



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:55 PM UTC

PDB ID : 4EOK / pdb_00004eok
Title : Thr 160 phosphorylated CDK2 H84S, Q85M, K89D - human cyclin A3 complex with the inhibitor NU6102
Authors : Echalier, A.; Cot, E.; Camasses, A.; Hodimont, E.; Hoh, F.; Sheinerman, F.; Krasinska, L.; Fisher, D.
Deposited on : 2012-04-14
Resolution : 2.57 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

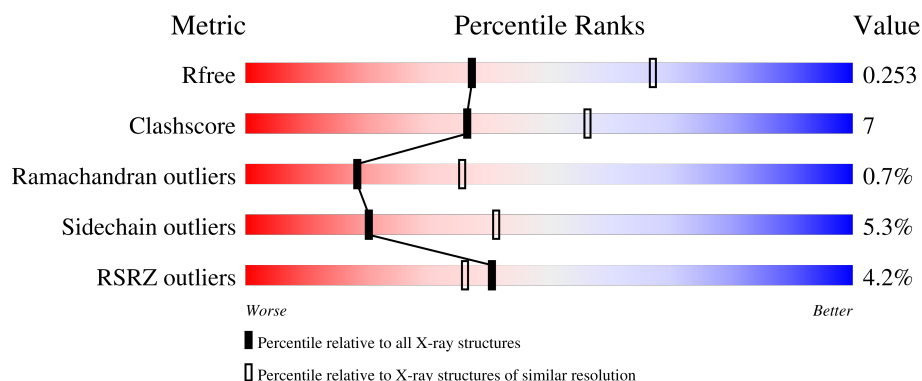
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.57 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	4770 (2.60-2.56)
Clashscore	190562	5124 (2.60-2.56)
Ramachandran outliers	187476	5046 (2.60-2.56)
Sidechain outliers	187428	5046 (2.60-2.56)
RSRZ outliers	180081	4770 (2.60-2.56)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	300	 3% 82% 15% ..
1	C	300	 8% 84% 13% ..
2	B	258	 2% 83% 14% .
2	D	258	 4% 85% 12% ..

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8994 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 Cyclin-dependent kinase 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	294	Total	C	N	O	P	S	0	0	0
			2362	1534	400	418	1	9			
1	C	300	Total	C	N	O	P	S	0	0	0
			2405	1559	406	430	1	9			

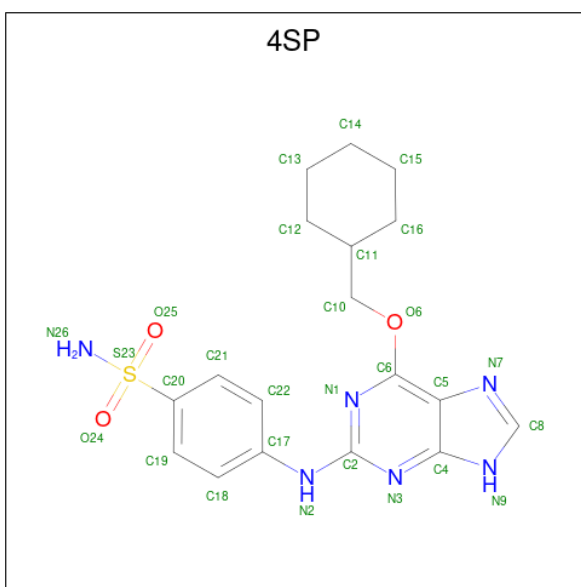
There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	LEU	-	expression tag	UNP P24941
A	-1	GLY	-	expression tag	UNP P24941
A	0	SER	-	expression tag	UNP P24941
A	84	SER	HIS	engineered mutation	UNP P24941
A	85	MET	GLN	engineered mutation	UNP P24941
A	89	ASP	LYS	engineered mutation	UNP P24941
C	-2	LEU	-	expression tag	UNP P24941
C	-1	GLY	-	expression tag	UNP P24941
C	0	SER	-	expression tag	UNP P24941
C	84	SER	HIS	engineered mutation	UNP P24941
C	85	MET	GLN	engineered mutation	UNP P24941
C	89	ASP	LYS	engineered mutation	UNP P24941

- Molecule 2 is a protein called Cyclin-A2.

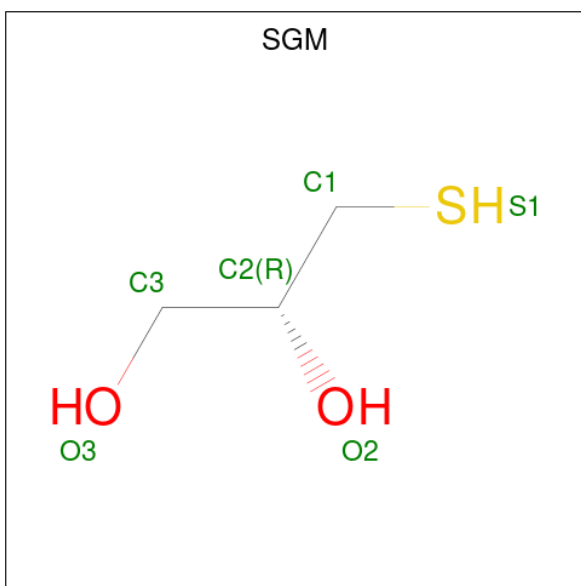
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	258	Total	C	N	O	S		0	0	0
			2083	1350	339	383	11				
2	D	256	Total	C	N	O	S		0	0	0
			2068	1339	337	381	11				

- Molecule 3 is O6-CYCLOHEXYLMETHOXY-2-(4'-SULPHAMOYLANILINO) PURINE (CCD ID: 4SP) (formula: C₁₈H₂₂N₆O₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			28	18	6	3	1		
3	C	1	Total	C	N	O	S	0	0
			28	18	6	3	1		

- Molecule 4 is MONOTHIOGLYCEROL (CCD ID: SGM) (formula: $C_3H_8O_2S$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	O	S	0	0
			6	3	2	1		
4	D	1	Total	C	O	S	0	0
			6	3	2	1		

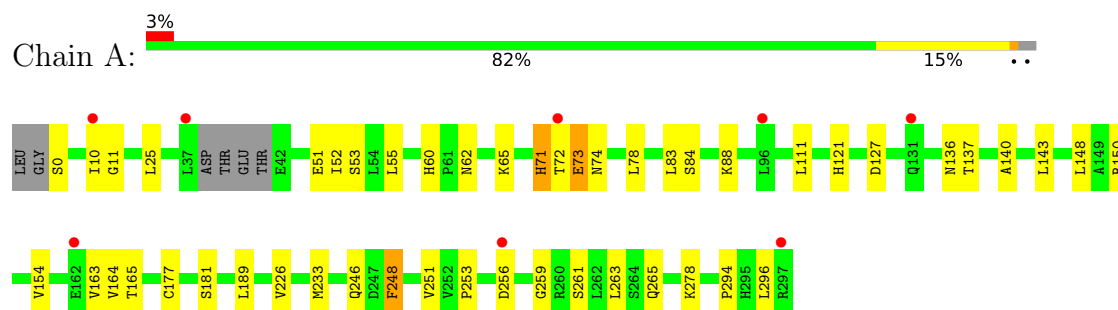
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	7	Total 7	O 7	0	0
5	B	1	Total 1	O 1	0	0

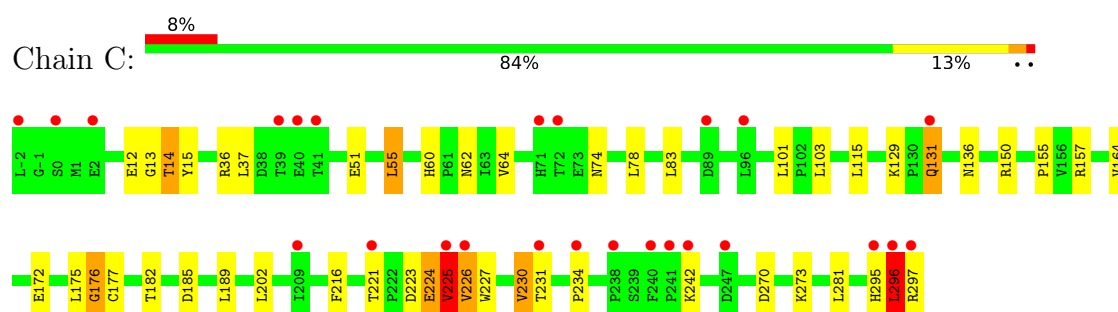
3 Residue-property plots [i](#)

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.

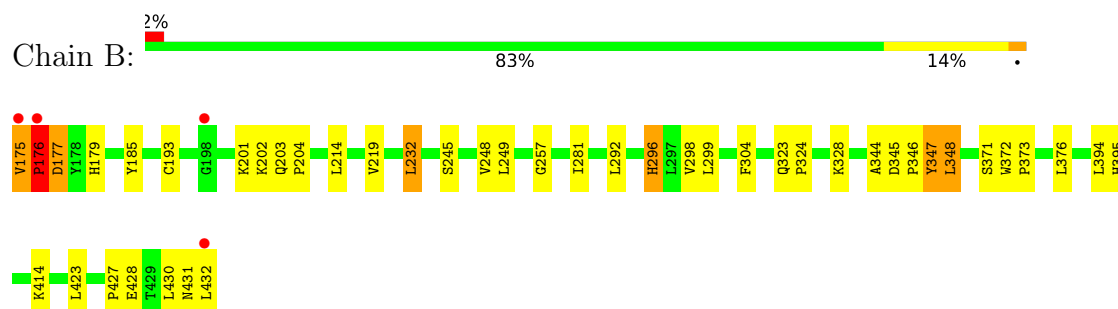
• Molecule 1: Cyclin-dependent kinase 2



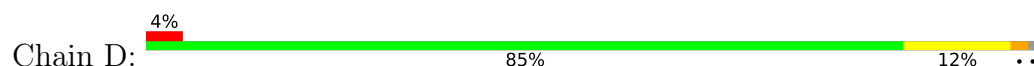
• Molecule 1: Cyclin-dependent kinase 2

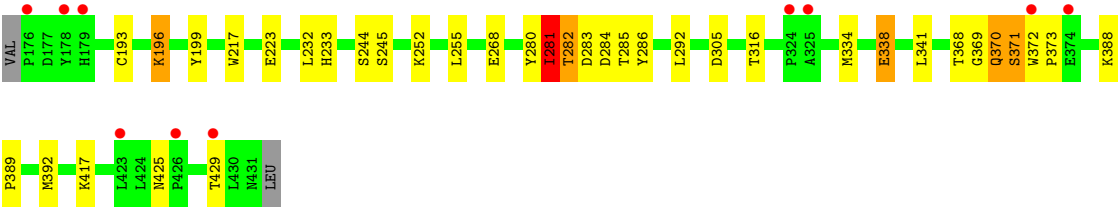


• Molecule 2: Cyclin-A2



• Molecule 2: Cyclin-A2





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	74.23Å 136.01Å 171.55Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.57 30.00 – 2.57	Depositor EDS
% Data completeness (in resolution range)	99.2 (30.00-2.57) 99.1 (30.00-2.57)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.06 (at 2.57Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.223 , 0.259 0.220 , 0.253	Depositor DCC
R_{free} test set	2845 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	52.3	Xtriage
Anisotropy	0.180	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 42.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8994	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.39% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: TPO, SGM, 4SP

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	0.55	1/2410 (0.0%)	0.86	4/3267 (0.1%)
1	C	0.58	0/2454	0.88	5/3329 (0.2%)
2	B	0.58	0/2133	0.86	3/2897 (0.1%)
2	D	0.49	0/2118	0.86	4/2875 (0.1%)
All	All	0.55	1/9115 (0.0%)	0.87	16/12368 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	71	HIS	CA-C	5.06	1.55	1.52

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	296	LEU	CB-CA-C	-12.74	91.22	111.48
1	C	297	ARG	N-CA-CB	9.25	126.23	110.50
1	A	253	PRO	N-CA-C	7.15	119.43	110.70
2	D	371	SER	N-CA-C	6.68	117.95	108.74
1	C	224	GLU	N-CA-C	-6.46	97.05	110.80
1	A	163	VAL	N-CA-C	6.29	122.42	109.34
2	B	177	ASP	N-CA-C	-6.12	104.22	113.89
2	B	432	LEU	N-CA-CB	5.82	120.39	110.50
2	D	425	ASN	CA-C-N	5.71	123.83	119.66
2	D	425	ASN	C-N-CA	5.71	123.83	119.66
1	A	11	GLY	N-CA-C	5.51	118.63	110.42
1	C	225	VAL	CB-CA-C	-5.44	102.36	111.29
1	C	296	LEU	N-CA-C	5.40	119.17	112.47
2	B	347	TYR	N-CA-C	5.37	119.31	112.87
1	A	71	HIS	N-CA-C	5.18	117.03	108.48
2	D	369	GLY	N-CA-C	-5.08	108.00	114.85

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	2362	0	2408	28	0
1	C	2405	0	2447	59	0
2	B	2083	0	2106	29	0
2	D	2068	0	2088	25	0
3	A	28	0	22	0	0
3	C	28	0	22	2	0
4	B	6	0	7	1	0
4	D	6	0	8	2	0
5	A	7	0	0	0	0
5	B	1	0	0	0	0
All	All	8994	0	9108	131	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 7.

All (131) 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)
2:B:193:CYS:SG	4:B:501:SGM:S1	2.32	1.27
1:C:224:GLU:OE2	1:C:231:THR:OG1	1.64	1.14
1:C:225:VAL:O	1:C:226:VAL:HG12	1.47	1.12
1:C:224:GLU:O	1:C:225:VAL:HG12	1.56	1.05
1:C:227:TRP:O	1:C:230:VAL:HG23	1.57	1.04
2:D:368:THR:OG1	2:D:370:GLN:HG3	1.66	0.95
1:A:73:GLU:HG3	1:A:74:ASN:HA	1.46	0.93
1:C:14:THR:HG22	1:C:15:TYR:H	1.36	0.90
1:C:14:THR:CG2	1:C:15:TYR:N	2.35	0.90
1:C:295:HIS:C	1:C:296:LEU:HG	1.96	0.89
1:C:14:THR:HG23	1:C:15:TYR:HD2	1.38	0.89
1:C:14:THR:HG22	1:C:15:TYR:N	1.88	0.87
1:A:60:HIS:HD2	1:A:62:ASN:H	1.17	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:226:VAL:CG1	1:C:227:TRP:N	2.39	0.85
2:D:371:SER:O	2:D:373:PRO:HD3	1.75	0.85
1:C:295:HIS:O	1:C:296:LEU:HD12	1.76	0.84
1:C:223:ASP:O	1:C:225:VAL:O	1.97	0.82
2:D:282:THR:HG23	2:D:285:THR:OG1	1.79	0.82
1:A:136:ASN:HD21	1:A:140:ALA:HB3	1.46	0.81
1:A:278:LYS:NZ	2:B:177:ASP:O	2.13	0.79
1:C:295:HIS:O	1:C:296:LEU:CG	2.30	0.79
1:C:295:HIS:O	1:C:296:LEU:CD1	2.30	0.79
1:C:295:HIS:O	1:C:296:LEU:HG	1.82	0.79
1:C:225:VAL:O	1:C:226:VAL:CG1	2.29	0.78
1:C:224:GLU:O	1:C:225:VAL:CG1	2.30	0.78
1:C:227:TRP:O	1:C:230:VAL:CG2	2.32	0.77
1:C:14:THR:HG23	1:C:15:TYR:CD2	2.19	0.77
1:C:223:ASP:O	1:C:226:VAL:HG12	1.86	0.75
2:D:371:SER:O	2:D:372:TRP:C	2.30	0.74
1:C:226:VAL:HG12	1:C:227:TRP:H	1.53	0.73
1:C:226:VAL:HG13	1:C:227:TRP:N	2.04	0.72
1:C:225:VAL:O	1:C:225:VAL:HG12	1.88	0.71
1:C:225:VAL:O	1:C:225:VAL:CG1	2.35	0.71
2:D:193:CYS:SG	4:D:501:SGM:S1	2.71	0.68
2:D:282:THR:HG23	2:D:282:THR:O	1.92	0.68
1:C:157:ARG:HH22	2:D:268:GLU:HG3	1.61	0.65
1:C:14:THR:CG2	1:C:15:TYR:CD2	2.79	0.65
1:C:175:LEU:O	1:C:177:CYS:N	2.30	0.65
1:A:256:ASP:HB3	1:A:259:GLY:H	1.62	0.63
2:D:371:SER:O	2:D:373:PRO:CD	2.46	0.63
2:D:282:THR:O	2:D:282:THR:CG2	2.42	0.62
1:C:175:LEU:O	1:C:176:GLY:C	2.42	0.61
1:C:223:ASP:C	1:C:224:GLU:O	2.32	0.61
1:C:224:GLU:O	1:C:225:VAL:CB	2.49	0.60
1:C:176:GLY:O	1:C:234:PRO:HG2	2.02	0.59
1:C:224:GLU:C	1:C:225:VAL:O	2.46	0.58
1:C:14:THR:CG2	1:C:15:TYR:HD2	2.12	0.57
1:A:73:GLU:CG	1:A:74:ASN:HA	2.27	0.57
1:A:60:HIS:CD2	1:A:62:ASN:H	2.10	0.56
1:A:294:PRO:HG2	1:A:296:LEU:HD22	1.86	0.56
1:C:13:GLY:O	1:C:14:THR:HG22	2.07	0.55
2:B:347:TYR:OH	2:B:394:LEU:HA	2.06	0.55
2:B:175:VAL:C	2:B:176:PRO:O	2.50	0.55
1:C:115:LEU:HD21	1:C:185:ASP:HB3	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:282:THR:HG23	2:D:285:THR:HG1	1.70	0.54
2:D:305:ASP:HB3	4:D:501:SGM:H12	1.90	0.54
1:A:71:HIS:HE2	2:B:296:HIS:CE1	2.26	0.53
1:A:71:HIS:HE2	2:B:296:HIS:CD2	2.27	0.53
2:B:175:VAL:O	2:B:176:PRO:O	2.28	0.52
1:C:224:GLU:OE2	1:C:231:THR:CB	2.57	0.51
2:D:388:LYS:O	2:D:392:MET:HG2	2.10	0.51
1:A:177:CYS:HB2	1:A:233:MET:HE3	1.92	0.51
1:C:51:GLU:O	1:C:55:LEU:HB2	2.10	0.51
1:C:227:TRP:HB3	1:C:230:VAL:HG21	1.92	0.51
1:A:51:GLU:O	1:A:55:LEU:HB2	2.10	0.51
2:D:233:HIS:CD2	2:D:341:LEU:HD11	2.46	0.51
1:C:223:ASP:O	1:C:224:GLU:C	2.54	0.51
1:C:270:ASP:HB3	1:C:273:LYS:HB2	1.91	0.50
1:C:14:THR:HG23	1:C:15:TYR:N	2.20	0.50
2:B:176:PRO:C	2:B:177:ASP:OD2	2.54	0.50
1:C:224:GLU:O	1:C:225:VAL:O	2.29	0.50
2:D:368:THR:CB	2:D:370:GLN:HG3	2.41	0.49
2:B:344:ALA:HB1	2:B:348:LEU:HD22	1.95	0.49
2:B:214:LEU:HD11	2:B:257:GLY:HA3	1.93	0.49
1:C:216:PHE:HB3	1:C:221:THR:HG22	1.95	0.49
1:A:0:SER:HA	1:A:72:THR:HG22	1.95	0.48
2:D:282:THR:O	2:D:283:ASP:HB2	2.11	0.48
1:A:111:LEU:HD13	1:A:189:LEU:HD21	1.95	0.48
2:B:430:LEU:O	2:B:431:ASN:HB2	2.13	0.48
2:D:280:TYR:C	2:D:282:THR:H	2.22	0.48
2:D:284:ASP:O	2:D:285:THR:C	2.57	0.48
2:D:388:LYS:HB3	2:D:389:PRO:HD3	1.96	0.48
1:A:127:ASP:OD1	1:A:165:THR:HG23	2.14	0.48
2:B:395:HIS:HE1	2:B:427:PRO:O	1.97	0.47
1:C:172:GLU:O	1:C:177:CYS:HB2	2.14	0.47
1:A:25:LEU:O	2:D:252:LYS:HG3	2.15	0.47
2:B:176:PRO:HG2	2:B:179:HIS:CE1	2.50	0.47
1:A:136:ASN:ND2	1:A:140:ALA:HB3	2.21	0.46
1:C:227:TRP:NE1	1:C:270:ASP:HA	2.30	0.46
1:C:224:GLU:H	1:C:224:GLU:HG2	1.45	0.45
2:D:196:LYS:HB2	2:D:244:SER:HB3	1.99	0.45
2:B:177:ASP:OD2	2:B:177:ASP:N	2.48	0.44
1:C:155:PRO:HD2	2:D:316:THR:HB	1.98	0.44
2:B:175:VAL:O	2:B:176:PRO:C	2.58	0.44
1:C:129:LYS:HG3	1:C:131:GLN:HG2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:0:SER:HA	1:A:72:THR:CG2	2.47	0.44
1:C:225:VAL:O	1:C:226:VAL:CB	2.64	0.44
2:B:219:VAL:HG22	2:B:232:LEU:HD11	1.99	0.44
1:A:71:HIS:NE2	2:B:296:HIS:NE2	2.59	0.44
1:C:189:LEU:HD23	1:C:189:LEU:HA	1.88	0.44
2:B:203:GLN:HA	2:B:204:PRO:HD3	1.87	0.44
2:D:334:MET:O	2:D:338:GLU:HB2	2.18	0.43
1:A:53:SER:HB3	2:B:304:PHE:O	2.18	0.43
1:A:71:HIS:CE1	1:A:73:GLU:HB2	2.53	0.43
1:A:121:HIS:HD2	2:B:185:TYR:CE1	2.36	0.43
2:B:376:LEU:HA	2:B:376:LEU:HD23	1.75	0.43
1:A:246:GLN:HE21	1:A:251:VAL:HG22	1.83	0.43
2:B:298:VAL:O	2:B:299:LEU:C	2.61	0.43
1:C:227:TRP:CD2	1:C:230:VAL:HG22	2.54	0.42
1:A:248:PHE:HE2	1:A:263:LEU:HG	1.84	0.42
1:A:137:THR:HG22	1:A:296:LEU:HD21	2.02	0.42
2:D:199:TYR:CD1	2:D:199:TYR:C	2.98	0.42
2:B:373:PRO:HD2	2:B:376:LEU:HD12	2.00	0.42
1:C:13:GLY:O	1:C:14:THR:CB	2.68	0.42
1:A:261:SER:O	1:A:265:GLN:HG3	2.20	0.42
1:C:60:HIS:CD2	1:C:62:ASN:H	2.38	0.42
1:A:52:ILE:HD11	1:A:78:LEU:HD21	2.00	0.42
2:D:217:TRP:CZ2	2:D:281:ILE:HD12	2.55	0.42
2:D:255:LEU:HB2	2:D:286:TYR:CE1	2.55	0.41
1:C:227:TRP:CZ3	1:C:230:VAL:HG13	2.54	0.41
1:C:64:VAL:HG21	3:C:301:ASP:C8	2.50	0.41
1:A:154:VAL:HG13	2:B:179:HIS:CE1	2.56	0.41
2:B:345:ASP:HA	2:B:346:PRO:HA	1.82	0.41
1:C:83:LEU:HD12	1:C:136:ASN:HB3	2.01	0.41
2:B:414:LYS:HE3	2:B:423:LEU:HD21	2.03	0.40
1:C:55:LEU:HD12	1:C:55:LEU:HA	1.97	0.40
2:B:323:GLN:HA	2:B:324:PRO:HA	1.81	0.40
2:B:371:SER:O	2:B:372:TRP:C	2.65	0.40
1:C:227:TRP:CD1	1:C:270:ASP:HA	2.56	0.40
2:B:248:VAL:HG12	2:B:249:LEU:O	2.21	0.40
1:C:64:VAL:HG21	3:C:301:ASP:H8	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	289/300 (96%)	272 (94%)	15 (5%)	2 (1%)	18	36
1	C	297/300 (99%)	280 (94%)	13 (4%)	4 (1%)	9	19
2	B	256/258 (99%)	250 (98%)	5 (2%)	1 (0%)	30	49
2	D	254/258 (98%)	240 (94%)	13 (5%)	1 (0%)	30	49
All	All	1096/1116 (98%)	1042 (95%)	46 (4%)	8 (1%)	18	36

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	176	PRO
1	C	176	GLY
1	C	164	VAL
1	C	225	VAL
1	A	164	VAL
2	D	281	ILE
1	A	73	GLU
1	C	182	THR

5.3.2 Protein sidechains

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	258/263 (98%)	247 (96%)	11 (4%)	26	49
1	C	263/263 (100%)	245 (93%)	18 (7%)	14	31

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	232/232 (100%)	220 (95%)	12 (5%)	21	42
2	D	230/232 (99%)	219 (95%)	11 (5%)	23	45
All	All	983/990 (99%)	931 (95%)	52 (5%)	20	41

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	ILE
1	A	65	LYS
1	A	83	LEU
1	A	84	SER
1	A	88	LYS
1	A	143	LEU
1	A	148	LEU
1	A	150	ARG
1	A	181	SER
1	A	226	VAL
1	A	248	PHE
2	B	175	VAL
2	B	176	PRO
2	B	201	LYS
2	B	202	LYS
2	B	232	LEU
2	B	245	SER
2	B	281	ILE
2	B	292	LEU
2	B	296	HIS
2	B	328	LYS
2	B	348	LEU
2	B	428	GLU
1	C	12	GLU
1	C	14	THR
1	C	36	ARG
1	C	37	LEU
1	C	55	LEU
1	C	74	ASN
1	C	78	LEU
1	C	101	LEU
1	C	103	LEU
1	C	131	GLN
1	C	150	ARG

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Mol	Chain	Res	Type
1	C	202	LEU
1	C	225	VAL
1	C	226	VAL
1	C	230	VAL
1	C	242	LYS
1	C	281	LEU
1	C	296	LEU
2	D	196	LYS
2	D	223	GLU
2	D	232	LEU
2	D	245	SER
2	D	281	ILE
2	D	282	THR
2	D	292	LEU
2	D	338	GLU
2	D	370	GLN
2	D	417	LYS
2	D	429	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	62	ASN
1	A	161	HIS
1	A	246	GLN
1	A	265	GLN
2	B	179	HIS
2	B	183	HIS
2	B	233	HIS
2	B	254	GLN
2	B	317	GLN
2	B	395	HIS
2	B	406	GLN
2	B	431	ASN
1	C	3	ASN
1	C	60	HIS
1	C	62	ASN
1	C	119	HIS
1	C	161	HIS
2	D	233	HIS
2	D	254	GLN
2	D	323	GLN

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Mol	Chain	Res	Type
2	D	370	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	TPO	A	160	1	8,10,11	0.69	0	10,14,16	1.24	0
1	TPO	C	160	1	8,10,11	0.81	0	10,14,16	1.09	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
1	TPO	A	160	1	-	0/9/11/13	-
1	TPO	C	160	1	-	0/9/11/13	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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
4	SGM	D	501	-	5,5,5	0.38	0	5,5,5	0.49	0
3	4SP	A	301	-	31,31,31	2.44	8 (25%)	43,44,44	2.18	10 (23%)
4	SGM	B	501	-	5,5,5	0.36	0	5,5,5	0.52	0
3	4SP	C	301	-	31,31,31	2.53	8 (25%)	43,44,44	1.92	9 (20%)

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
4	SGM	D	501	-	-	1/4/4/4	-
3	4SP	A	301	-	-	4/15/23/23	0/4/4/4
4	SGM	B	501	-	-	3/4/4/4	-
3	4SP	C	301	-	-	2/15/23/23	0/4/4/4

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	301	4SP	C20-S23	-10.29	1.61	1.77
3	A	301	4SP	C20-S23	-9.81	1.62	1.77
3	C	301	4SP	C5-C4	4.87	1.46	1.39
3	A	301	4SP	C5-C4	4.74	1.46	1.39
3	A	301	4SP	S23-N26	-4.19	1.52	1.60
3	C	301	4SP	S23-N26	-3.87	1.52	1.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	301	4SP	O25-S23	3.16	1.49	1.43
3	C	301	4SP	O25-S23	3.05	1.49	1.43
3	C	301	4SP	O24-S23	2.96	1.48	1.43
3	C	301	4SP	C6-N1	2.88	1.36	1.32
3	A	301	4SP	O24-S23	2.76	1.48	1.43
3	A	301	4SP	C6-N1	2.66	1.36	1.32
3	C	301	4SP	C5-N7	-2.28	1.34	1.39
3	A	301	4SP	C5-N7	-2.19	1.35	1.39
3	A	301	4SP	C8-N7	2.13	1.36	1.32
3	C	301	4SP	C17-N2	-2.03	1.36	1.40

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	301	4SP	O25-S23-O24	-6.54	108.74	118.80
3	C	301	4SP	O25-S23-O24	-5.46	110.40	118.80
3	A	301	4SP	C5-C4-N3	-4.75	121.89	126.55
3	A	301	4SP	C2-N1-C6	4.71	123.48	115.38
3	C	301	4SP	C2-N1-C6	4.60	123.30	115.38
3	C	301	4SP	C5-C4-N3	-4.28	122.36	126.55
3	A	301	4SP	C5-N7-C8	4.09	108.10	103.48
3	C	301	4SP	C5-C6-N1	-3.95	118.21	123.49
3	A	301	4SP	N3-C2-N1	-3.66	120.26	126.26
3	C	301	4SP	C5-N7-C8	3.48	107.41	103.48
3	A	301	4SP	C4-C5-N7	-3.34	106.04	110.67
3	A	301	4SP	C5-C6-N1	-3.29	119.08	123.49
3	C	301	4SP	C4-C5-N7	-3.17	106.27	110.67
3	C	301	4SP	N3-C2-N1	-3.05	121.27	126.26
3	A	301	4SP	C6-C5-N7	2.98	137.32	133.82
3	A	301	4SP	O25-S23-C20	2.95	110.69	107.35
3	A	301	4SP	O6-C6-C5	2.73	120.33	116.73
3	C	301	4SP	O6-C6-N1	2.50	123.36	120.02
3	C	301	4SP	C6-C5-N7	2.18	136.39	133.82

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	301	4SP	O6-C10-C11-C12
4	B	501	SGM	C1-C2-C3-O3
3	C	301	4SP	O6-C10-C11-C16
3	A	301	4SP	O6-C10-C11-C12

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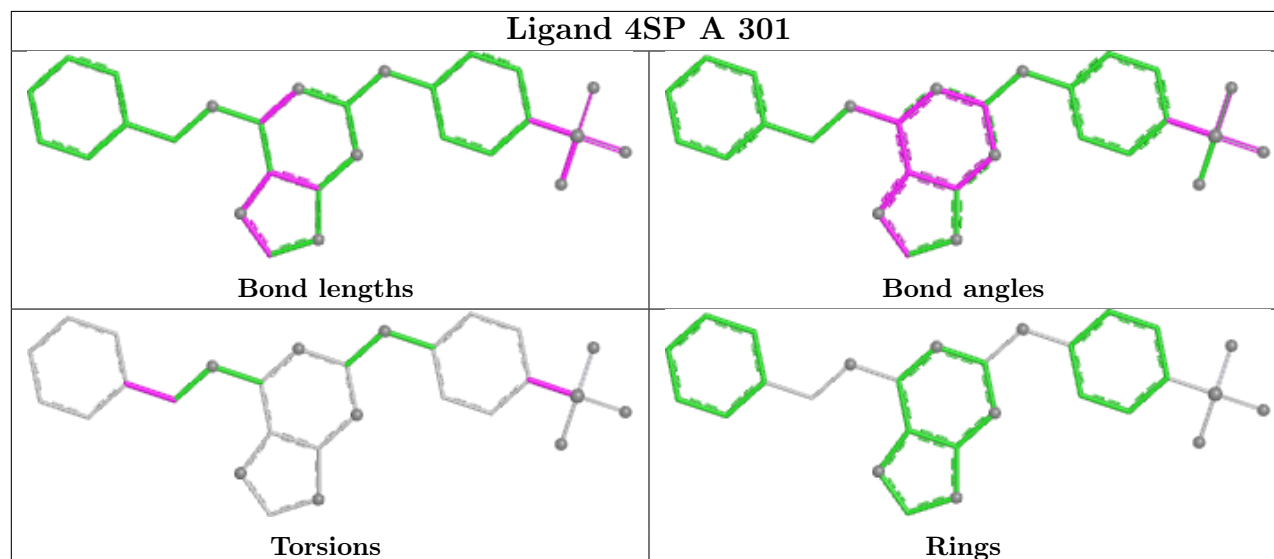
Mol	Chain	Res	Type	Atoms
4	B	501	SGM	S1-C1-C2-O2
4	D	501	SGM	S1-C1-C2-O2
4	B	501	SGM	O2-C2-C3-O3
3	A	301	4SP	O6-C10-C11-C16
3	A	301	4SP	C19-C20-S23-O24
3	A	301	4SP	C21-C20-S23-O24

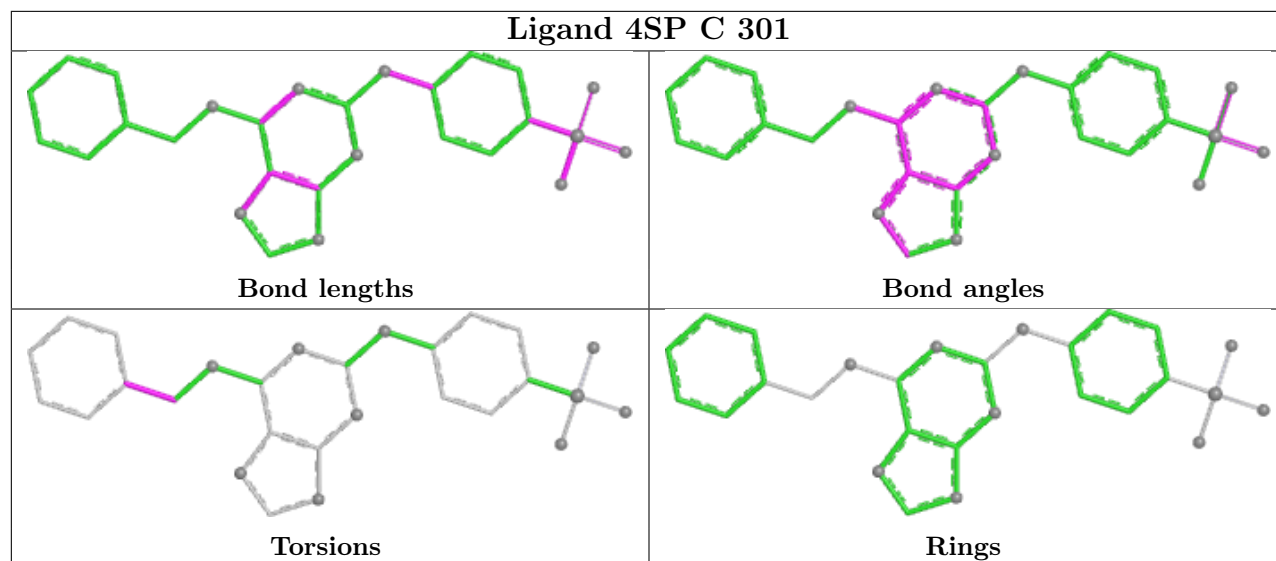
There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	501	SGM	2	0
4	B	501	SGM	1	0
3	C	301	4SP	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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, 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	293/300 (97%)	-0.08	8 (2%) 56 52	18, 43, 71, 84	2 (0%)
1	C	299/300 (99%)	0.55	25 (8%) 17 14	49, 75, 109, 130	1 (0%)
2	B	258/258 (100%)	-0.07	4 (1%) 70 67	33, 54, 75, 86	0
2	D	256/258 (99%)	0.46	10 (3%) 43 39	46, 75, 119, 136	0
All	All	1106/1116 (99%)	0.22	47 (4%) 40 36	18, 61, 107, 136	3 (0%)

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	131	GLN	8.4
2	B	175	VAL	6.5
1	C	296	LEU	5.9
1	A	256	ASP	5.7
1	C	-2	LEU	5.5
1	C	297	ARG	4.6
1	A	162	GLU	4.6
2	B	176	PRO	4.6
2	D	176	PRO	4.2
1	C	40	GLU	3.9
2	B	432	LEU	3.6
1	C	295	HIS	3.1
1	C	242	LYS	3.1
2	D	429	THR	3.0
2	D	374	GLU	3.0
1	C	131	GLN	2.9
2	D	324	PRO	2.9
1	C	39	THR	2.8
1	C	234	PRO	2.8
2	D	179	HIS	2.7
1	C	221	THR	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	240	PHE	2.6
2	D	372	TRP	2.6
1	C	231	THR	2.6
1	C	41	THR	2.6
1	A	297	ARG	2.5
1	A	96	LEU	2.5
1	C	247	ASP	2.5
1	C	71	HIS	2.5
1	C	89	ASP	2.4
1	C	226	VAL	2.4
1	A	72	THR	2.4
1	C	96	LEU	2.4
1	C	72	THR	2.4
2	B	198	GLY	2.4
1	A	10	ILE	2.3
1	C	225	VAL	2.3
1	C	238	PRO	2.3
2	D	423	LEU	2.3
1	C	2	GLU	2.3
1	C	241	PRO	2.3
1	C	0	SER	2.3
2	D	426	PRO	2.2
1	C	209	ILE	2.2
2	D	325	ALA	2.1
2	D	178	TYR	2.1
1	A	37	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
1	TPO	C	160	11/12	0.96	0.08	65,71,74,75	0
1	TPO	A	160	11/12	0.98	0.06	39,42,43,43	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

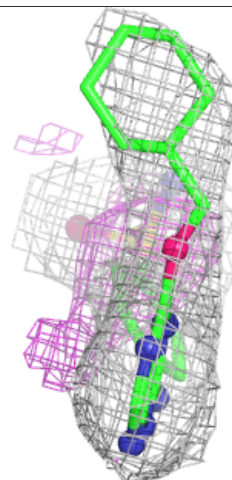
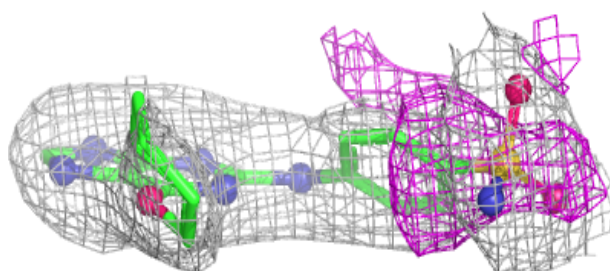
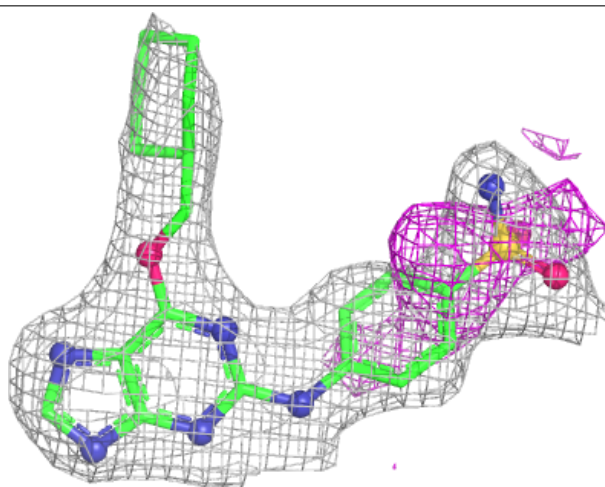
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	SGM	D	501	6/6	0.87	0.17	79,79,80,81	0
4	SGM	B	501	6/6	0.90	0.16	68,68,69,70	0
3	4SP	C	301	28/28	0.90	0.12	68,69,75,75	0
3	4SP	A	301	28/28	0.96	0.07	43,47,52,53	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.

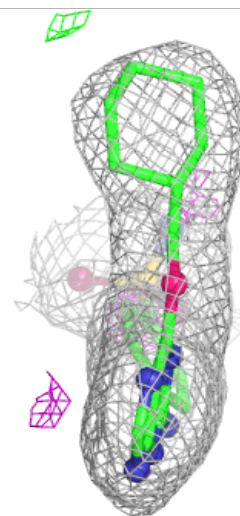
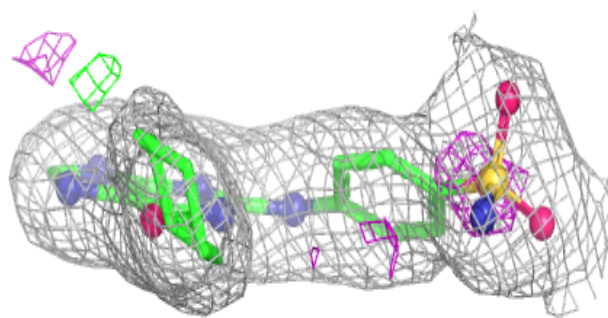
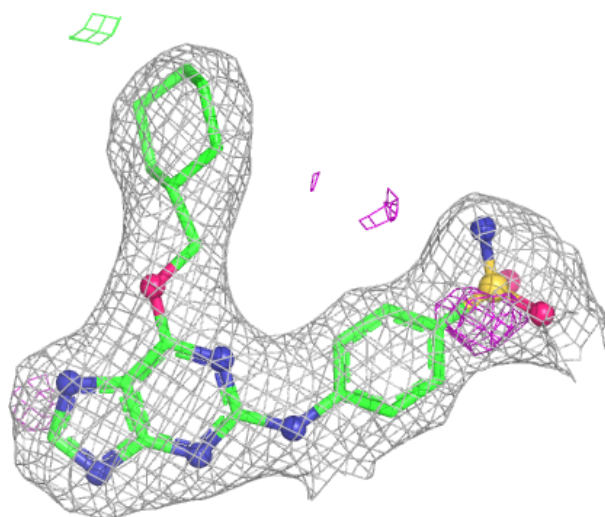
Electron density around 4SP C 301:

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 4SP A 301:

$2mF_o-DF_c$ (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.