Full wwPDB X-ray Structure Validation Report (i)

May 22, 2020 – 06:28 pm BST

PDB ID	:	6BAB
Title	:	The structure of human CamKII with bound inhibitor
Authors	:	Somoza, J.R.; Villasenor, A.G.
Deposited on	:	2017-10-12
Resolution	:	1.91 Å(reported)

The following versions of software and data (see references (i)) 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 ⓘ

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

The reported resolution of this entry is 1.91 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.
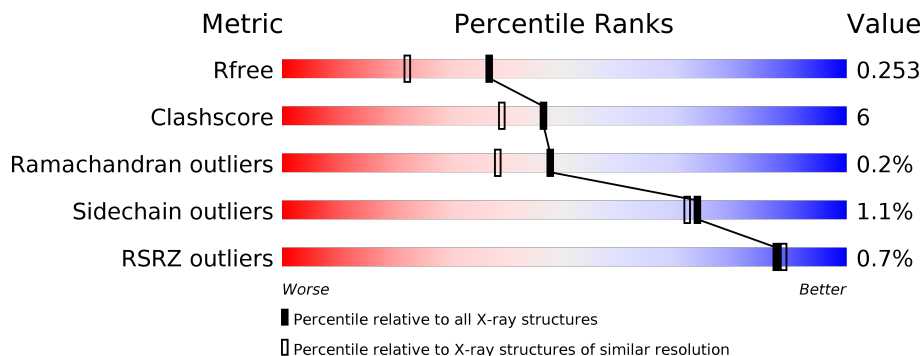
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	7937 (1.94-1.90)
Clashscore	141614	8644 (1.94-1.90)
Ramachandran outliers	138981	8530 (1.94-1.90)
Sidechain outliers	138945	8530 (1.94-1.90)
RSRZ outliers	127900	7793 (1.94-1.90)

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	302	84% 12% •
1	B	302	% 79% 14% • 6%
1	C	302	% 79% 14% • 6%
1	D	302	86% 11% •

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 10369 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 Calcium/calmodulin-dependent protein kinase type II subunit delta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	290	Total	C	N	O	S	0	1	0
			2331	1488	407	423	13			
1	B	285	Total	C	N	O	S	0	1	0
			2296	1466	402	415	13			
1	C	284	Total	C	N	O	S	0	2	0
			2297	1468	402	414	13			
1	D	292	Total	C	N	O	S	0	1	1
			2335	1490	408	424	13			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP Q6PHZ2
A	2	HIS	-	expression tag	UNP Q6PHZ2
A	3	MET	-	expression tag	UNP Q6PHZ2
B	1	GLY	-	expression tag	UNP Q6PHZ2
B	2	HIS	-	expression tag	UNP Q6PHZ2
B	3	MET	-	expression tag	UNP Q6PHZ2
C	1	GLY	-	expression tag	UNP Q6PHZ2
C	2	HIS	-	expression tag	UNP Q6PHZ2
C	3	MET	-	expression tag	UNP Q6PHZ2
D	2	GLY	-	expression tag	UNP Q6PHZ2
D	3	HIS	-	expression tag	UNP Q6PHZ2
D	4	MET	-	expression tag	UNP Q6PHZ2

- Molecule 2 is N-[(2S)-2-(diethylamino)propyl]-2-(3-hydroxyazetidin-1-yl)-6-[5-(thiophen-2-yl)pyrazolo[1,5-a]pyrimidin-3-yl]pyridine-4-carboxamide (three-letter code: D0S) (formula: $C_{26}H_{31}N_7O_2S$).
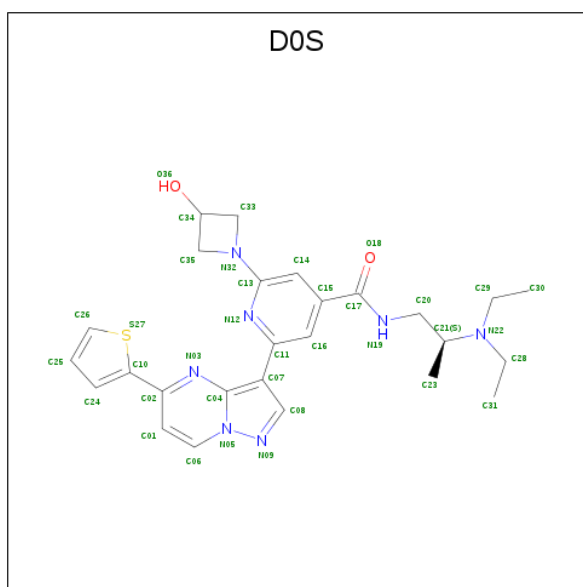
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			36	26	7	2	1		
2	B	1	Total	C	N	O	S	0	0
			36	26	7	2	1		
2	C	1	Total	C	N	O	S	0	0
			36	26	7	2	1		
2	D	1	Total	C	N	O	S	0	0
			36	26	7	2	1		

- Molecule 3 is L(+)-TARTARIC ACID (three-letter code: TLA) (formula: $C_4H_6O_6$).
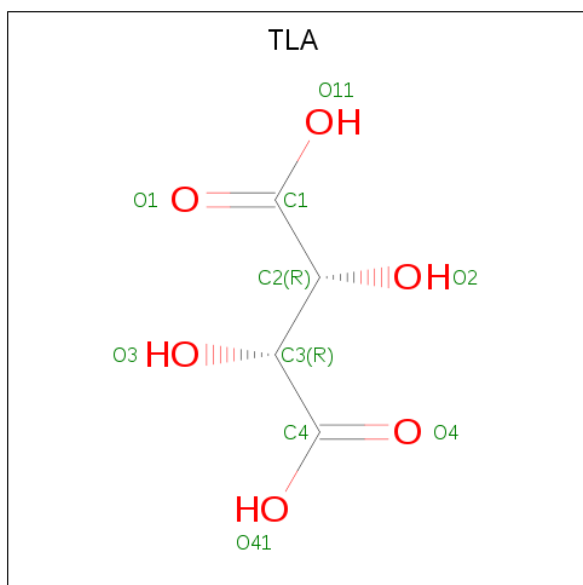
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 10	C 4	O 6	0	0
3	B	1	Total 10	C 4	O 6	0	0
3	C	1	Total 10	C 4	O 6	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	248	Total 248	O 248	0	0
4	B	221	Total 221	O 221	0	0
4	C	247	Total 247	O 247	0	0
4	D	220	Total 220	O 220	0	0

3 Residue-property plots ⓘ

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: Calcium/calmodulin-dependent protein kinase type II subunit delta
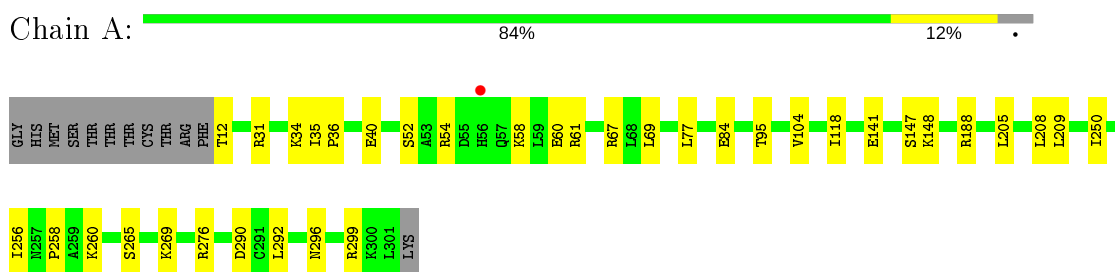
- Molecule 1: Calcium/calmodulin-dependent protein kinase type II subunit delta
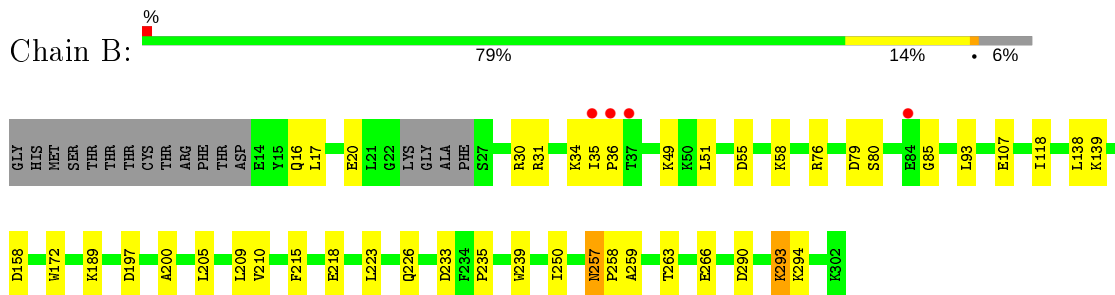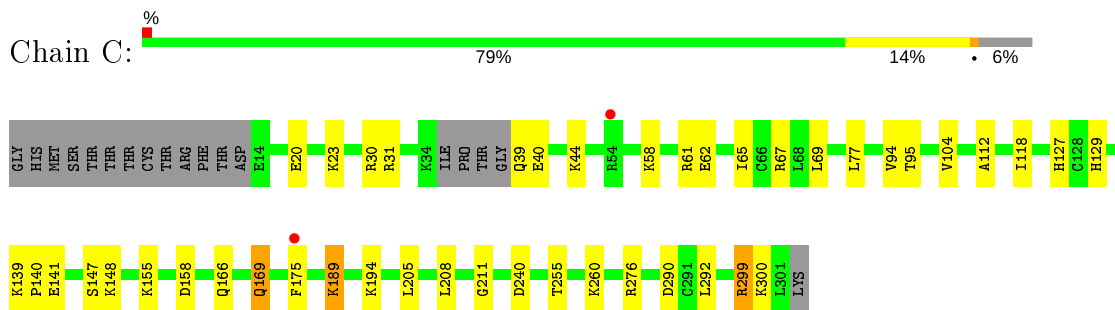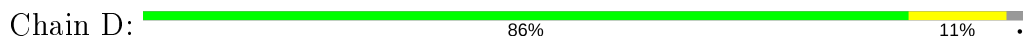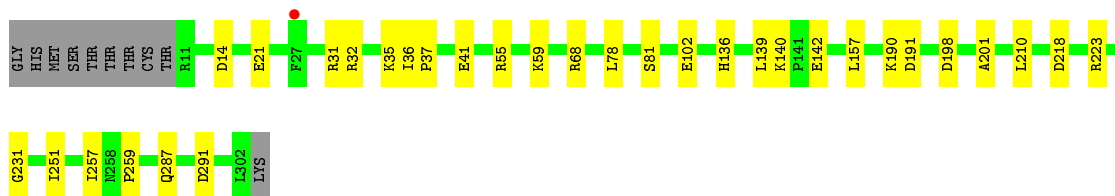

- Molecule 1: Calcium/calmodulin-dependent protein kinase type II subunit delta

- Molecule 1: Calcium/calmodulin-dependent protein kinase type II subunit delta

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	54.25Å 67.57Å 82.84Å 93.34° 92.93° 90.11°	Depositor
Resolution (Å)	54.18 – 1.91 54.18 – 1.69	Depositor EDS
% Data completeness (in resolution range)	86.7 (54.18-1.91) 79.5 (54.18-1.69)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.97 (at 1.69Å)	Xtriage
Refinement program	PHENIX 1.12_2829	Depositor
R, R_{free}	0.190 , 0.253 0.190 , 0.253	Depositor DCC
R_{free} test set	1330 reflections (1.16%)	wwPDB-VP
Wilson B-factor (Å^2)	17.6	Xtriage
Anisotropy	0.558	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 49.4	EDS
L-test for twinning[2]	$< |L| > = 0.49, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.030 for h,-k,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	10369	wwPDB-VP
Average B, all atoms (Å^2)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.17% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: TLA, D0S

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	0.37	0/2390	0.53	0/3233
1	B	0.37	0/2353	0.53	0/3181
1	C	0.38	0/2354	0.55	0/3181
1	D	0.35	0/2393	0.51	0/3235
All	All	0.36	0/9490	0.53	0/12830

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 (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	2331	0	2322	33	0
1	B	2296	0	2293	33	0
1	C	2297	0	2290	32	0
1	D	2335	0	2321	21	0
2	A	36	0	0	0	0
2	B	36	0	0	1	0
2	C	36	0	0	0	0
2	D	36	0	0	1	0
3	A	10	0	4	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	10	0	4	0	0
3	C	10	0	4	0	0
4	A	248	0	0	16	2
4	B	221	0	0	13	1
4	C	247	0	0	10	0
4	D	220	0	0	7	1
All	All	10369	0	9238	118	2

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 6.

All (118) 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:276:ARG:NH1	4:A:502:HOH:O	2.10	0.83
1:D:198:ASP:O	4:D:501:HOH:O	1.94	0.83
1:C:276:ARG:NH2	4:C:504:HOH:O	2.17	0.76
1:C:240:ASP:OD1	4:C:501:HOH:O	2.06	0.73
1:B:200:ALA:HB3	4:B:503:HOH:O	1.89	0.72
1:A:35:ILE:HG13	1:A:36:PRO:HD3	1.70	0.72
1:A:12:THR:O	4:A:501:HOH:O	2.07	0.71
1:C:290:ASP:OD2	4:C:502:HOH:O	2.07	0.71
1:B:107:GLU:OE2	4:B:501:HOH:O	2.09	0.70
1:C:127:HIS:NE2	4:C:507:HOH:O	2.25	0.69
1:A:256:ILE:O	4:A:503:HOH:O	2.11	0.68
2:B:401:D0S:O36	4:B:502:HOH:O	2.11	0.67
1:B:51:LEU:HB3	1:B:55:ASP:HB2	1.75	0.67
1:D:14:ASP:OD2	4:D:502:HOH:O	2.12	0.67
1:B:189:LYS:NZ	4:B:507:HOH:O	2.26	0.67
1:A:290:ASP:OD1	4:A:504:HOH:O	2.12	0.67
1:D:136:HIS:CD2	1:D:157:LEU:HD21	2.29	0.67
1:B:226:GLN:HB2	4:B:505:HOH:O	1.95	0.66
1:C:31:ARG:NH1	1:C:40:GLU:OE2	2.29	0.66
1:C:290:ASP:OD1	4:C:503:HOH:O	2.12	0.66
1:B:139:LYS:NZ	4:B:509:HOH:O	2.28	0.65
1:B:197:ASP:O	4:B:503:HOH:O	2.14	0.65
1:C:139:LYS:NZ	4:C:512:HOH:O	2.30	0.64
1:B:31:ARG:HE	1:B:93:LEU:HD21	1.63	0.64
1:B:34:LYS:HG2	1:B:36:PRO:HD2	1.79	0.64
1:B:49:LYS:HG3	1:B:85:GLY:HA2	1.80	0.63
1:A:61:ARG:NH2	4:A:514:HOH:O	2.30	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:67:ARG:NH2	4:A:506:HOH:O	2.31	0.63
1:A:118:ILE:HG13	1:A:205:LEU:HD13	1.84	0.59
1:B:118:ILE:HG13	1:B:205:LEU:HD13	1.83	0.59
1:C:276:ARG:NH1	4:C:520:HOH:O	2.36	0.58
1:A:52:SER:OG	1:A:58:LYS:NZ	2.37	0.58
1:C:112:ALA:O	1:C:276:ARG:HD2	2.03	0.58
1:C:140:PRO:HB2	1:C:299:ARG:HH12	1.68	0.57
1:D:68:ARG:HG2	1:D:78:LEU:HD23	1.86	0.57
1:A:188:ARG:NH2	4:A:516:HOH:O	2.33	0.57
1:B:290:ASP:O	1:B:293:LYS:HG2	2.04	0.56
1:C:118:ILE:HG13	1:C:205:LEU:HD13	1.87	0.56
1:D:218:ASP:OD1	1:D:223:ARG:NH1	2.38	0.56
1:A:84:GLU:H	1:A:84:GLU:CD	2.10	0.53
1:B:138:LEU:HB3	4:B:503:HOH:O	2.08	0.53
1:C:129:HIS:HB3	1:C:194:LYS:HD3	1.89	0.53
1:B:223:LEU:HD12	4:B:505:HOH:O	2.08	0.53
1:D:210:LEU:HD12	1:D:251:ILE:HD11	1.91	0.53
1:C:67:ARG:HG3	1:C:77:LEU:HD23	1.91	0.52
1:A:67:ARG:HG3	1:A:77:LEU:HD23	1.90	0.51
1:C:23:LYS:NZ	4:C:527:HOH:O	2.41	0.51
1:C:95:THR:CG2	1:C:147:SER:HB2	2.40	0.51
1:D:102:GLU:HG2	4:D:506:HOH:O	2.10	0.51
1:D:201:ALA:HB3	4:D:501:HOH:O	2.11	0.50
1:D:55:ARG:HG3	1:D:59:LYS:HE2	1.92	0.50
1:B:20:GLU:HA	1:B:30:ARG:HG2	1.93	0.49
1:B:209:LEU:HD12	1:B:250:ILE:HD11	1.96	0.48
1:B:258:PRO:HD3	4:B:524:HOH:O	2.12	0.48
1:A:31:ARG:HD2	1:A:40:GLU:OE1	2.13	0.48
1:D:21:GLU:HA	1:D:31:ARG:HG2	1.96	0.48
1:B:215:PHE:HB3	4:B:505:HOH:O	2.13	0.48
1:D:191:ASP:OD2	4:D:503:HOH:O	2.20	0.48
1:D:287:GLN:NE2	1:D:291:ASP:OD1	2.45	0.48
1:C:104:VAL:HG12	1:C:292:LEU:HB3	1.95	0.48
1:A:54:ARG:NE	4:A:525:HOH:O	2.46	0.47
1:A:296:ASN:OD1	1:A:299:ARG:NH1	2.37	0.47
1:D:68:ARG:NH2	1:D:81:SER:HB3	2.29	0.47
2:D:401:D0S:O36	4:D:504:HOH:O	2.20	0.47
1:C:141:GLU:HG3	1:C:299:ARG:NH2	2.30	0.47
1:D:35:LYS:HG3	1:D:37:PRO:HD2	1.96	0.47
1:B:76:ARG:NE	4:B:514:HOH:O	2.37	0.47
1:C:39:GLN:N	4:C:538:HOH:O	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:269:LYS:HE3	4:A:505:HOH:O	2.15	0.47
1:B:257:ASN:HD22	1:B:259:ALA:H	1.63	0.47
1:A:296:ASN:HA	1:A:299:ARG:NH1	2.30	0.46
1:A:118:ILE:HG12	1:A:208:LEU:HD12	1.97	0.46
1:C:166:GLN:H	1:C:169:GLN:HG2	1.80	0.46
1:C:300:LYS:NZ	4:C:537:HOH:O	2.48	0.46
1:B:263:THR:OG1	1:B:266:GLU:HG3	2.15	0.46
1:A:104:VAL:HG12	1:A:292:LEU:HB3	1.98	0.46
1:A:299:ARG:HD2	4:A:509:HOH:O	2.16	0.46
1:C:169:GLN:O	1:C:169:GLN:HG3	2.15	0.46
1:C:44:LYS:NZ	1:C:62:GLU:OE2	2.38	0.46
1:B:210:VAL:HG11	1:B:239:TRP:CE2	2.51	0.46
1:B:49:LYS:HB2	1:B:49:LYS:HE2	1.75	0.46
1:C:175:PHE:HE2	1:C:189:LYS:HZ1	1.63	0.45
1:C:20:GLU:HA	1:C:30:ARG:HG2	1.98	0.45
1:C:95:THR:HG23	1:C:147:SER:HB2	1.97	0.45
1:B:218:GLU:OE2	1:C:260:LYS:HE2	2.16	0.45
1:A:60:GLU:OE2	4:A:506:HOH:O	2.21	0.45
1:D:259:PRO:HD3	4:D:508:HOH:O	2.16	0.45
1:B:79:ASP:OD1	1:B:80:SER:N	2.50	0.45
1:D:231:GLY:N	1:D:257:ILE:HD11	2.32	0.44
1:B:58:LYS:NZ	4:B:504:HOH:O	2.19	0.44
1:A:188:ARG:NH2	4:A:503:HOH:O	2.38	0.44
1:A:260:LYS:NZ	4:A:517:HOH:O	2.35	0.44
1:B:17:LEU:HD13	1:B:30:ARG:NH1	2.32	0.44
1:A:95:THR:OG1	1:A:147:SER:HB2	2.18	0.44
1:C:141:GLU:HG3	1:C:299:ARG:HH22	1.83	0.44
1:D:140:LYS:HE3	1:D:142:GLU:HB2	1.99	0.43
1:B:235:PRO:HD2	1:B:239:TRP:CD1	2.53	0.43
1:D:36:ILE:HB	1:D:37:PRO:HD3	2.00	0.43
1:D:231:GLY:CA	1:D:257:ILE:HD11	2.49	0.43
1:C:211:GLY:HA2	1:C:292:LEU:HD13	2.00	0.43
1:C:58:LYS:HG2	1:C:61:ARG:HH21	1.84	0.43
1:B:293:LYS:HZ2	1:B:294:LYS:HG2	1.84	0.43
1:D:32:ARG:NH1	1:D:41:GLU:OE2	2.51	0.43
1:A:118:ILE:HA	1:A:118:ILE:HD13	1.94	0.42
1:A:34:LYS:HG2	1:A:36:PRO:HD2	2.01	0.42
1:A:141:GLU:OE2	4:A:507:HOH:O	2.22	0.42
1:A:258:PRO:HD3	4:A:503:HOH:O	2.18	0.42
1:C:94:VAL:HG11	1:C:155:LYS:HG3	2.02	0.42
1:B:172:TRP:CZ3	1:B:189:LYS:HA	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:209:LEU:HD12	1:A:250:ILE:HD11	2.01	0.41
1:C:148:LYS:HB2	1:D:190:LYS:HB3	2.02	0.41
1:C:61:ARG:O	1:C:65:ILE:HG13	2.20	0.41
1:A:265:SER:OG	4:A:505:HOH:O	2.15	0.41
1:A:292:LEU:HD23	1:A:292:LEU:HA	1.96	0.41
1:A:148:LYS:HB2	1:B:189:LYS:HB3	2.02	0.41
1:A:104:VAL:CG1	1:A:292:LEU:HB3	2.50	0.40
1:B:290:ASP:HA	1:B:293:LYS:HE3	2.04	0.40
1:B:16:GLN:HB2	1:B:35:ILE:HD11	2.02	0.40

All (2) 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)
4:A:701:HOH:O	4:B:625:HOH:O[1_655]	2.15	0.05
4:A:712:HOH:O	4:D:668:HOH:O[1_465]	2.16	0.04

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	289/302 (96%)	284 (98%)	5 (2%)	0	100	100
1	B	282/302 (93%)	274 (97%)	7 (2%)	1 (0%)	34	24
1	C	282/302 (93%)	276 (98%)	5 (2%)	1 (0%)	34	24
1	D	289/302 (96%)	283 (98%)	6 (2%)	0	100	100
All	All	1142/1208 (94%)	1117 (98%)	23 (2%)	2 (0%)	47	38

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	158	ASP
1	C	158	ASP

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	250/260 (96%)	249 (100%)	1 (0%)	91	91
1	B	247/260 (95%)	244 (99%)	3 (1%)	71	69
1	C	246/260 (95%)	240 (98%)	6 (2%)	49	41
1	D	249/260 (96%)	248 (100%)	1 (0%)	91	91
All	All	992/1040 (95%)	981 (99%)	11 (1%)	73	72

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

Mol	Chain	Res	Type
1	A	69	LEU
1	B	233	ASP
1	B	257	ASN
1	B	293	LYS
1	C	69	LEU
1	C	169	GLN
1	C	189	LYS
1	C	208	LEU
1	C	255	THR
1	C	299	ARG
1	D	139	LEU

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

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 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	#$|Z| > 2$
2	D0S	B	401	-	31,40,40	1.79	5 (16%)	32,57,57	1.40	4 (12%)
3	TLA	C	402	-	3,9,9	1.73	1 (33%)	6,12,12	1.22	0
2	D0S	C	401	-	31,40,40	1.67	5 (16%)	32,57,57	1.28	4 (12%)
2	D0S	A	401	-	31,40,40	1.67	4 (12%)	32,57,57	1.48	6 (18%)
3	TLA	A	402	-	3,9,9	2.03	2 (66%)	6,12,12	0.87	0
3	TLA	B	402	-	3,9,9	1.73	2 (66%)	6,12,12	1.12	1 (16%)
2	D0S	D	401	-	31,40,40	1.75	5 (16%)	32,57,57	1.30	5 (15%)

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	D0S	B	401	-	-	3/19/37/37	0/5/5/5
3	TLA	C	402	-	-	0/4/12/12	-
2	D0S	C	401	-	-	2/19/37/37	0/5/5/5
2	D0S	A	401	-	-	2/19/37/37	0/5/5/5
3	TLA	A	402	-	-	0/4/12/12	-
3	TLA	B	402	-	-	0/4/12/12	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	D0S	D	401	-	-	6/19/37/37	0/5/5/5

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	401	D0S	C01-C02	5.10	1.50	1.38
2	A	401	D0S	C01-C02	5.07	1.50	1.38
2	C	401	D0S	C01-C02	5.00	1.50	1.38
2	B	401	D0S	C01-C02	4.87	1.50	1.38
2	C	401	D0S	C35-N32	-4.81	1.42	1.47
2	D	401	D0S	C35-N32	-4.58	1.42	1.47
2	B	401	D0S	C35-N32	-4.53	1.42	1.47
2	D	401	D0S	C33-N32	-4.49	1.42	1.47
2	B	401	D0S	C33-N32	-4.40	1.42	1.47
2	A	401	D0S	C35-N32	-4.28	1.42	1.47
2	C	401	D0S	C33-N32	-4.09	1.43	1.47
2	A	401	D0S	C33-N32	-3.99	1.43	1.47
2	B	401	D0S	C07-C11	-3.23	1.44	1.49
2	D	401	D0S	C07-C11	-2.56	1.45	1.49
2	D	401	D0S	C17-N19	2.51	1.39	1.33
2	A	401	D0S	C07-C11	-2.46	1.46	1.49
3	A	402	TLA	O2-C2	-2.45	1.37	1.42
2	B	401	D0S	C10-S27	-2.45	1.70	1.72
3	A	402	TLA	O3-C3	-2.34	1.38	1.42
3	C	402	TLA	O2-C2	-2.16	1.38	1.42
2	C	401	D0S	C07-C11	-2.14	1.46	1.49
3	B	402	TLA	O3-C3	-2.10	1.38	1.42
2	C	401	D0S	C17-N19	2.04	1.38	1.33
3	B	402	TLA	O2-C2	-2.00	1.38	1.42

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	D0S	C06-C01-C02	-4.12	115.05	118.03
2	C	401	D0S	C06-C01-C02	-3.85	115.24	118.03
2	B	401	D0S	C06-C01-C02	-3.65	115.39	118.03
2	A	401	D0S	C23-C21-N22	-3.26	108.44	114.31
2	B	401	D0S	C23-C21-N22	-3.03	108.85	114.31
2	D	401	D0S	C06-C01-C02	-2.84	115.98	118.03
2	A	401	D0S	C15-C14-C13	2.83	118.76	117.18
2	A	401	D0S	C14-C13-N32	-2.77	119.00	122.29
2	D	401	D0S	C14-C13-N32	-2.69	119.10	122.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	401	D0S	C07-C11-N12	-2.55	112.81	116.14
2	D	401	D0S	C23-C21-N22	-2.49	109.82	114.31
2	B	401	D0S	C15-C14-C13	2.48	118.57	117.18
2	B	401	D0S	C25-C26-S27	-2.47	110.98	112.98
3	B	402	TLA	C1-C2-C3	-2.31	108.13	113.11
2	A	401	D0S	N12-C13-N32	2.30	119.13	116.55
2	D	401	D0S	N12-C13-N32	2.27	119.10	116.55
2	D	401	D0S	C15-C14-C13	2.27	118.45	117.18
2	C	401	D0S	C16-C11-C07	2.24	125.36	121.05
2	C	401	D0S	C15-C14-C13	2.05	118.33	117.18
2	A	401	D0S	C07-C11-N12	-2.05	113.46	116.14

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	401	D0S	N19-C20-C21-C23
2	B	401	D0S	N19-C20-C21-N22
2	B	401	D0S	C30-C29-N22-C28
2	C	401	D0S	C20-C21-N22-C29
2	D	401	D0S	C20-C21-N22-C28
2	D	401	D0S	C20-C21-N22-C29
2	D	401	D0S	C23-C21-N22-C28
2	D	401	D0S	C23-C21-N22-C29
2	D	401	D0S	C30-C29-N22-C21
2	C	401	D0S	N19-C20-C21-C23
2	D	401	D0S	C30-C29-N22-C28
2	A	401	D0S	C23-C21-N22-C28
2	A	401	D0S	C23-C21-N22-C29

There are no ring outliers.
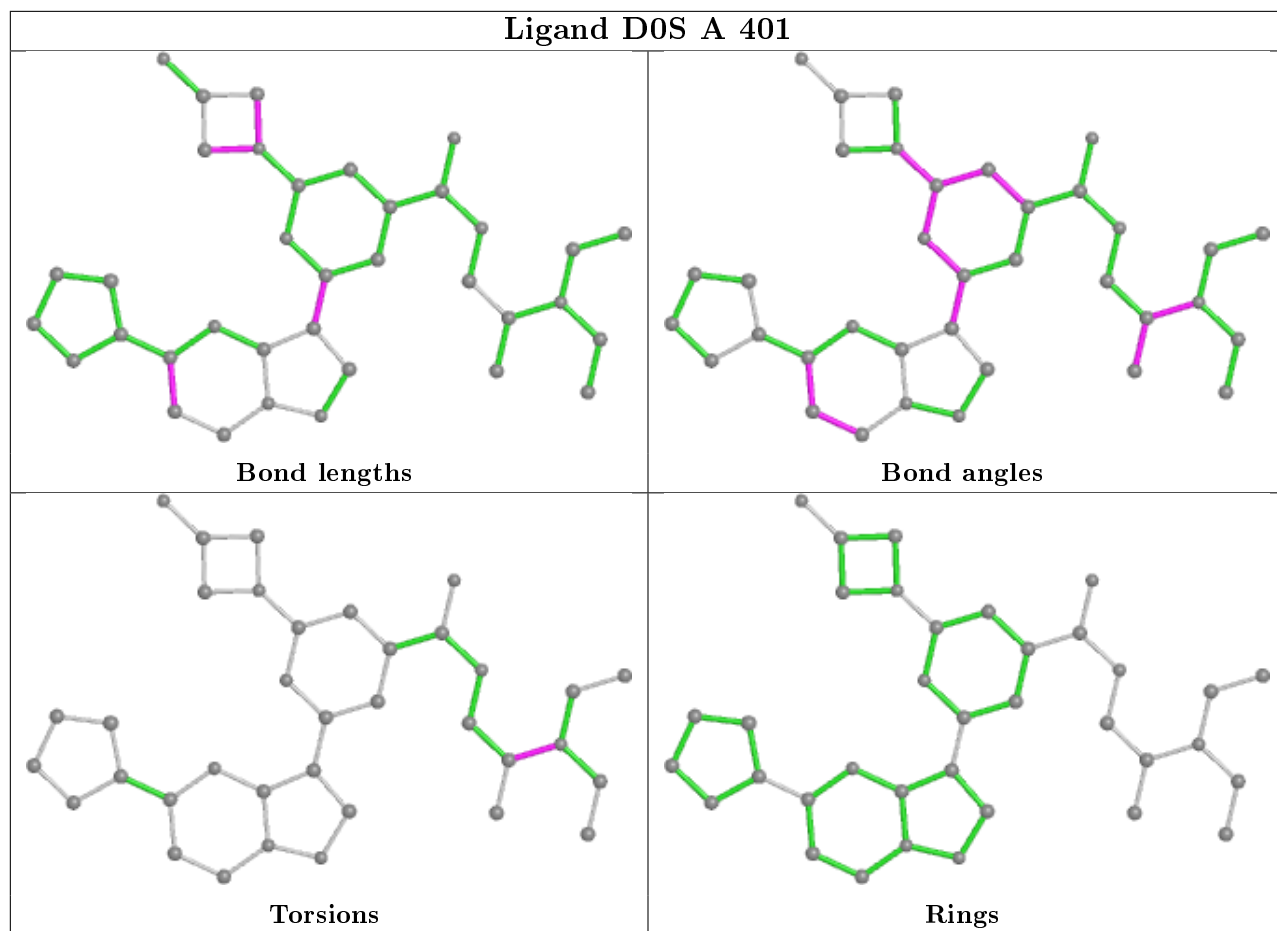
2 monomers are involved in 2 short contacts:

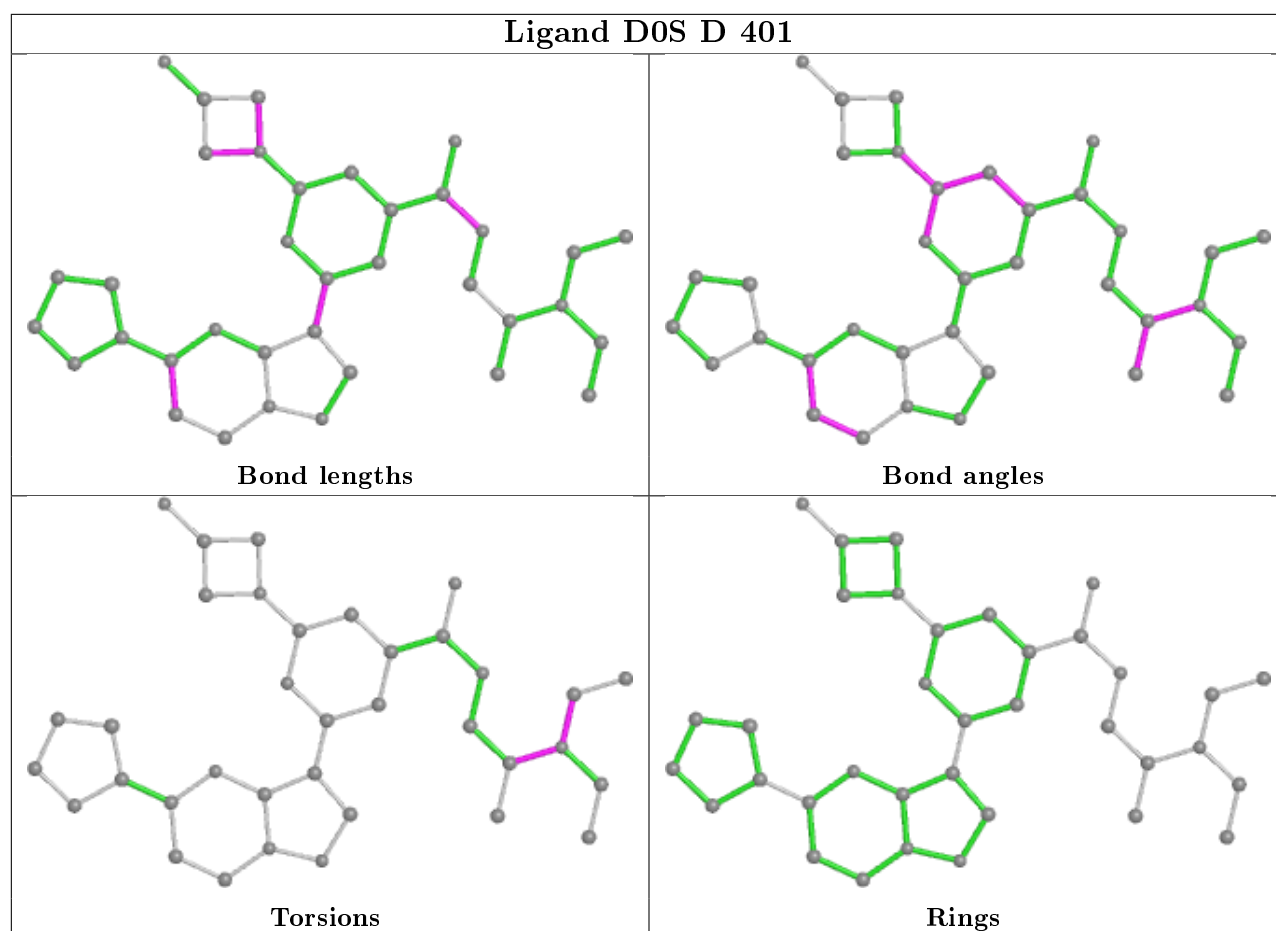| Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	401	D0S	1	0
2	D	401	D0S	1	0

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 D0S B 401

Bond lengths

Bond angles

Torsions

Rings

Ligand D0S C 401

Bond lengths

Bond angles

Torsions

Rings

Ligand D0S A 401

Bond lengths

Bond angles

Torsions

Rings

Ligand D0S D 401

Bond lengths

Bond angles

Torsions

Rings
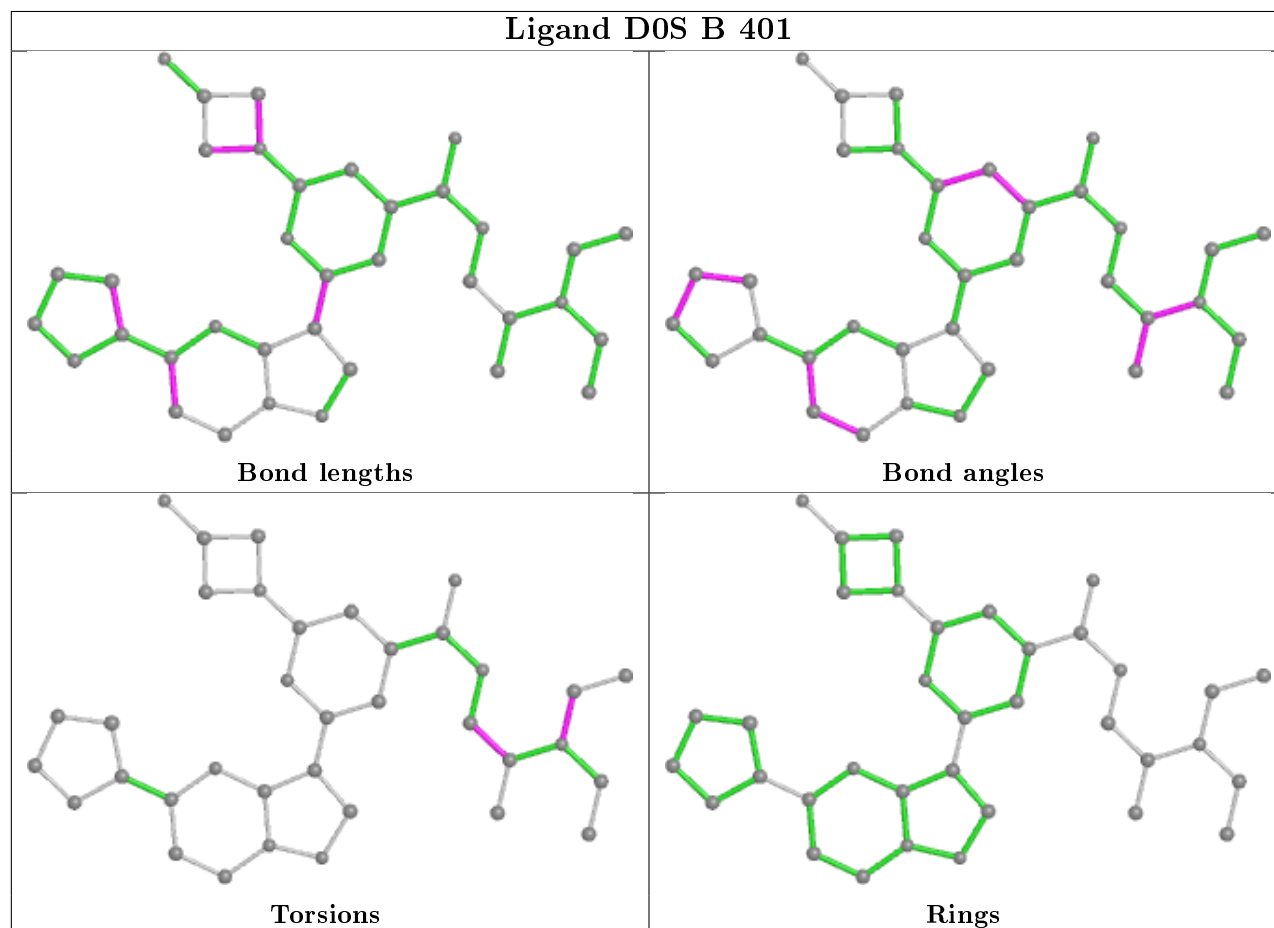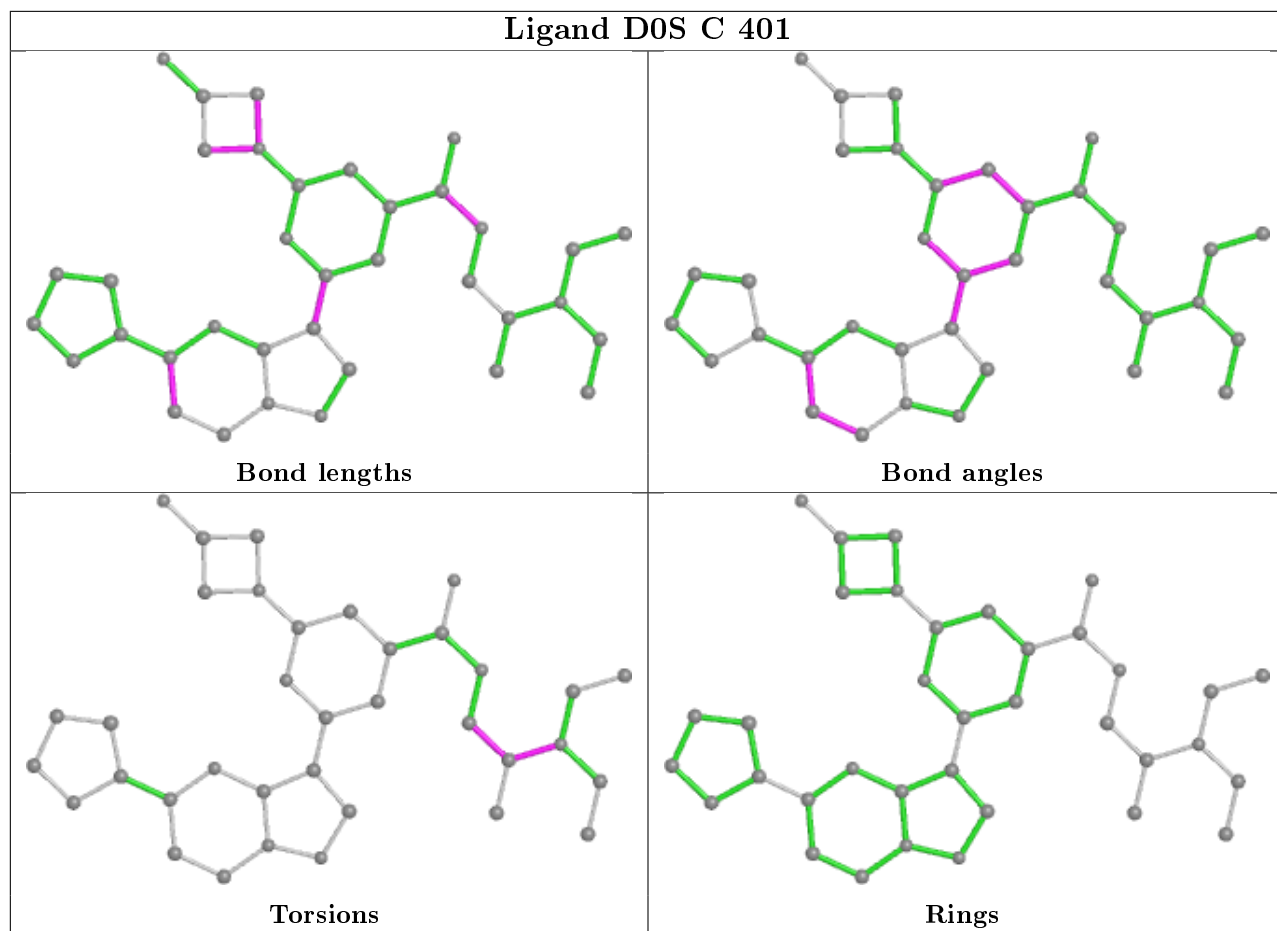
5.7 Other polymers (i)

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 (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	290/302 (96%)	-0.39	1 (0%)	94	94	14, 22, 36, 47	0
1	B	285/302 (94%)	-0.32	4 (1%)	75	77	12, 24, 42, 59	0
1	C	284/302 (94%)	-0.41	2 (0%)	87	89	13, 21, 35, 51	0
1	D	292/302 (96%)	-0.30	1 (0%)	94	94	12, 24, 45, 53	0
All	All	1151/1208 (95%)	-0.35	8 (0%)	87	89	12, 23, 40, 59	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	27	PHE	3.0
1	C	54	ARG	2.9
1	B	84	GLU	2.7
1	C	175	PHE	2.6
1	B	36	PRO	2.4
1	B	35	ILE	2.4
1	B	37	THR	2.2
1	A	56	HIS	2.1

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, 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	TLA	B	402	10/10	0.90	0.11	29,33,36,38	0
3	TLA	C	402	10/10	0.91	0.09	22,28,32,32	0
3	TLA	A	402	10/10	0.94	0.08	23,29,32,33	0
2	D0S	D	401	36/36	0.95	0.09	18,26,36,42	0
2	D0S	A	401	36/36	0.96	0.10	13,17,24,30	0
2	D0S	B	401	36/36	0.96	0.08	18,24,30,39	0
2	D0S	C	401	36/36	0.97	0.07	13,18,22,25	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.
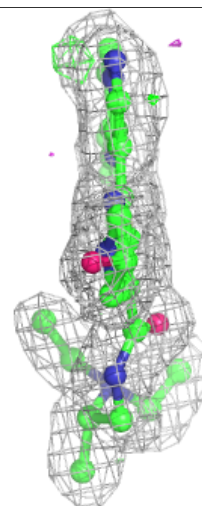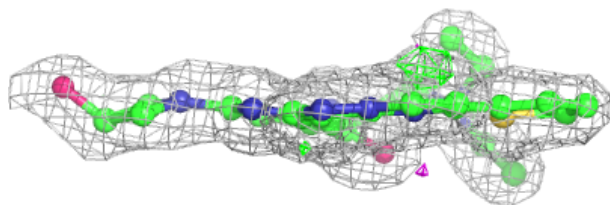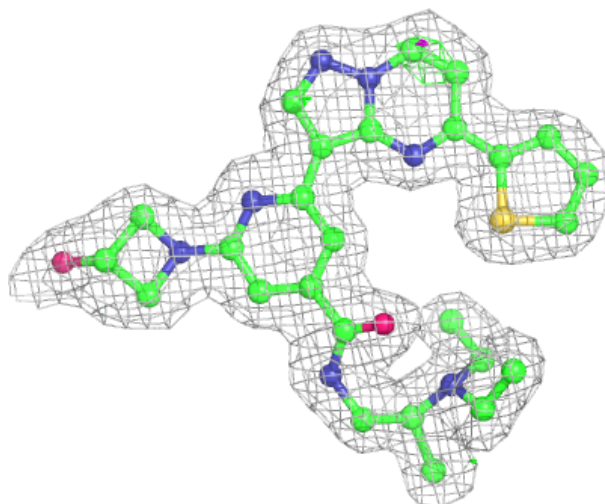
Electron density around D0S D 401:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
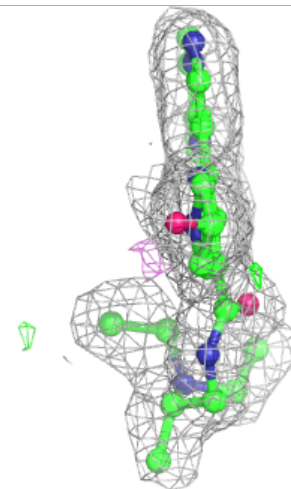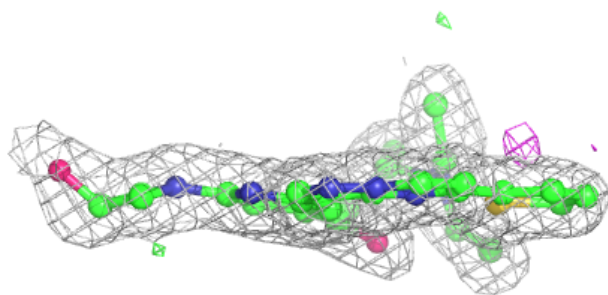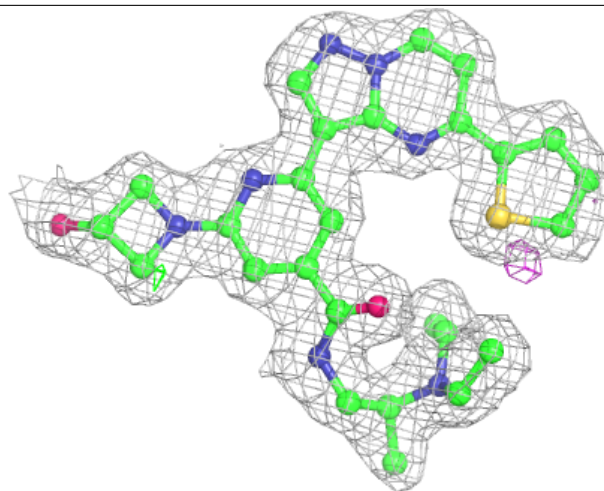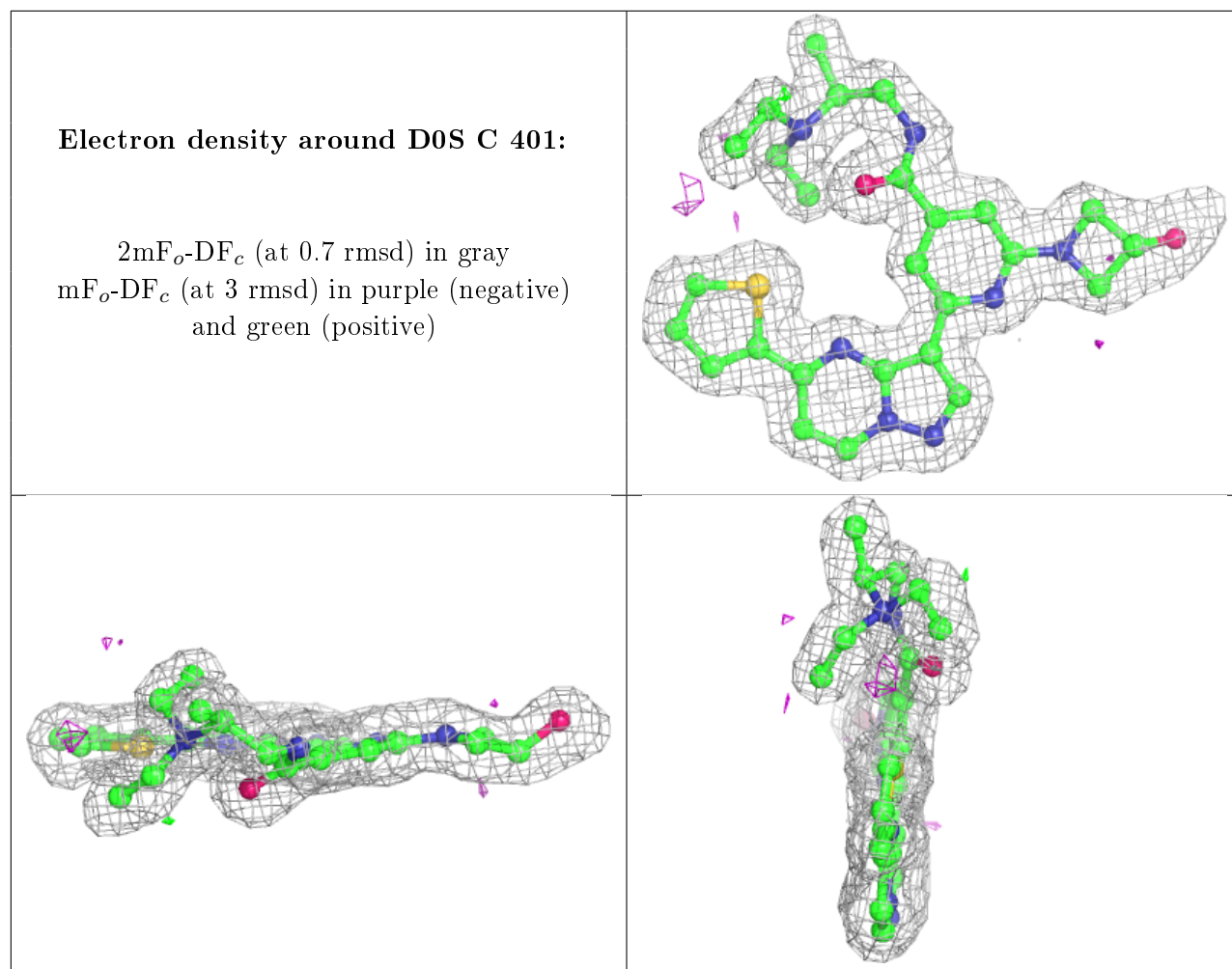and green (positive)
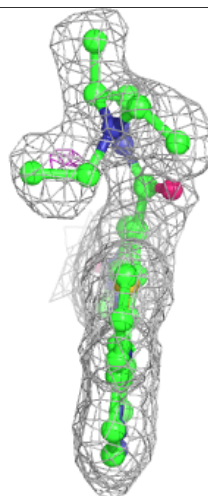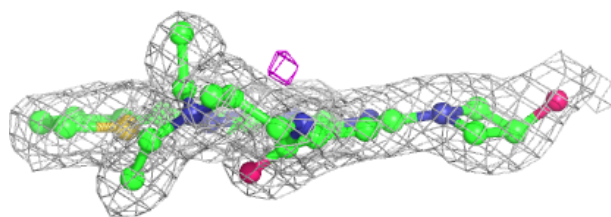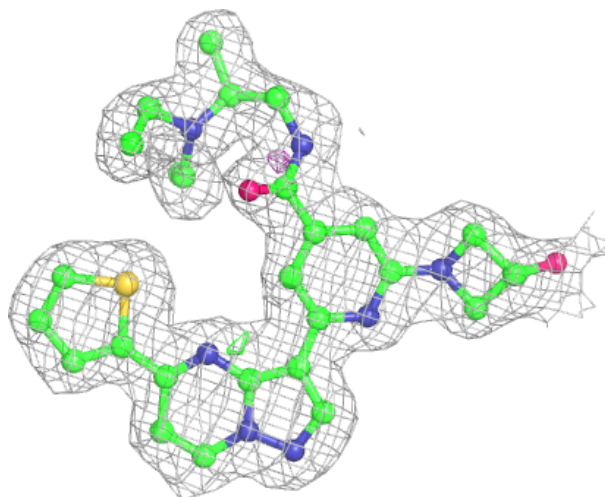
Electron density around D0S A 401:

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

Electron density around D0S B 401:

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 D0S C 401:

$2mF_o$-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.