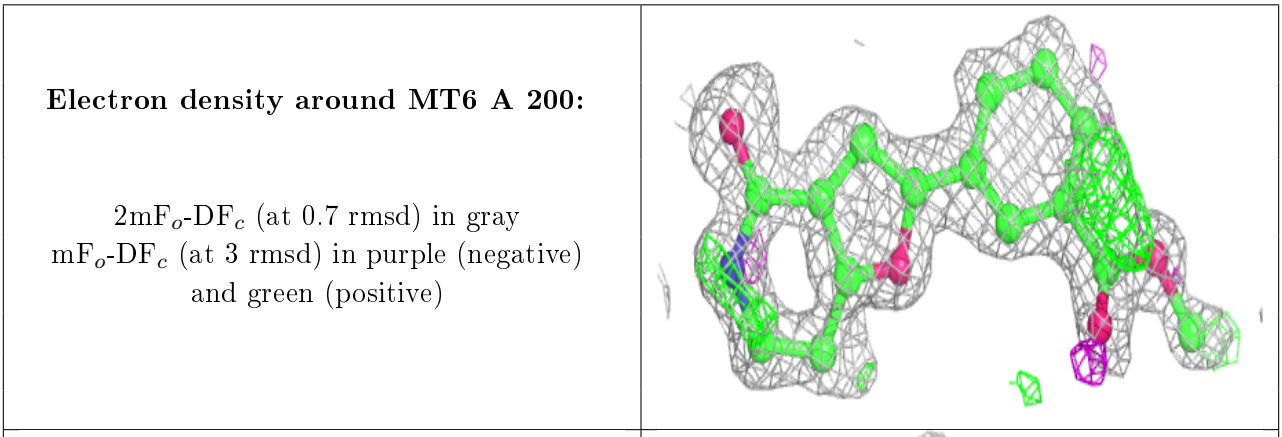
Electron density around P6G C 202:

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



Electron density around MT6 A 200:

$2mF_o$-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.