Full wwPDB X-ray Structure Validation Report ⓘ

Oct 8, 2023 – 07:17 PM EDT

PDB ID	:	6W7E
Title	:	K2P2.1 (TREK-1), 30 mM K+
Authors	:	Lolicato, M.; Minor, D.L.
Deposited on	:	2020-03-19
Resolution	:	3.29 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:

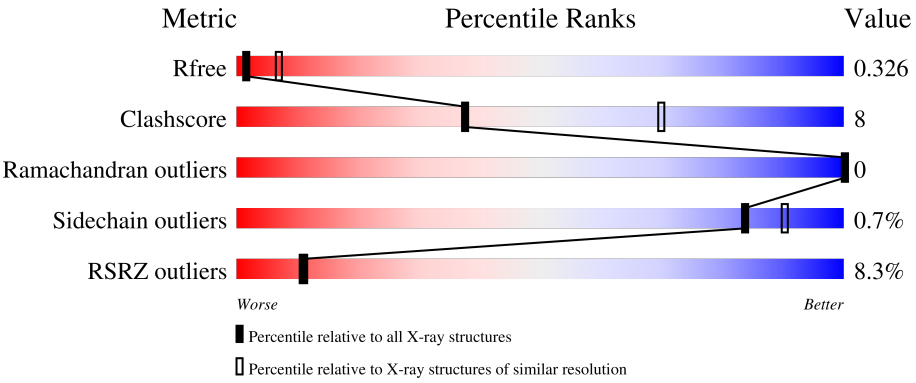
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 3.29 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	1149 (3.34-3.26)
Clashscore	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)
RSRZ outliers	127900	1115 (3.34-3.26)

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 <=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	312	5% 64% 16% 19%
1	B	312	9% 71% 15% 14%

2 Entry composition (i)

There are 9 unique types of molecules in this entry. The entry contains 4204 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 Potassium channel subfamily K member 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	252	Total	C	N	O	S	0	0	0
			1971	1319	310	338	4			
1	B	268	Total	C	N	O	S	0	1	0
			2102	1406	333	358	5			

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	20	MET	-	initiating methionine	UNP P97438
A	84	ARG	LYS	conflict	UNP P97438
A	85	GLU	GLN	conflict	UNP P97438
A	86	LYS	THR	conflict	UNP P97438
A	88	LEU	ILE	conflict	UNP P97438
A	89	ARG	ALA	conflict	UNP P97438
A	90	ALA	GLN	conflict	UNP P97438
A	92	PRO	ALA	conflict	UNP P97438
A	95	SER	ASN	conflict	UNP P97438
A	96	ASP	SER	conflict	UNP P97438
A	97	GLN	THR	conflict	UNP P97438
A	119	ALA	ASN	conflict	UNP P97438
A	300	ALA	SER	conflict	UNP P97438
A	306	ALA	GLU	conflict	UNP P97438
A	323	SER	-	expression tag	UNP P97438
A	324	ASN	-	expression tag	UNP P97438
A	325	SER	-	expression tag	UNP P97438
A	326	LEU	-	expression tag	UNP P97438
A	327	GLU	-	expression tag	UNP P97438
A	328	VAL	-	expression tag	UNP P97438
A	329	LEU	-	expression tag	UNP P97438
A	330	PHE	-	expression tag	UNP P97438
A	331	GLN	-	expression tag	UNP P97438
B	20	MET	-	initiating methionine	UNP P97438
B	84	ARG	LYS	conflict	UNP P97438

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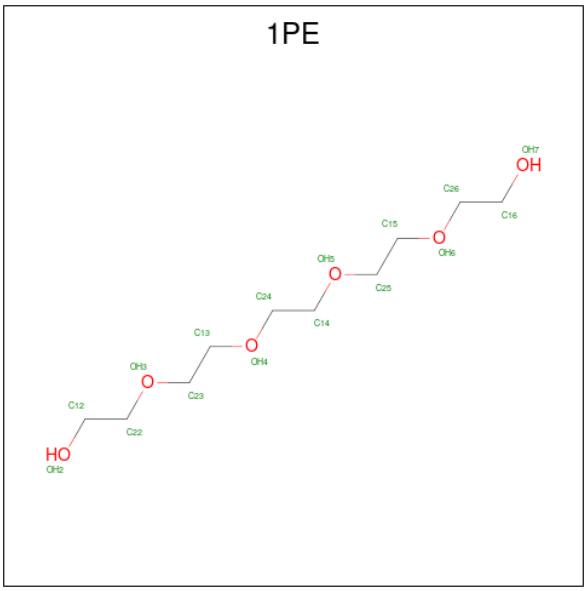
Chain	Residue	Modelled	Actual	Comment	Reference
B	85	GLU	GLN	conflict	UNP P97438
B	86	LYS	THR	conflict	UNP P97438
B	88	LEU	ILE	conflict	UNP P97438
B	89	ARG	ALA	conflict	UNP P97438
B	90	ALA	GLN	conflict	UNP P97438
B	92	PRO	ALA	conflict	UNP P97438
B	95	SER	ASN	conflict	UNP P97438
B	96	ASP	SER	conflict	UNP P97438
B	97	GLN	THR	conflict	UNP P97438
B	119	ALA	ASN	conflict	UNP P97438
B	300	ALA	SER	conflict	UNP P97438
B	306	ALA	GLU	conflict	UNP P97438
B	323	SER	-	expression tag	UNP P97438
B	324	ASN	-	expression tag	UNP P97438
B	325	SER	-	expression tag	UNP P97438
B	326	LEU	-	expression tag	UNP P97438
B	327	GLU	-	expression tag	UNP P97438
B	328	VAL	-	expression tag	UNP P97438
B	329	LEU	-	expression tag	UNP P97438
B	330	PHE	-	expression tag	UNP P97438
B	331	GLN	-	expression tag	UNP P97438

- Molecule 2 is CADMIUM ION (three-letter code: CD) (formula: Cd).

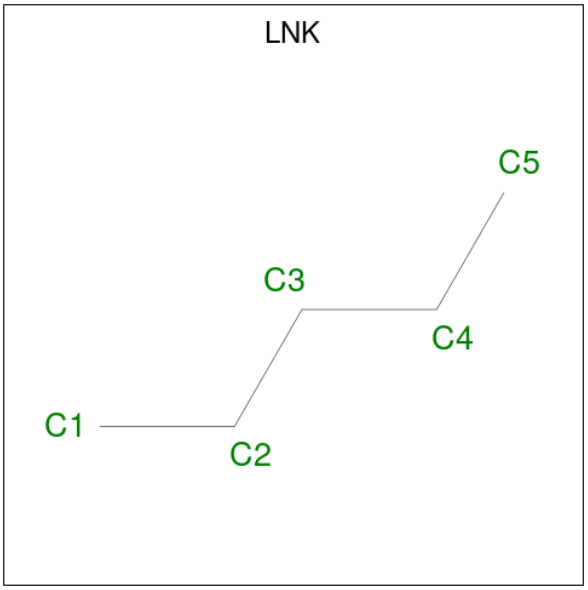
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total Cd 2 2	0	0
2	B	2	Total Cd 2 2	0	0

- Molecule 3 is PENTAETHYLENE GLYCOL (three-letter code: 1PE) (formula: $C_{10}H_{22}O_6$).



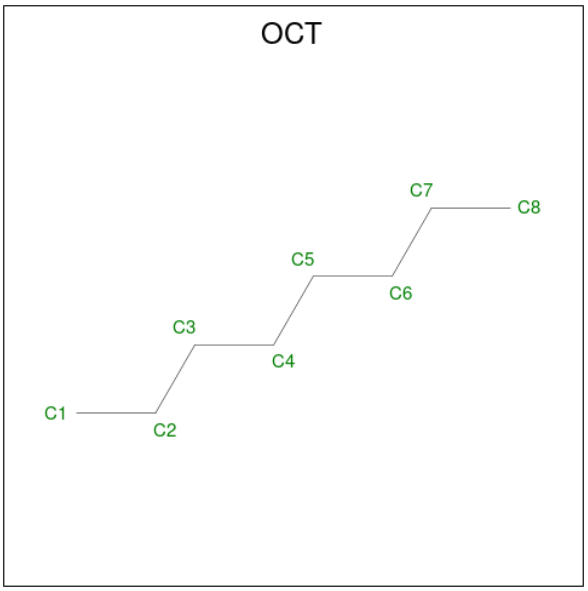
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 16 10 6	0	0

- Molecule 4 is PENTANE (three-letter code: LNK) (formula: C_5H_{12}).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C 5 5	0	0
4	B	1	Total C 5 5	0	0

- Molecule 5 is N-OCTANE (three-letter code: OCT) (formula: C_8H_{18}).

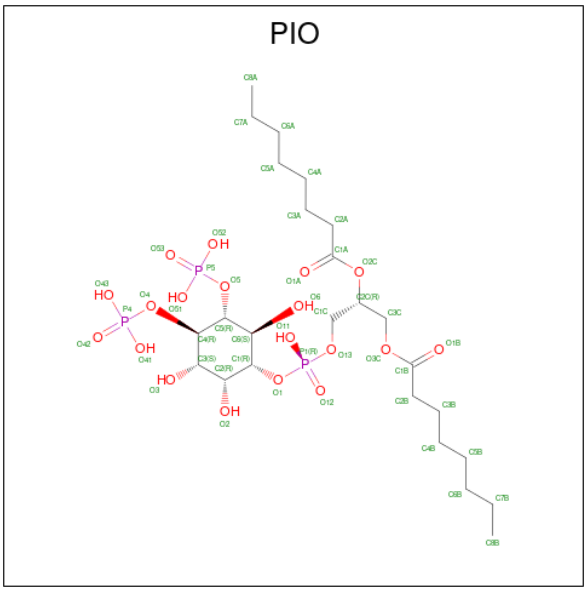


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C 8 8	0	0
5	B	1	Total C 8 8	0	0
5	B	1	Total C 8 8	0	0

- Molecule 6 is POTASSIUM ION (three-letter code: K) (formula: K).

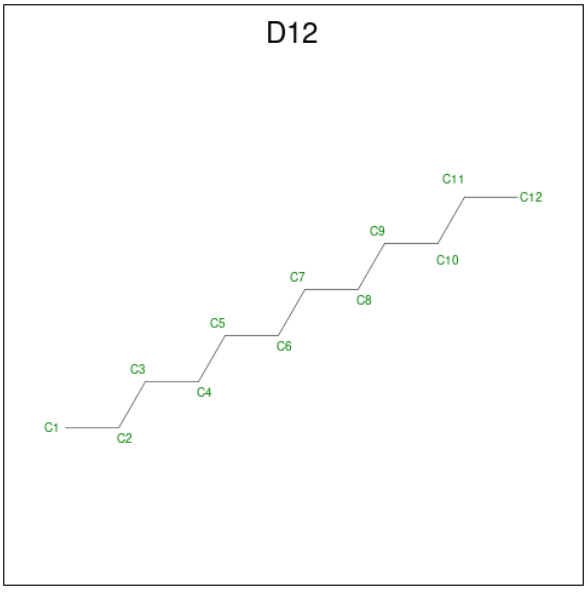
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total K 1 1	0	0
6	B	1	Total K 1 1	0	0

- Molecule 7 is [(2R)-2-octanoyloxy-3-[oxidanyl-[(1R,2R,3S,4R,5R,6S)-2,3,6-tris(oxidanyl)-4,5-diphosphonooxy-cyclohexyl]oxy-phosphoryl]oxy-propyl] octanoate (three-letter code: PIO) (formula: $C_{25}H_{49}O_{19}P_3$).



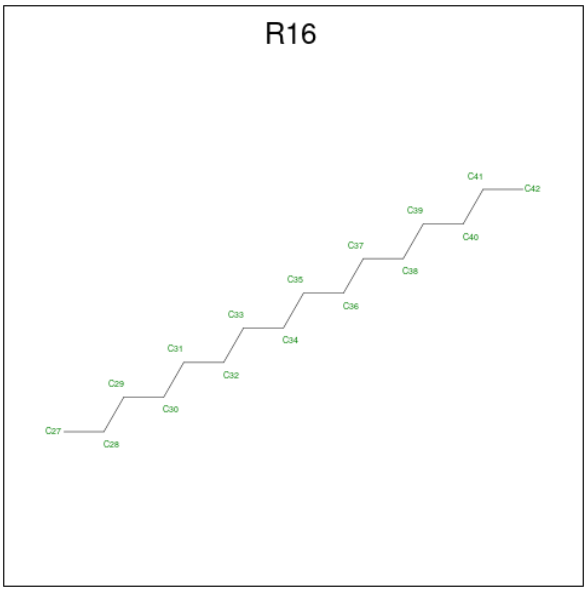
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	O	P	0	0
			47	25	19	3		

- Molecule 8 is DODECANE (three-letter code: D12) (formula: $C_{12}H_{26}$).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	1	Total	C	0	0
			12	12		

- Molecule 9 is HEXADECANE (three-letter code: R16) (formula: $C_{16}H_{34}$).



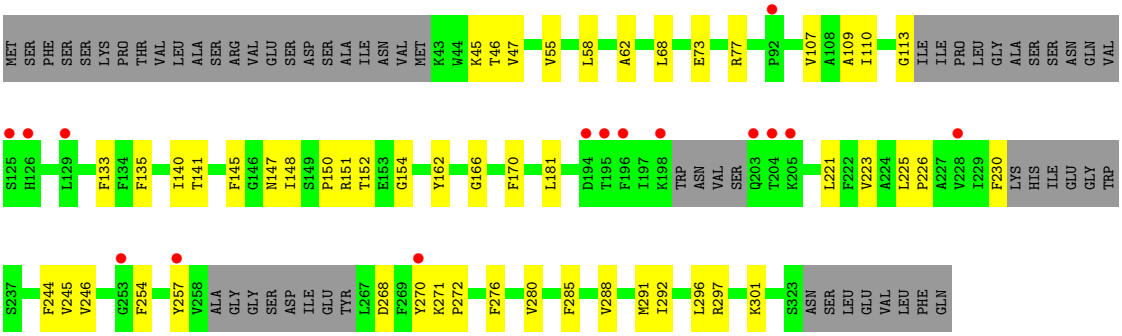
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	B	1	Total C 16 16	0	0

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.

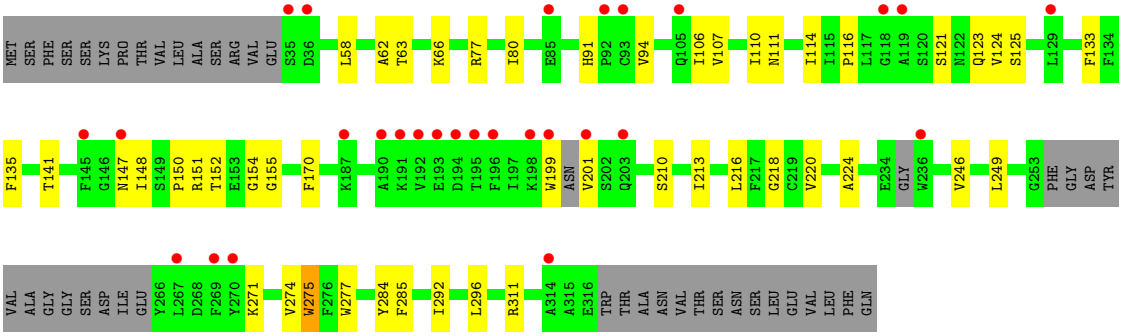
• Molecule 1: Potassium channel subfamily K member 2

Chain A:



• Molecule 1: Potassium channel subfamily K member 2

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	67.37Å 122.53Å 126.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	14.94 – 3.29 14.94 – 3.29	Depositor EDS
% Data completeness (in resolution range)	100.0 (14.94-3.29) 100.0 (14.94-3.29)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.01 (at 3.25Å)	Xtriage
Refinement program	BUSTER 2.10.3 (6-FEB-2020)	Depositor
R, R_{free}	0.288 , 0.307 0.302 , 0.326	Depositor DCC
R_{free} test set	878 reflections (5.37%)	wwPDB-VP
Wilson B-factor (Å^2)	174.0	Xtriage
Anisotropy	0.288	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 199.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	0.024 for -h,l,k	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	4204	wwPDB-VP
Average B, all atoms (Å^2)	237.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.84% 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: R16, CD, PIO, K, OCT, D12, 1PE, LNK

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	0.28	0/2015	0.52	1/2735 (0.0%)
1	B	0.26	0/2152	0.46	0/2925
All	All	0.27	0/4167	0.49	1/5660 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	151	ARG	NE-CZ-NH2	-6.96	116.82	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1971	0	2037	39	0
1	B	2102	0	2166	38	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	16	0	22	0	0
4	A	5	0	12	1	0
4	B	5	0	12	0	0
5	A	8	0	18	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	16	0	36	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
7	A	47	0	44	2	0
8	B	12	0	26	0	0
9	B	16	0	34	0	0
All	All	4204	0	4407	66	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 8.

All (66) 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:B:271:LYS:O	1:B:275[B]:TRP:N	2.17	0.77
1:A:254:PHE:HE2	1:A:257:TYR:HB2	1.51	0.76
1:A:254:PHE:CE2	1:A:257:TYR:HB2	2.29	0.67
1:B:107:VAL:HA	1:B:110:ILE:HD12	1.75	0.66
1:A:246:VAL:HA	1:A:285:PHE:HE2	1.59	0.66
1:B:152:THR:HG22	1:B:154:GLY:H	1.61	0.64
1:A:221:LEU:HA	1:A:225:LEU:HD12	1.80	0.64
1:A:133:PHE:HB2	1:B:62:ALA:HB2	1.81	0.62
1:B:121:SER:O	1:B:123:GLN:NE2	2.34	0.60
1:B:111:ASN:HB3	1:B:151:ARG:NH2	2.20	0.57
1:A:133:PHE:CD1	1:B:58:LEU:HB3	2.41	0.56
1:A:110:ILE:HD11	1:B:110:ILE:HD13	1.90	0.54
1:A:62:ALA:HB2	1:B:133:PHE:HB2	1.89	0.53
1:A:244:PHE:HD1	1:A:254:PHE:CE2	2.26	0.53
1:B:199:TRP:O	1:B:201:VAL:N	2.41	0.52
1:A:133:PHE:HE1	1:B:58:LEU:HD13	1.75	0.51
1:B:213:ILE:HD12	1:B:216:LEU:HD23	1.92	0.51
4:A:404:LNK:H11	7:A:407:PIO:H7AA	1.93	0.51
1:B:77:ARG:O	1:B:80:ILE:HG22	2.10	0.51
1:B:218:GLY:HA3	1:B:284:TYR:CZ	2.46	0.51
1:B:63:THR:HA	1:B:66:LYS:HE2	1.93	0.50
1:B:147:ASN:OD1	1:B:148:ILE:N	2.42	0.50
1:B:135:PHE:CZ	1:B:150:PRO:HD3	2.46	0.50
1:B:91:HIS:O	1:B:94:VAL:HG12	2.12	0.50
1:A:109:ALA:O	1:A:113:GLY:N	2.40	0.50
1:A:77:ARG:NH2	1:B:124:VAL:O	2.38	0.49
1:A:58:LEU:HB3	1:B:133:PHE:CD1	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:221:LEU:O	1:A:226:PRO:HD3	2.12	0.49
1:A:145:PHE:HE1	1:A:254:PHE:HB3	1.78	0.49
1:B:220:VAL:HA	1:B:224:ALA:HB3	1.96	0.48
1:A:68:LEU:HD13	1:B:155:GLY:HA2	1.95	0.48
1:A:288:VAL:HA	1:A:291:MET:HE2	1.95	0.47
1:B:106:ILE:O	1:B:110:ILE:HG13	2.15	0.47
1:B:246:VAL:HA	1:B:285:PHE:HE2	1.78	0.47
1:A:230:PHE:HB3	1:A:244:PHE:CE2	2.50	0.47
1:A:107:VAL:HA	1:A:110:ILE:HD12	1.96	0.47
1:B:274:VAL:O	1:B:277:TRP:HB3	2.15	0.47
1:B:114:ILE:HD12	1:B:116:PRO:HG3	1.96	0.47
1:A:181:LEU:HD22	1:A:280:VAL:HG13	1.97	0.46
1:A:45:LYS:HG2	1:A:47:VAL:H	1.80	0.46
1:A:152:THR:HG22	1:A:154:GLY:H	1.79	0.46
1:A:268:ASP:C	1:A:270:TYR:H	2.19	0.46
1:B:141:THR:HG22	1:B:170:PHE:CZ	2.50	0.46
1:A:135:PHE:CZ	1:A:150:PRO:HD3	2.50	0.46
1:A:141:THR:HG22	1:A:170:PHE:CZ	2.51	0.45
1:B:218:GLY:HA3	1:B:284:TYR:CE1	2.52	0.45
1:A:147:ASN:CG	1:A:148:ILE:HD12	2.37	0.45
1:B:210:SER:O	1:B:213:ILE:HG22	2.17	0.45
1:A:55:VAL:HG22	1:B:275[B]:TRP:CH2	2.51	0.45
1:A:73:GLU:HG2	1:A:77:ARG:HH11	1.82	0.44
1:A:223:VAL:HA	1:A:245:VAL:HG11	2.00	0.44
1:B:292:ILE:O	1:B:296:LEU:HG	2.18	0.44
1:A:46:THR:HG21	7:A:407:PIO:O6	2.18	0.43
1:B:111:ASN:O	1:B:151:ARG:NH2	2.43	0.43
1:B:124:VAL:HG12	1:B:125:SER:N	2.34	0.43
1:A:162:TYR:OH	1:B:58:LEU:HD23	2.19	0.43
1:A:271:LYS:HG3	1:A:272:PRO:HD3	2.01	0.43
1:A:292:ILE:O	1:A:296:LEU:HG	2.19	0.41
1:B:141:THR:HG22	1:B:170:PHE:CE2	2.55	0.41
1:B:249:LEU:HB2	1:B:285:PHE:CE2	2.55	0.41
1:A:73:GLU:OE2	1:A:77:ARG:NH1	2.53	0.41
1:A:133:PHE:CE1	1:B:58:LEU:HB3	2.55	0.41
1:A:58:LEU:HB3	1:B:133:PHE:CE1	2.55	0.41
1:A:145:PHE:CE1	1:A:254:PHE:HB3	2.55	0.41
1:A:140:ILE:HG22	1:A:166:GLY:HA3	2.03	0.40
1:A:297:ARG:O	1:A:301:LYS:HG2	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	242/312 (78%)	235 (97%)	7 (3%)	0	100	100
1	B	261/312 (84%)	249 (95%)	12 (5%)	0	100	100
All	All	503/624 (81%)	484 (96%)	19 (4%)	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	208/260 (80%)	207 (100%)	1 (0%)	88	93
1	B	222/260 (85%)	219 (99%)	3 (1%)	67	82
All	All	430/520 (83%)	426 (99%)	4 (1%)	84	87

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	276	PHE
1	B	275[A]	TRP
1	B	275[B]	TRP
1	B	311	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry

Of 15 ligands modelled in this entry, 6 are monoatomic - leaving 9 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	$\#\|Z\| > 2$
7	PIO	A	407	-	47,47,47	1.18	7 (14%)	61,65,65	1.05	4 (6%)
5	OCT	B	404	-	7,7,7	0.31	0	6,6,6	0.74	0
9	R16	B	408	-	15,15,15	0.29	0	14,14,14	0.89	0
5	OCT	A	405	-	7,7,7	0.31	0	6,6,6	0.72	0
3	1PE	A	403	-	15,15,15	0.54	0	14,14,14	0.26	0
5	OCT	B	405	-	7,7,7	0.31	0	6,6,6	0.74	0
4	LNK	B	403	-	4,4,4	0.32	0	3,3,3	0.56	0
8	D12	B	406	-	11,11,11	0.31	0	10,10,10	0.85	0
4	LNK	A	404	-	4,4,4	0.32	0	3,3,3	0.54	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
7	PIO	A	407	-	-	19/44/68/68	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	OCT	B	404	-	-	3/5/5/5	-
9	R16	B	408	-	-	4/13/13/13	-
5	OCT	A	405	-	-	0/5/5/5	-
3	1PE	A	403	-	-	5/13/13/13	-
5	OCT	B	405	-	-	2/5/5/5	-
4	LNK	B	403	-	-	1/2/2/2	-
8	D12	B	406	-	-	1/9/9/9	-
4	LNK	A	404	-	-	1/2/2/2	-

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	407	PIO	P4-O4	3.24	1.65	1.59
7	A	407	PIO	P5-O5	3.22	1.65	1.59
7	A	407	PIO	O2C-C2C	-2.37	1.40	1.46
7	A	407	PIO	O2C-C1A	2.24	1.40	1.34
7	A	407	PIO	O3C-C3C	-2.18	1.40	1.45
7	A	407	PIO	O3C-C1B	2.11	1.39	1.33
7	A	407	PIO	P1-O1	2.06	1.65	1.60

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	A	407	PIO	O2C-C1A-C2A	3.96	120.04	111.50
7	A	407	PIO	C5-C6-C1	2.64	114.44	108.96
7	A	407	PIO	O3C-C1B-C2B	2.40	119.44	111.91
7	A	407	PIO	C2-C3-C4	2.07	114.41	109.68

There are no chirality outliers.

All (36) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	407	PIO	C1C-O13-P1-O1
7	A	407	PIO	C3-C4-O4-P4
7	A	407	PIO	O2C-C2C-C3C-O3C
3	A	403	1PE	OH5-C14-C24-OH4
7	A	407	PIO	C2B-C1B-O3C-C3C
7	A	407	PIO	O1B-C1B-O3C-C3C
3	A	403	1PE	OH4-C13-C23-OH3
3	A	403	1PE	OH6-C15-C25-OH5

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Mol	Chain	Res	Type	Atoms
3	A	403	1PE	OH7-C16-C26-OH6
9	B	408	R16	C37-C38-C39-C40
7	A	407	PIO	C5-C4-O4-P4
7	A	407	PIO	C2A-C3A-C4A-C5A
7	A	407	PIO	O1A-C1A-O2C-C2C
7	A	407	PIO	C2A-C1A-O2C-C2C
5	B	405	OCT	C2-C3-C4-C5
9	B	408	R16	C31-C32-C33-C34
7	A	407	PIO	C1C-C2C-C3C-O3C
7	A	407	PIO	C2B-C3B-C4B-C5B
5	B	404	OCT	C1-C2-C3-C4
5	B	404	OCT	C5-C6-C7-C8
7	A	407	PIO	C4A-C5A-C6A-C7A
4	A	404	LNK	C2-C3-C4-C5
4	B	403	LNK	C2-C3-C4-C5
7	A	407	PIO	C5-O5-P5-O53
8	B	406	D12	C11-C10-C9-C8
7	A	407	PIO	C2C-C1C-O13-P1
5	B	405	OCT	C1-C2-C3-C4
5	B	404	OCT	C3-C4-C5-C6
9	B	408	R16	C33-C34-C35-C36
9	B	408	R16	C39-C40-C41-C42
7	A	407	PIO	O13-C1C-C2C-O2C
7	A	407	PIO	C5A-C6A-C7A-C8A
3	A	403	1PE	C13-C23-OH3-C22
7	A	407	PIO	C1B-C2B-C3B-C4B
7	A	407	PIO	O13-C1C-C2C-C3C
7	A	407	PIO	C4-O4-P4-O41

There are no ring outliers.

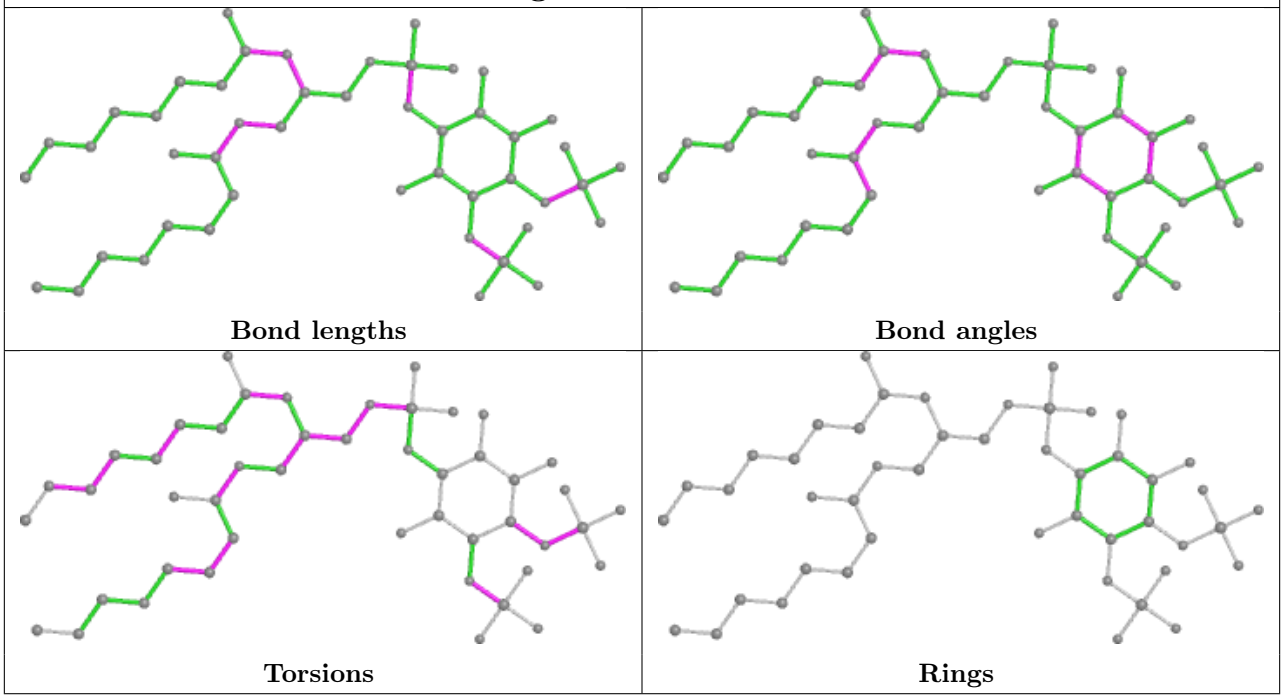
2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	407	PIO	2	0
4	A	404	LNK	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 PIO A 407



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	274:VAL	C	275[B]:TRP	N	3.23

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	252/312 (80%)	0.02	15 (5%) 21 21	128, 238, 300, 300	0
1	B	268/312 (85%)	0.19	28 (10%) 6 6	129, 254, 300, 300	0
All	All	520/624 (83%)	0.11	43 (8%) 11 11	128, 248, 300, 300	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	93	CYS	8.2
1	B	191	LYS	8.1
1	B	92	PRO	7.8
1	A	198	LYS	7.4
1	B	199	TRP	6.6
1	B	195	THR	6.1
1	B	201	VAL	5.2
1	A	196	PHE	5.0
1	A	204	THR	4.2
1	B	236	TRP	4.2
1	A	270	TYR	4.1
1	A	125	SER	4.0
1	B	194	ASP	4.0
1	B	269	PHE	3.9
1	A	195	THR	3.7
1	B	129	LEU	3.7
1	B	192	VAL	3.5
1	A	253	GLY	3.5
1	A	203	GLN	3.4
1	A	228	VAL	3.4
1	A	126	HIS	3.4
1	A	257	TYR	3.2
1	B	314	ALA	3.1
1	A	92	PRO	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	193	GLU	3.0
1	B	105	GLN	2.9
1	B	190	ALA	2.9
1	B	196	PHE	2.9
1	B	198	LYS	2.9
1	A	205	LYS	2.8
1	B	203	GLN	2.8
1	B	85	GLU	2.7
1	B	36	ASP	2.7
1	B	118	GLY	2.6
1	B	145	PHE	2.5
1	A	194	ASP	2.4
1	B	119	ALA	2.4
1	B	147	ASN	2.3
1	B	270	TYR	2.3
1	B	267	LEU	2.2
1	B	187	LYS	2.2
1	B	35	SER	2.2
1	A	129	LEU	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 monosaccharides 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
3	1PE	A	403	16/16	0.61	0.16	276,294,300,300	0
7	PIO	A	407	47/47	0.64	0.39	178,300,300,300	0
2	CD	B	402	1/1	0.65	0.13	300,300,300,300	1
9	R16	B	408	16/16	0.81	0.15	229,257,294,294	0

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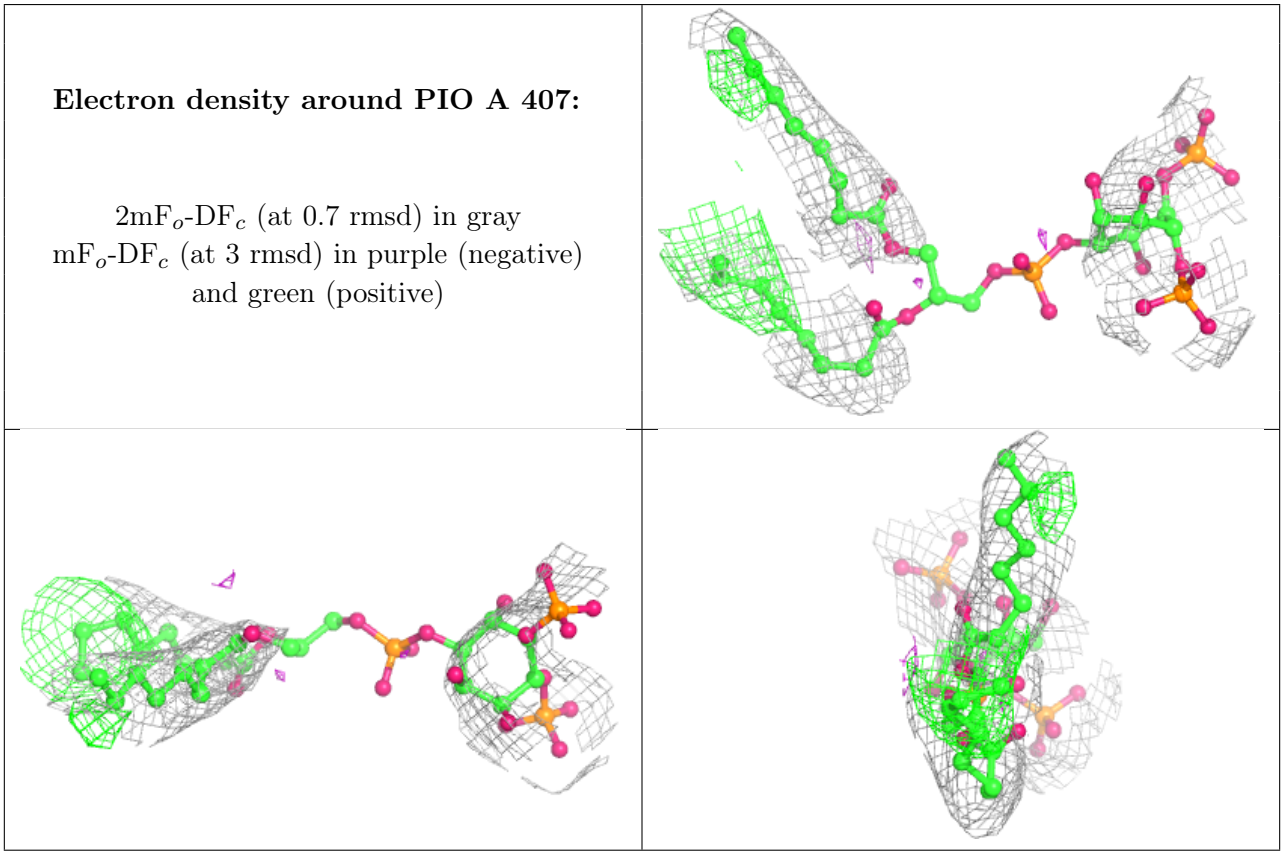
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	LNK	B	403	5/5	0.84	0.41	227,227,228,230	0
4	LNK	A	404	5/5	0.85	0.25	175,176,179,180	0
8	D12	B	406	12/12	0.86	0.21	185,190,192,193	0
5	OCT	A	405	8/8	0.87	0.12	200,215,235,236	0
2	CD	A	402	1/1	0.89	0.21	295,295,295,295	1
6	K	A	406	1/1	0.90	0.10	155,155,155,155	0
5	OCT	B	404	8/8	0.91	0.41	188,192,201,201	0
5	OCT	B	405	8/8	0.91	0.16	175,177,185,186	0
2	CD	A	401	1/1	0.94	0.12	237,237,237,237	0
2	CD	B	401	1/1	0.97	0.20	300,300,300,300	1
6	K	B	407	1/1	0.98	0.11	136,136,136,136	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 PIO A 407:

$2mF_o$-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

There are no such residues in this entry.