Full wwPDB X-ray Structure Validation Report ⓘ

Jun 6, 2023 – 08:30 pm BST

PDB ID	:	8BZX
Title	:	1-deoxy-D-xylulose 5-phosphate synthase from Klebsiella pneumoniae (kpDXPS),co-crystal with thiamine monophosphate analog
Authors	:	Hamid, R.
Deposited on	:	2022-12-15
Resolution	:	2.05 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:

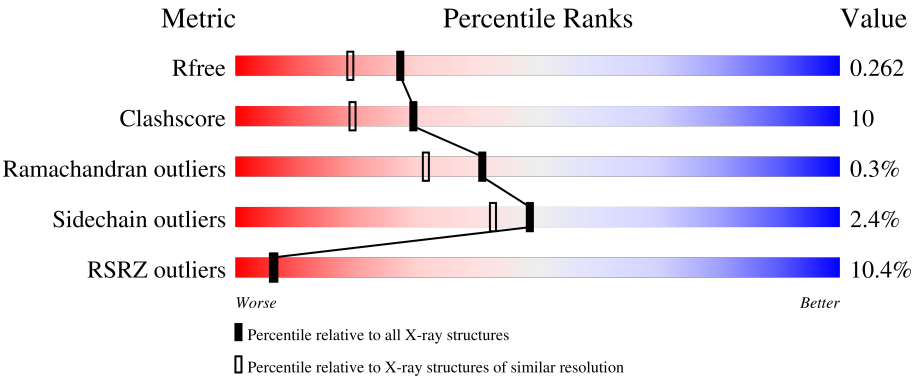
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.33
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.33

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 2.05 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	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

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	586	9% 77% 15% 7%
1	B	586	11% 76% 20%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 8819 atoms, of which 40 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.

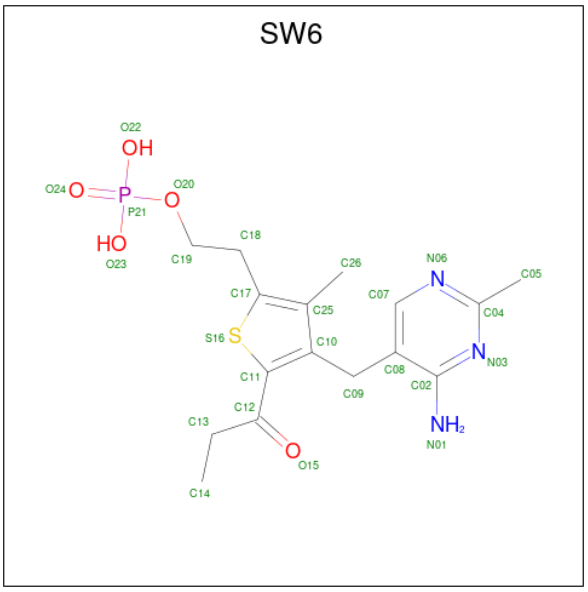
- Molecule 1 is a protein called 1-deoxy-D-xylulose-5-phosphate synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	546	Total	C	N	O	S	0	0	0
			4162	2647	717	778	20			
1	B	568	Total	C	N	O	S	0	0	0
			4332	2755	749	808	20			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	198	GLY	-	linker	UNP A0A486V6R5
A	199	GLY	-	linker	UNP A0A486V6R5
A	200	GLY	-	linker	UNP A0A486V6R5
A	201	GLY	-	linker	UNP A0A486V6R5
A	202	GLY	-	linker	UNP A0A486V6R5
A	203	GLY	-	linker	UNP A0A486V6R5
A	204	GLY	-	linker	UNP A0A486V6R5
B	198	GLY	-	linker	UNP A0A486V6R5
B	199	GLY	-	linker	UNP A0A486V6R5
B	200	GLY	-	linker	UNP A0A486V6R5
B	201	GLY	-	linker	UNP A0A486V6R5
B	202	GLY	-	linker	UNP A0A486V6R5
B	203	GLY	-	linker	UNP A0A486V6R5
B	204	GLY	-	linker	UNP A0A486V6R5

- Molecule 2 is 2-[4-[(4-azanyl-2-methyl-pyrimidin-5-yl)methyl]-3-methyl-5-propanoyl-thiophen-2-yl]ethyl dihydrogen phosphate (three-letter code: SW6) (formula: $C_{16}H_{22}N_3O_5PS$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	P	S	0	0
			46	16	20	3	5	1	1		
2	B	1	Total	C	H	N	O	P	S	0	0
			46	16	20	3	5	1	1		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	B	2	Total	Mg	0	0
			2	2		

- Molecule 4 is water.

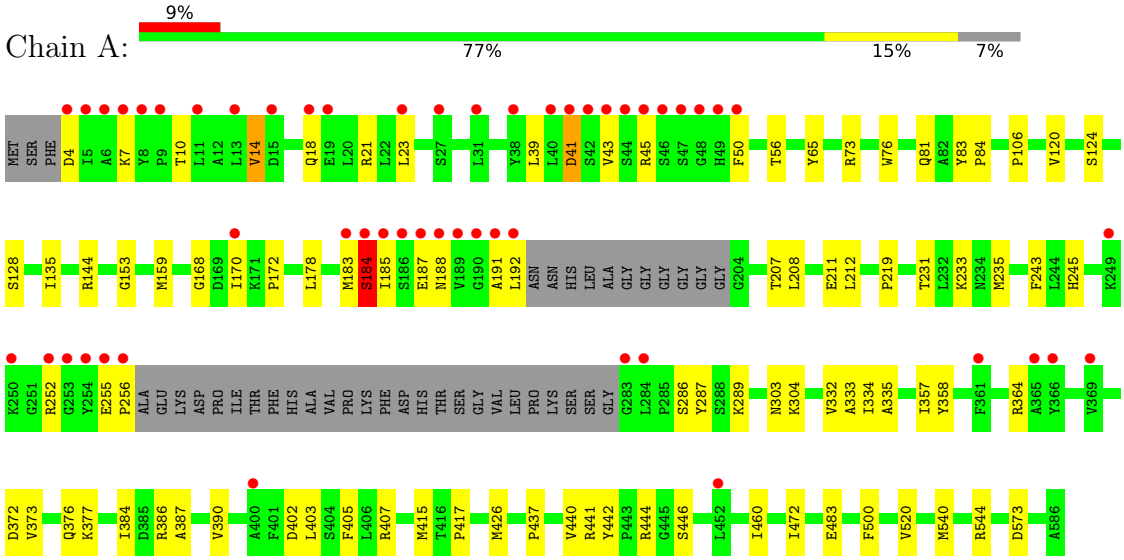
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	128	Total	O	0	0
			128	128		
4	B	102	Total	O	0	0
			102	102		

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.

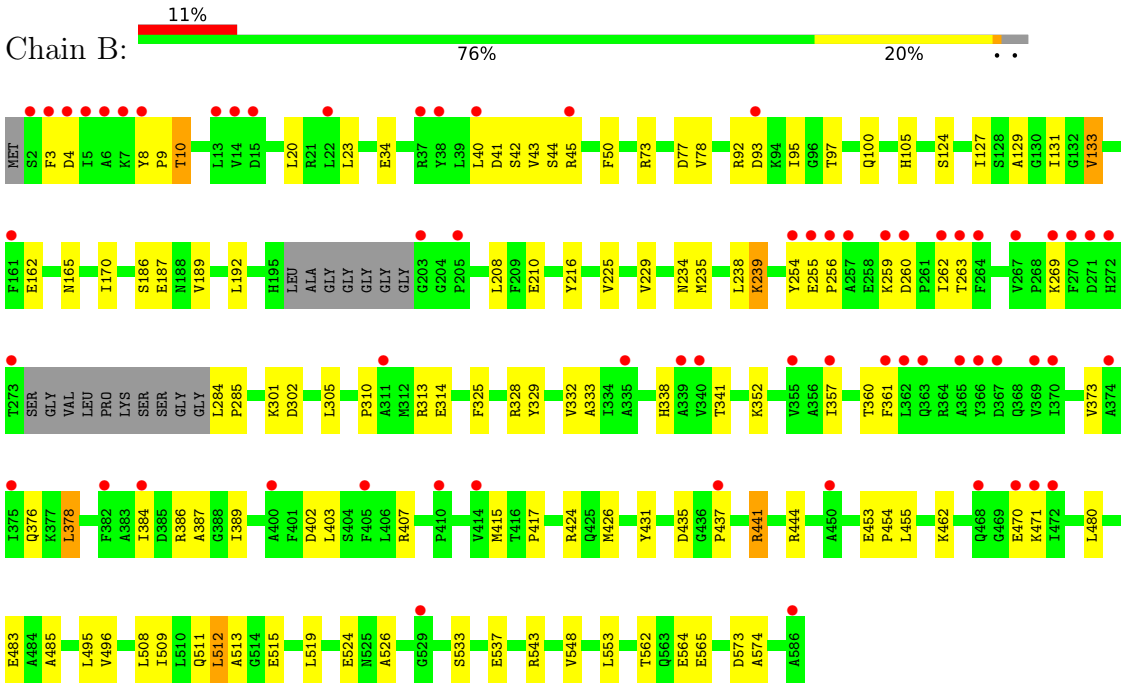
• Molecule 1: 1-deoxy-D-xylulose-5-phosphate synthase

Chain A:



• Molecule 1: 1-deoxy-D-xylulose-5-phosphate synthase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	119.25Å 150.97Å 142.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.79 – 2.05 46.79 – 2.05	Depositor EDS
% Data completeness (in resolution range)	99.8 (46.79-2.05) 99.8 (46.79-2.05)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.17 (at 2.05Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.217 , 0.264 0.217 , 0.262	Depositor DCC
R_{free} test set	3953 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å^2)	35.0	Xtriage
Anisotropy	0.725	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 44.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	8819	wwPDB-VP
Average B, all atoms (Å^2)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.25% 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: SW6, MG

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	0.39	0/4247	0.58	0/5757
1	B	0.37	0/4424	0.57	0/5999
All	All	0.38	0/8671	0.57	0/11756

There are no bond length outliers.

There are no bond angle outliers.

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	4162	0	4164	77	0
1	B	4332	0	4313	92	0
2	A	26	20	0	1	0
2	B	26	20	0	0	0
3	A	1	0	0	0	0
3	B	2	0	0	0	0
4	A	128	0	0	3	0
4	B	102	0	0	7	0
All	All	8779	40	8477	162	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 10.

All (162) 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:43:VAL:HG11	1:A:50:PHE:HB3	1.26	1.07
1:B:235:MET:HA	1:B:238:LEU:HD23	1.39	1.01
1:B:8:TYR:HA	1:B:34:GLU:OE2	1.62	0.99
1:A:183:MET:HB3	1:A:187:GLU:HA	1.46	0.98
1:A:415:MET:HE3	1:A:426:MET:HB3	1.47	0.95
1:A:386:ARG:HD2	1:A:444:ARG:HB2	1.47	0.93
1:A:403:LEU:HD21	1:A:441:ARG:HD3	1.50	0.92
1:A:415:MET:CE	1:A:426:MET:HB3	2.10	0.82
1:A:402:ASP:OD2	1:A:441:ARG:HD2	1.81	0.80
1:A:43:VAL:CG1	1:A:50:PHE:HB3	2.10	0.78
1:B:403:LEU:HD21	1:B:441:ARG:HD3	1.66	0.78
1:B:533:SER:O	1:B:537:GLU:HG3	1.84	0.77
1:B:562:THR:HG22	1:B:565:GLU:H	1.49	0.77
1:B:373:VAL:HG12	1:B:437:PRO:HG3	1.66	0.76
1:A:41:ASP:O	1:A:45:ARG:HD3	1.88	0.74
1:B:10:THR:OG1	1:B:34:GLU:OE1	2.06	0.73
1:A:207:THR:O	1:A:211:GLU:HG2	1.89	0.73
1:A:73:ARG:HD2	1:A:144:ARG:HD3	1.73	0.71
1:B:41:ASP:O	1:B:45:ARG:HG3	1.91	0.69
1:A:43:VAL:HG11	1:A:50:PHE:CB	2.14	0.69
1:B:403:LEU:O	1:B:407:ARG:HB2	1.94	0.68
1:A:4:ASP:N	1:A:7:LYS:HZ3	1.92	0.68
1:B:403:LEU:CD2	1:B:441:ARG:HD3	2.24	0.68
1:B:508:LEU:O	1:B:512:LEU:HG	1.94	0.67
1:B:341:THR:HB	4:B:701:HOH:O	1.94	0.66
1:B:45:ARG:O	1:B:269:LYS:HD2	1.94	0.66
1:B:424:ARG:HH21	1:B:455:LEU:HD11	1.60	0.66
1:A:415:MET:HE2	1:A:440:VAL:HG22	1.77	0.66
1:B:386:ARG:HD2	1:B:444:ARG:HB2	1.79	0.65
1:A:124:SER:HB2	1:A:159:MET:CE	2.27	0.64
1:A:159:MET:HE2	1:A:364:ARG:NH1	2.13	0.64
1:A:403:LEU:CD2	1:A:441:ARG:HD3	2.26	0.63
1:A:415:MET:CE	1:A:440:VAL:HG22	2.28	0.63
1:B:9:PRO:HD2	1:B:34:GLU:OE2	1.98	0.63
1:A:135:ILE:CD1	1:A:172:PRO:HB3	2.28	0.63
1:B:562:THR:HB	1:B:565:GLU:HB2	1.81	0.62
4:A:824:HOH:O	1:B:170:ILE:HD11	1.98	0.62
1:B:496:VAL:HG21	1:B:508:LEU:HD21	1.81	0.61
1:A:472:ILE:HD11	1:A:520:VAL:HG21	1.84	0.60
1:A:387:ALA:HB1	1:A:441:ARG:CZ	2.32	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:338:HIS:HA	4:B:701:HOH:O	2.02	0.60
1:B:424:ARG:NH2	1:B:455:LEU:HD11	2.16	0.60
1:A:183:MET:CB	1:A:187:GLU:HA	2.27	0.59
1:A:303:ASN:OD1	1:A:304:LYS:HE2	2.02	0.58
1:A:128:SER:HB3	4:B:701:HOH:O	2.02	0.58
1:B:302:ASP:O	1:B:328:ARG:NH2	2.36	0.58
1:A:377:LYS:HE2	4:A:703:HOH:O	2.04	0.58
1:A:335:ALA:HB1	1:B:162:GLU:OE1	2.03	0.57
1:B:511:GLN:HG3	1:B:515:GLU:OE2	2.04	0.57
1:B:9:PRO:CD	1:B:34:GLU:OE2	2.52	0.57
1:B:483:GLU:HG2	1:B:573:ASP:HA	1.85	0.57
1:B:402:ASP:OD1	1:B:441:ARG:HD2	2.05	0.56
1:B:480:LEU:HD21	1:B:524:GLU:OE1	2.05	0.56
1:A:231:THR:HG22	1:A:235:MET:CE	2.36	0.55
1:A:56:THR:HG21	1:A:81:GLN:HG3	1.89	0.55
1:A:219:PRO:HA	1:A:245:HIS:O	2.07	0.55
1:A:483:GLU:HG2	1:A:573:ASP:HA	1.88	0.55
1:B:129:ALA:O	1:B:133:VAL:HG13	2.06	0.55
1:B:192:LEU:HD23	4:B:793:HOH:O	2.05	0.55
1:A:124:SER:HB2	1:A:159:MET:HE3	1.88	0.55
1:A:415:MET:HE1	1:A:426:MET:O	2.07	0.54
1:A:255:GLU:HB3	1:A:256:PRO:HD3	1.90	0.54
1:B:210:GLU:OE1	1:B:216:TYR:HB3	2.08	0.54
1:B:43:VAL:HG12	1:B:50:PHE:HD2	1.73	0.53
1:A:170:ILE:CG2	1:A:172:PRO:HD3	2.38	0.53
1:B:192:LEU:HD13	1:B:208:LEU:HD22	1.91	0.53
1:B:509:ILE:O	1:B:512:LEU:HD12	2.08	0.52
1:B:20:LEU:HA	1:B:23:LEU:CD2	2.39	0.52
1:B:543:ARG:HH11	1:B:543:ARG:HG2	1.75	0.52
1:A:170:ILE:HG22	1:A:172:PRO:HD3	1.92	0.51
1:A:332:VAL:O	1:A:333:ALA:HB3	2.10	0.51
1:B:234:ASN:O	1:B:238:LEU:HD22	2.10	0.51
1:B:45:ARG:HA	1:B:269:LYS:HD2	1.92	0.51
1:B:470:GLU:O	1:B:471:LYS:HB2	2.11	0.51
1:A:208:LEU:HD12	1:B:208:LEU:HD12	1.92	0.51
1:B:313:ARG:HB2	1:B:329:TYR:OH	2.10	0.51
1:B:186:SER:HB3	1:B:314:GLU:OE1	2.11	0.51
1:A:358:TYR:CD2	1:A:386:ARG:HG2	2.47	0.50
1:B:305:LEU:HD23	1:B:431:TYR:CE1	2.46	0.50
1:B:485:ALA:HA	1:B:495:LEU:HD22	1.93	0.50
1:A:18:GLN:HE21	1:A:21:ARG:NH2	2.10	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:MET:HA	1:A:188:ASN:H	1.76	0.49
1:B:376:GLN:CB	1:B:378:LEU:HD22	2.43	0.49
1:A:124:SER:O	1:A:159:MET:HE3	2.13	0.49
1:A:373:VAL:HG12	1:A:437:PRO:HG3	1.93	0.49
1:A:386:ARG:HB3	1:A:390:VAL:HG12	1.94	0.49
1:B:97:THR:O	1:B:100:GLN:HG3	2.14	0.48
1:B:526:ALA:HA	1:B:553:LEU:HB2	1.94	0.48
1:A:168:GLY:HA3	1:A:212:LEU:O	2.13	0.48
1:B:483:GLU:HG3	1:B:574:ALA:N	2.28	0.48
1:A:335:ALA:HB1	1:B:162:GLU:CD	2.34	0.48
1:A:191:ALA:HB3	1:B:165:ASN:OD1	2.14	0.48
1:A:153:GLY:C	1:A:334:ILE:HD12	2.34	0.48
1:A:386:ARG:CD	1:A:444:ARG:HB2	2.33	0.48
1:A:415:MET:HE3	1:A:426:MET:CB	2.32	0.48
1:B:255:GLU:HG2	1:B:259:LYS:HD2	1.95	0.48
1:A:231:THR:CG2	1:A:235:MET:CE	2.92	0.48
1:B:254:TYR:CZ	1:B:256:PRO:HG2	2.48	0.47
1:B:519:LEU:HB2	1:B:548:VAL:HG22	1.96	0.47
1:B:234:ASN:O	1:B:238:LEU:CD2	2.63	0.47
1:B:389:ILE:HD11	1:B:553:LEU:HD21	1.97	0.46
1:A:184:SER:HB2	1:A:185:ILE:H	1.52	0.46
1:A:357:ILE:O	1:A:384:ILE:HA	2.15	0.46
1:A:135:ILE:HD11	1:A:172:PRO:HB3	1.96	0.46
1:B:332:VAL:O	1:B:333:ALA:HB3	2.16	0.46
1:A:287:TYR:HB3	1:A:442:TYR:CD2	2.51	0.46
1:A:208:LEU:HD12	1:B:208:LEU:CD1	2.47	0.45
1:A:286:SER:HA	1:A:446:SER:HA	1.98	0.45
1:A:358:TYR:CE2	1:A:386:ARG:HG2	2.51	0.45
1:B:105:HIS:HD2	4:B:796:HOH:O	1.99	0.45
1:A:233:LYS:HE3	1:A:233:LYS:HB2	1.54	0.45
1:B:187:GLU:OE2	1:B:262:ILE:HD11	2.17	0.45
1:B:352:LYS:NZ	4:B:707:HOH:O	2.50	0.45
1:B:284:LEU:HB3	1:B:285:PRO:HD2	1.99	0.45
1:B:40:LEU:O	1:B:44:SER:HB2	2.17	0.44
1:B:325:PHE:HB3	1:B:328:ARG:HG3	1.99	0.44
1:B:512:LEU:HD12	1:B:513:ALA:N	2.32	0.44
1:B:543:ARG:HG2	1:B:543:ARG:NH1	2.33	0.44
1:B:192:LEU:CD1	1:B:208:LEU:HD22	2.47	0.44
1:A:540:MET:HB3	1:B:548:VAL:O	2.18	0.44
1:A:372:ASP:O	1:A:376:GLN:HG3	2.15	0.44
1:A:14:VAL:HG22	1:A:14:VAL:O	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:21:ARG:HG2	1:A:65:TYR:HA	2.00	0.44
1:A:106:PRO:HD2	4:A:722:HOH:O	2.17	0.44
1:B:415:MET:HB3	1:B:426:MET:SD	2.58	0.44
1:B:509:ILE:HA	1:B:512:LEU:HD11	1.99	0.44
1:B:186:SER:HA	1:B:262:ILE:HG12	2.01	0.43
1:B:77:ASP:OD1	1:B:78:VAL:HG23	2.18	0.43
1:B:387:ALA:HB1	1:B:441:ARG:CZ	2.48	0.43
1:A:81:GLN:HG2	1:A:81:GLN:O	2.17	0.43
1:B:417:PRO:HD2	1:B:441:ARG:O	2.19	0.43
1:B:496:VAL:HG21	1:B:508:LEU:CD2	2.49	0.43
1:A:10:THR:HG22	1:A:23:LEU:HD11	2.00	0.42
1:B:225:VAL:O	1:B:229:VAL:HG23	2.18	0.42
1:B:95:ILE:HD12	1:B:95:ILE:HA	1.92	0.42
1:B:192:LEU:HD13	1:B:208:LEU:CD2	2.49	0.42
1:B:360:THR:HG23	1:B:361:PHE:CD1	2.54	0.42
1:B:92:ARG:NH1	1:B:93:ASP:OD1	2.52	0.42
1:B:254:TYR:CE2	1:B:256:PRO:HG2	2.55	0.42
1:B:3:PHE:CG	1:B:92:ARG:NH1	2.88	0.42
1:B:376:GLN:HB2	1:B:378:LEU:HD22	2.02	0.42
1:A:178:LEU:HB2	1:A:243:PHE:CZ	2.55	0.42
1:A:460:ILE:HA	1:A:500:PHE:CZ	2.54	0.42
1:B:562:THR:HG22	1:B:564:GLU:N	2.34	0.42
1:B:352:LYS:HD3	1:B:431:TYR:CZ	2.54	0.42
1:A:83:TYR:HB2	1:A:84:PRO:HD3	2.01	0.41
1:B:260:ASP:OD2	1:B:263:THR:HB	2.20	0.41
1:A:208:LEU:CD1	1:B:208:LEU:CD1	2.98	0.41
1:A:76:TRP:O	1:A:120:VAL:HG11	2.20	0.41
1:B:357:ILE:O	1:B:384:ILE:HA	2.20	0.41
1:B:8:TYR:CA	1:B:34:GLU:OE2	2.52	0.41
1:B:453:GLU:HB3	1:B:454:PRO:HD2	2.03	0.41
1:A:387:ALA:HB1	1:A:441:ARG:NE	2.35	0.41
1:A:417:PRO:HD2	1:A:441:ARG:O	2.20	0.41
1:B:73:ARG:HA	4:B:741:HOH:O	2.21	0.41
1:B:127:ILE:O	1:B:131:ILE:HG13	2.21	0.41
1:A:10:THR:CG2	1:A:23:LEU:HD11	2.51	0.40
1:A:472:ILE:HD11	1:A:520:VAL:CG2	2.48	0.40
1:B:239:LYS:HA	1:B:239:LYS:HD2	1.82	0.40
1:A:415:MET:HE1	1:A:426:MET:HB3	2.00	0.40
1:A:184:SER:HB3	2:A:601:SW6:O20	2.22	0.40
1:A:402:ASP:HA	1:A:405:PHE:CE2	2.57	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	540/586 (92%)	519 (96%)	20 (4%)	1 (0%)	47 39
1	B	562/586 (96%)	540 (96%)	20 (4%)	2 (0%)	34 24
All	All	1102/1172 (94%)	1059 (96%)	40 (4%)	3 (0%)	41 31

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	184	SER
1	B	4	ASP
1	B	310	PRO

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	436/466 (94%)	427 (98%)	9 (2%)	53 48
1	B	453/466 (97%)	441 (97%)	12 (3%)	46 39
All	All	889/932 (95%)	868 (98%)	21 (2%)	49 42

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	VAL
1	A	39	LEU
1	A	41	ASP

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Mol	Chain	Res	Type
1	A	184	SER
1	A	192	LEU
1	A	252	ARG
1	A	289	LYS
1	A	407	ARG
1	A	544	ARG
1	B	10	THR
1	B	42	SER
1	B	124	SER
1	B	133	VAL
1	B	189	VAL
1	B	239	LYS
1	B	301	LYS
1	B	378	LEU
1	B	435	ASP
1	B	441	ARG
1	B	462	LYS
1	B	512	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	GLN
1	A	100	GLN
1	A	105	HIS
1	A	234	ASN

5.3.3 RNA (i)

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 3 are monoatomic - leaving 2 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	SW6	B	601	3	23,27,27	2.88	7 (30%)	29,39,39	1.47	6 (20%)
2	SW6	A	601	3	23,27,27	2.57	6 (26%)	29,39,39	1.40	4 (13%)

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	SW6	B	601	3	-	0/12/17/17	0/2/2/2
2	SW6	A	601	3	-	1/12/17/17	0/2/2/2

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	SW6	C18-C17	8.52	1.54	1.50
2	A	601	SW6	C18-C17	6.60	1.53	1.50
2	B	601	SW6	C17-S16	-6.20	1.62	1.74
2	A	601	SW6	C10-C25	5.38	1.53	1.37
2	A	601	SW6	C17-S16	-5.32	1.64	1.74
2	B	601	SW6	C10-C25	5.20	1.53	1.37
2	A	601	SW6	C02-N01	4.85	1.46	1.34
2	B	601	SW6	C02-N01	4.77	1.46	1.34
2	A	601	SW6	C09-C08	2.47	1.57	1.52
2	A	601	SW6	C13-C12	2.30	1.54	1.50
2	B	601	SW6	C13-C12	2.26	1.54	1.50
2	B	601	SW6	P21-O20	2.15	1.67	1.60
2	B	601	SW6	O15-C12	-2.04	1.19	1.22

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	601	SW6	C07-N06-C04	3.42	121.79	115.96
2	A	601	SW6	C07-N06-C04	3.32	121.61	115.96
2	B	601	SW6	C08-C07-N06	-3.27	118.38	123.82
2	B	601	SW6	N01-C02-N03	2.91	121.15	117.03
2	A	601	SW6	C08-C07-N06	-2.63	119.43	123.82
2	B	601	SW6	N06-C04-N03	-2.38	121.45	125.54
2	A	601	SW6	N06-C04-N03	-2.37	121.47	125.54
2	A	601	SW6	C09-C10-C25	-2.33	122.33	126.49
2	B	601	SW6	C08-C02-N01	-2.24	119.01	122.19
2	B	601	SW6	C07-C08-C02	2.02	118.47	115.72

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	SW6	C19-O20-P21-O24

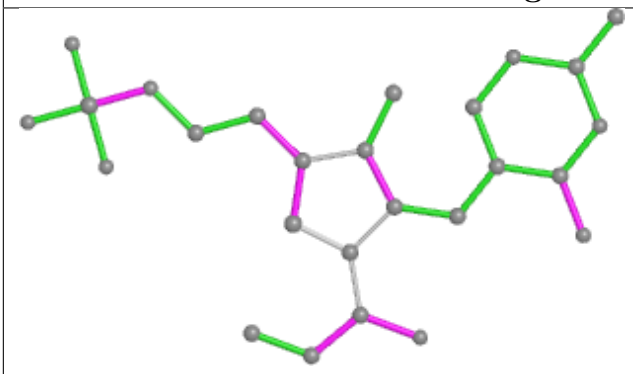
There are no ring outliers.

1 monomer is involved in 1 short contact:

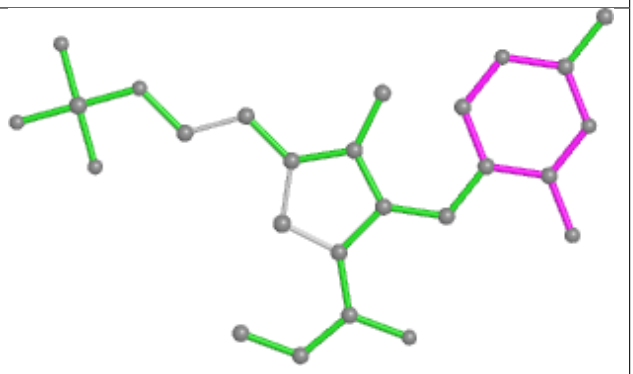
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	SW6	1	0

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.

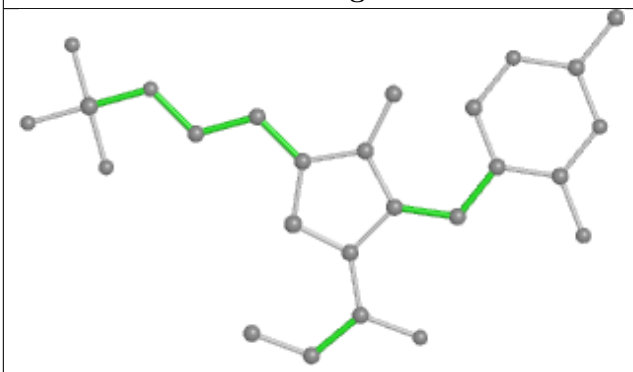
Ligand SW6 B 601



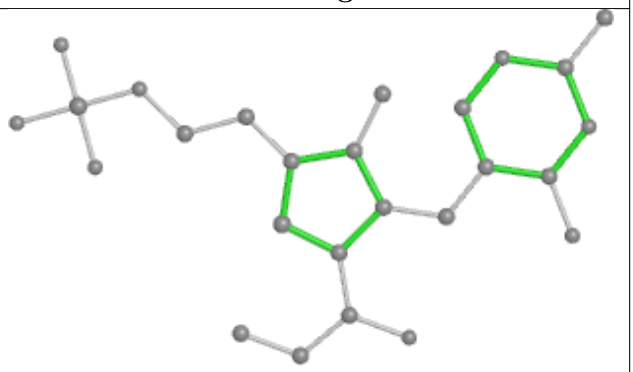
Bond lengths



Bond angles

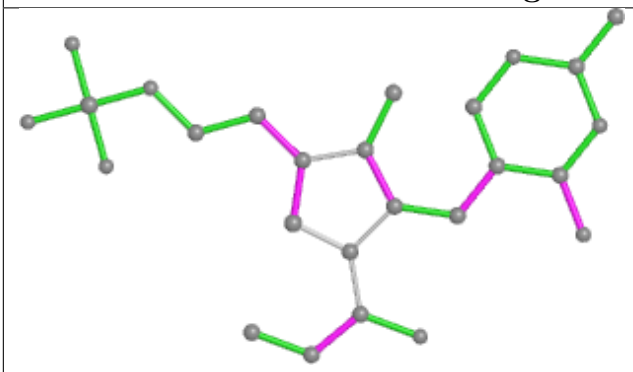


Torsions

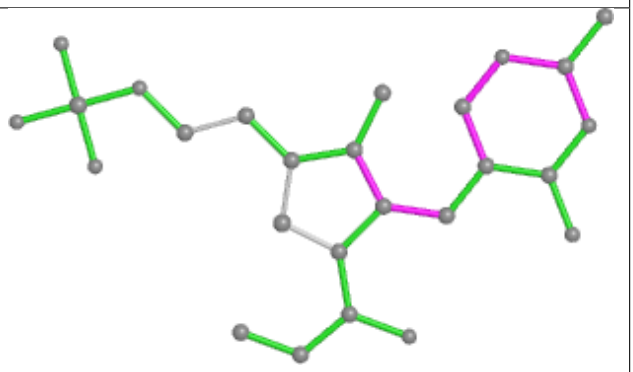


Rings

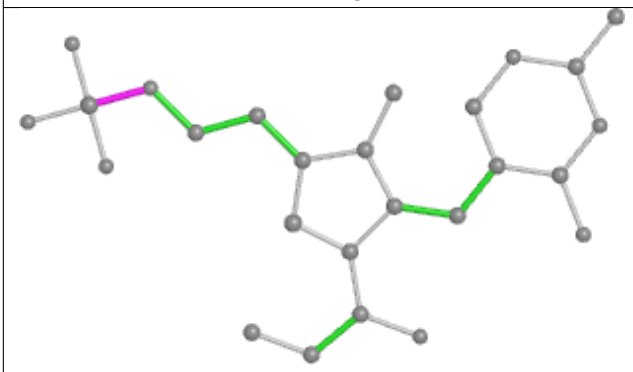
Ligand SW6 A 601



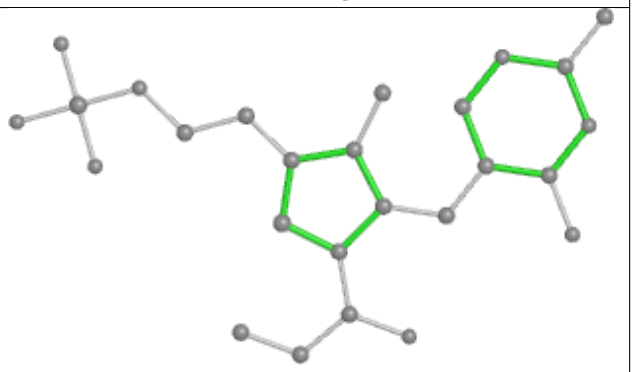
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

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	546/586 (93%)	0.58	52 (9%) 8 9	32, 44, 81, 130	0
1	B	568/586 (96%)	0.70	64 (11%) 5 5	33, 48, 77, 107	0
All	All	1114/1172 (95%)	0.64	116 (10%) 6 6	32, 45, 80, 130	0

All (116) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	183	MET	9.3
1	A	186	SER	9.1
1	A	45	ARG	8.8
1	A	185	ILE	6.1
1	B	5	ILE	5.5
1	A	192	LEU	5.4
1	A	255	GLU	5.4
1	B	3	PHE	5.3
1	A	184	SER	5.2
1	A	254	TYR	5.2
1	B	2	SER	4.7
1	A	256	PRO	4.7
1	A	41	ASP	4.4
1	B	270	PHE	4.3
1	B	586	ALA	4.3
1	B	273	THR	4.1
1	B	272	HIS	4.1
1	A	43	VAL	3.9
1	A	50	PHE	3.7
1	A	44	SER	3.6
1	A	188	ASN	3.5
1	A	187	GLU	3.5
1	B	255	GLU	3.5
1	B	259	LYS	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	40	LEU	3.4
1	B	40	LEU	3.4
1	A	284	LEU	3.4
1	A	46	SER	3.3
1	A	189	VAL	3.3
1	A	47	SER	3.3
1	B	6	ALA	3.3
1	A	42	SER	3.2
1	B	8	TYR	3.2
1	B	271	ASP	3.2
1	A	11	LEU	3.2
1	B	362	LEU	3.1
1	B	361	PHE	3.1
1	A	252	ARG	3.1
1	B	472	ILE	3.0
1	A	23	LEU	3.0
1	B	369	VAL	3.0
1	B	14	VAL	3.0
1	A	31	LEU	3.0
1	B	370	ILE	2.9
1	A	283	GLY	2.9
1	B	38	TYR	2.9
1	B	254	TYR	2.9
1	A	249	LYS	2.9
1	B	7	LYS	2.9
1	B	93	ASP	2.9
1	A	253	GLY	2.8
1	A	5	ILE	2.8
1	B	262	ILE	2.8
1	B	37	ARG	2.7
1	B	367	ASP	2.7
1	A	15	ASP	2.7
1	A	38	TYR	2.7
1	A	191	ALA	2.7
1	B	468	GLN	2.7
1	A	170	ILE	2.6
1	B	374	ALA	2.6
1	A	13	LEU	2.6
1	B	161	PHE	2.6
1	A	190	GLY	2.6
1	B	340	VAL	2.6
1	B	4	ASP	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	203	GLY	2.6
1	B	267	VAL	2.5
1	B	264	PHE	2.5
1	B	339	ALA	2.5
1	A	361	PHE	2.5
1	B	357	ILE	2.5
1	B	470	GLU	2.5
1	A	7	LYS	2.5
1	A	250	LYS	2.5
1	B	355	VAL	2.4
1	A	366	TYR	2.4
1	A	365	ALA	2.4
1	B	260	ASP	2.4
1	A	8	TYR	2.4
1	B	257	ALA	2.4
1	B	256	PRO	2.4
1	B	263	THR	2.4
1	B	471	LYS	2.4
1	A	4	ASP	2.4
1	B	384	ILE	2.4
1	B	22	LEU	2.4
1	B	366	TYR	2.4
1	B	45	ARG	2.4
1	B	335	ALA	2.4
1	A	48	GLY	2.3
1	B	15	ASP	2.3
1	B	363	GLN	2.3
1	A	19	GLU	2.3
1	B	311	ALA	2.2
1	B	382	PHE	2.2
1	B	405	PHE	2.2
1	B	437	PRO	2.2
1	A	400	ALA	2.2
1	B	410	PRO	2.2
1	B	365	ALA	2.2
1	A	49	HIS	2.2
1	A	6	ALA	2.1
1	B	13	LEU	2.1
1	B	205	PRO	2.1
1	B	414	VAL	2.1
1	B	529	GLY	2.1
1	A	27	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	400	ALA	2.1
1	B	269	LYS	2.1
1	A	369	VAL	2.0
1	B	450	ALA	2.0
1	A	18	GLN	2.0
1	A	9	PRO	2.0
1	A	452	LEU	2.0
1	B	375	ILE	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)

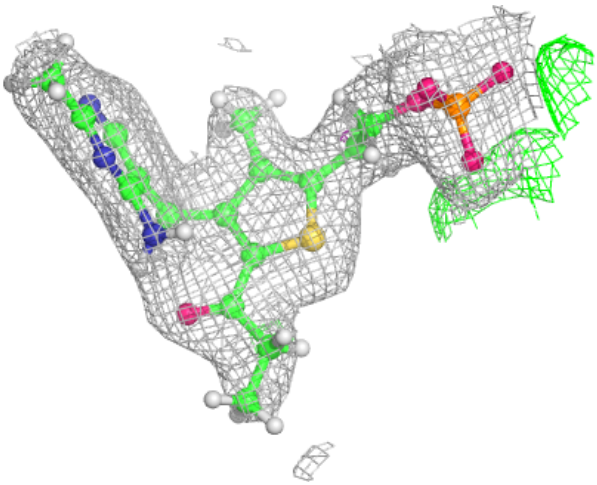
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

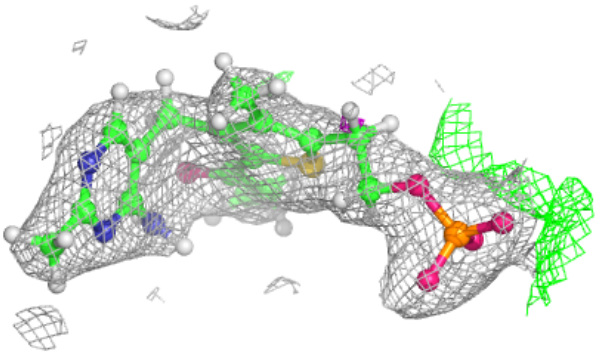
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	MG	A	602	1/1	0.77	0.28	59,59,59,59	0
3	MG	B	602	1/1	0.88	0.23	46,46,46,46	0
3	MG	B	603	1/1	0.89	0.35	59,59,59,59	0
2	SW6	B	601	26/26	0.96	0.14	33,44,57,57	0
2	SW6	A	601	26/26	0.96	0.14	35,47,62,63	0

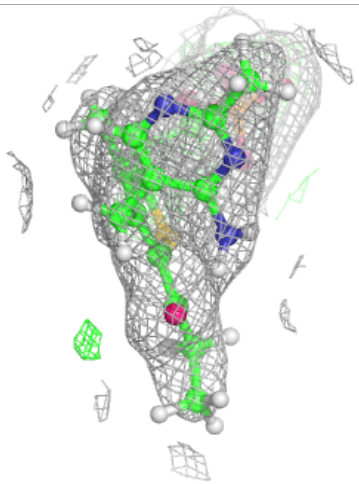
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around SW6 B 601:

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

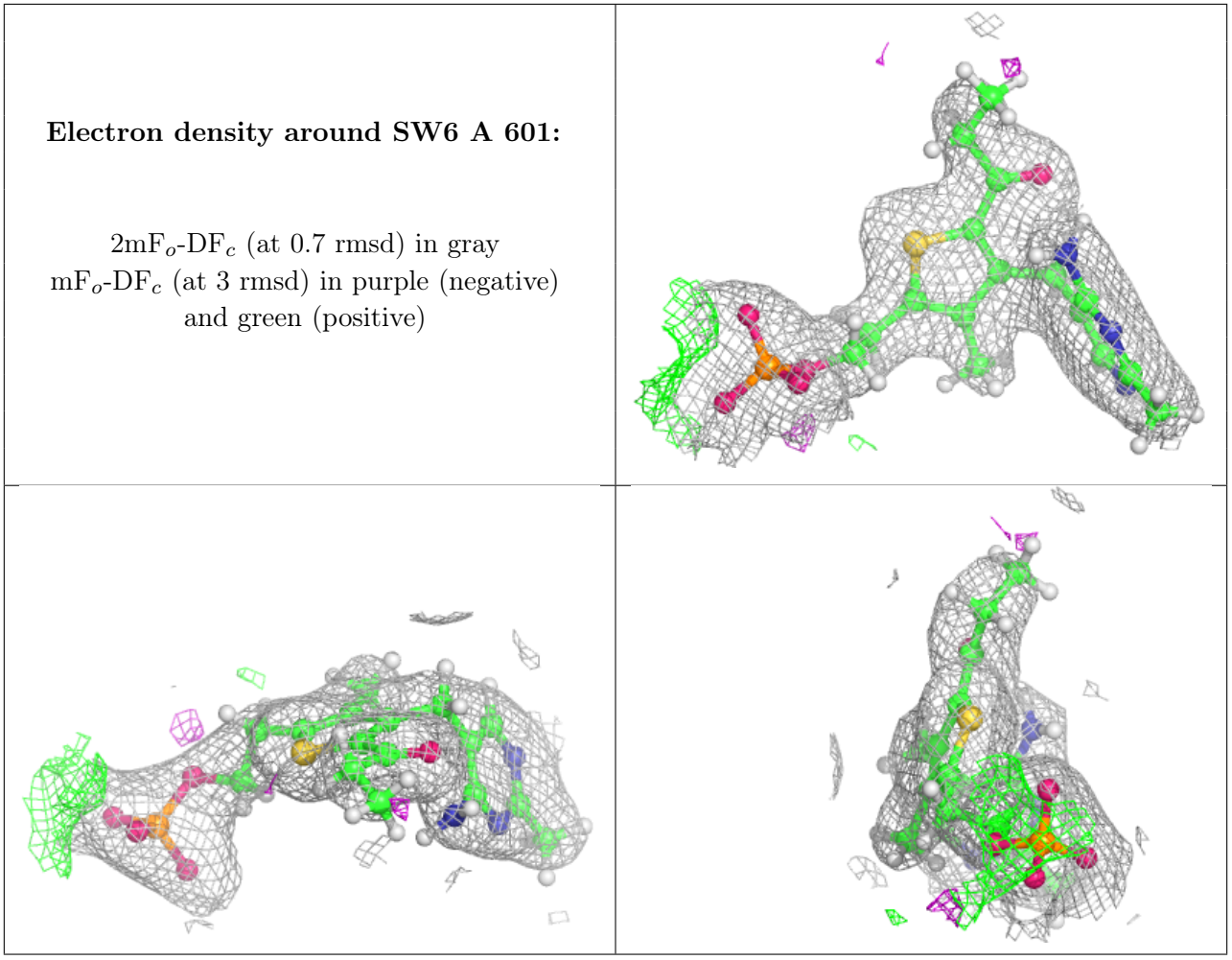






Electron density around SW6 A 601:

$2mF_o$-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.