



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:52 PM UTC

PDB ID : 8BUF / pdb_00008buf
Title : Structure of DDB1 bound to Z12-engaged CDK12-cyclin K
Authors : Kozicka, Z.; Kempf, G.; Petzold, G.; Thoma, N.H.
Deposited on : 2022-11-30
Resolution : 3.30 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

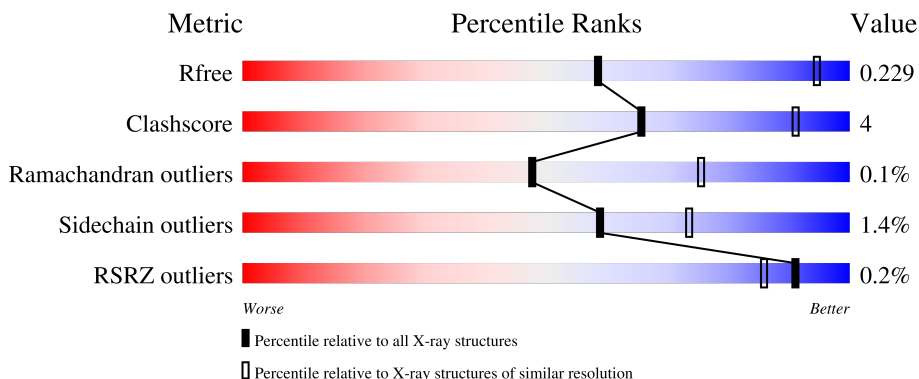
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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	1169 (3.32-3.28)
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)
RSRZ outliers	180081	1169 (3.32-3.28)

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	840	89% (green), 10% (yellow), 1% (orange), 0% (red), 0% (grey)
1	D	840	88% (green), 10% (yellow), 1% (orange), 0% (red), 0% (grey)
1	G	840	86% (green), 12% (yellow), 1% (orange), 0% (red), 0% (grey)
2	B	344	76% (green), 16% (yellow), 7% (orange), 0% (red), 0% (grey)
2	E	344	82% (green), 13% (yellow), 0% (orange), 0% (red), 0% (grey)

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Mol	Chain	Length	Quality of chain
2	H	344	 81% 11% 8%
3	C	271	 85% 7% 9%
3	F	271	 84% 7% 8%
3	I	271	 83% 8% 9%

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 67286 atoms, of which 33481 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 DNA damage-binding protein 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	826	12937	4105	6450	1094	1252	36	6450	0	0
1	D	827	12957	4111	6462	1095	1253	36	6500	0	0
1	G	826	12940	4106	6454	1093	1251	36	6454	0	0

There are 39 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP Q16531
A	-2	GLY	-	expression tag	UNP Q16531
A	-1	GLY	-	expression tag	UNP Q16531
A	0	ARG	-	expression tag	UNP Q16531
A	700	GLY	-	linker	UNP Q16531
A	701	ASN	-	linker	UNP Q16531
A	702	GLY	-	linker	UNP Q16531
A	703	ASN	-	linker	UNP Q16531
A	704	SER	-	linker	UNP Q16531
A	705	GLY	-	linker	UNP Q16531
A	706	GLU	-	linker	UNP Q16531
A	707	ILE	-	linker	UNP Q16531
A	708	GLN	-	linker	UNP Q16531
D	-3	GLY	-	expression tag	UNP Q16531
D	-2	GLY	-	expression tag	UNP Q16531
D	-1	GLY	-	expression tag	UNP Q16531
D	0	ARG	-	expression tag	UNP Q16531
D	700	GLY	-	linker	UNP Q16531
D	701	ASN	-	linker	UNP Q16531
D	702	GLY	-	linker	UNP Q16531
D	703	ASN	-	linker	UNP Q16531
D	704	SER	-	linker	UNP Q16531
D	705	GLY	-	linker	UNP Q16531

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Chain	Residue	Modelled	Actual	Comment	Reference
D	706	GLU	-	linker	UNP Q16531
D	707	ILE	-	linker	UNP Q16531
D	708	GLN	-	linker	UNP Q16531
G	-3	GLY	-	expression tag	UNP Q16531
G	-2	GLY	-	expression tag	UNP Q16531
G	-1	GLY	-	expression tag	UNP Q16531
G	0	ARG	-	expression tag	UNP Q16531
G	700	GLY	-	linker	UNP Q16531
G	701	ASN	-	linker	UNP Q16531
G	702	GLY	-	linker	UNP Q16531
G	703	ASN	-	linker	UNP Q16531
G	704	SER	-	linker	UNP Q16531
G	705	GLY	-	linker	UNP Q16531
G	706	GLU	-	linker	UNP Q16531
G	707	ILE	-	linker	UNP Q16531
G	708	GLN	-	linker	UNP Q16531

- Molecule 2 is a protein called Cyclin-dependent kinase 12.

Mol	Chain	Residues	Atoms							ZeroOcc	AltConf	Trace
			Total	C	H	N	O	P	S			
2	B	319	Total	C	H	N	O	P	S	2643	0	0
			5214	1661	2622	437	477	1	16			
2	E	329	Total	C	H	N	O	P	S	2697	0	0
			5384	1723	2697	454	492	1	17			
2	H	318	Total	C	H	N	O	P	S	2611	0	0
			5195	1655	2611	436	476	1	16			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	709	GLY	-	expression tag	UNP Q9NYV4
B	710	GLY	-	expression tag	UNP Q9NYV4
B	711	GLY	-	expression tag	UNP Q9NYV4
B	965	ARG	LYS	engineered mutation	UNP Q9NYV4
B	1052	GLN	-	expression tag	UNP Q9NYV4
E	709	GLY	-	expression tag	UNP Q9NYV4
E	710	GLY	-	expression tag	UNP Q9NYV4
E	711	GLY	-	expression tag	UNP Q9NYV4
E	965	ARG	LYS	engineered mutation	UNP Q9NYV4
E	1052	GLN	-	expression tag	UNP Q9NYV4
H	709	GLY	-	expression tag	UNP Q9NYV4
H	710	GLY	-	expression tag	UNP Q9NYV4

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Chain	Residue	Modelled	Actual	Comment	Reference
H	711	GLY	-	expression tag	UNP Q9NYV4
H	965	ARG	LYS	engineered mutation	UNP Q9NYV4
H	1052	GLN	-	expression tag	UNP Q9NYV4

- Molecule 3 is a protein called Cyclin-K.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
3	C	247	Total	C	H	N	O	S	2039	0	0
			4092	1335	2039	343	362	13			
3	F	248	Total	C	H	N	O	S	2048	0	0
			4111	1341	2048	346	363	13			
3	I	247	Total	C	H	N	O	S	2041	0	0
			4094	1335	2041	343	362	13			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-3	GLY	-	expression tag	UNP O75909
C	-2	GLY	-	expression tag	UNP O75909
C	-1	GLY	-	expression tag	UNP O75909
C	0	ARG	-	expression tag	UNP O75909
F	-3	GLY	-	expression tag	UNP O75909
F	-2	GLY	-	expression tag	UNP O75909
F	-1	GLY	-	expression tag	UNP O75909
F	0	ARG	-	expression tag	UNP O75909
I	-3	GLY	-	expression tag	UNP O75909
I	-2	GLY	-	expression tag	UNP O75909
I	-1	GLY	-	expression tag	UNP O75909
I	0	ARG	-	expression tag	UNP O75909

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

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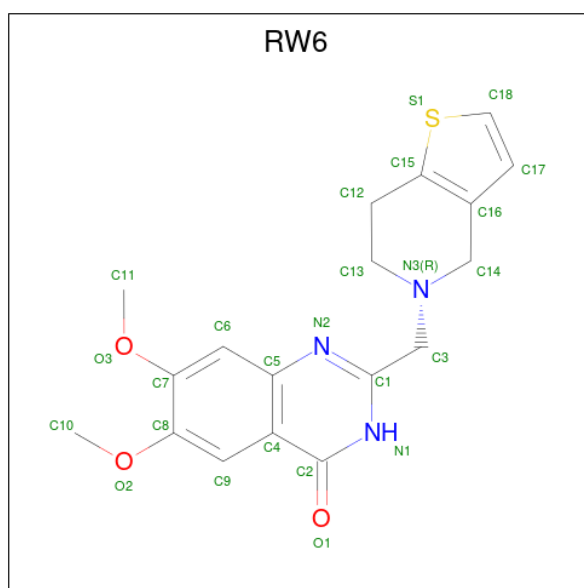
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
4	D	1	5	4	1	0	0
4	D	1	5	4	1	0	0
4	D	1	5	4	1	0	0
4	D	1	5	4	1	0	0
4	D	1	5	4	1	0	0
4	D	1	5	4	1	0	0
4	D	1	5	4	1	0	0
4	E	1	5	4	1	0	0
4	E	1	5	4	1	0	0
4	E	1	5	4	1	0	0
4	E	1	5	4	1	0	0
4	F	1	5	4	1	0	0
4	F	1	5	4	1	0	0
4	F	1	5	4	1	0	0
4	F	1	5	4	1	0	0
4	G	1	5	4	1	0	0
4	G	1	5	4	1	0	0
4	G	1	5	4	1	0	0
4	G	1	5	4	1	0	0
4	G	1	5	4	1	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	G	1	Total	O	S	0	0
			5	4	1		
4	G	1	Total	O	S	0	0
			5	4	1		
4	G	1	Total	O	S	0	0
			5	4	1		
4	H	1	Total	O	S	0	0
			5	4	1		
4	H	1	Total	O	S	0	0
			5	4	1		
4	H	1	Total	O	S	0	0
			5	4	1		
4	H	1	Total	O	S	0	0
			5	4	1		
4	H	1	Total	O	S	0	0
			5	4	1		
4	I	1	Total	O	S	0	0
			5	4	1		
4	I	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is 2-(6,7-dihydro-4 {H}-thieno[3,2-c]pyridin-5-ylmethyl)-6,7-dimethoxy-3 {H}-quinazolin-4-one (CCD ID: RW6) (formula: C₁₈H₁₉N₃O₃S) (labeled as "Ligand of Interest" by depositor).

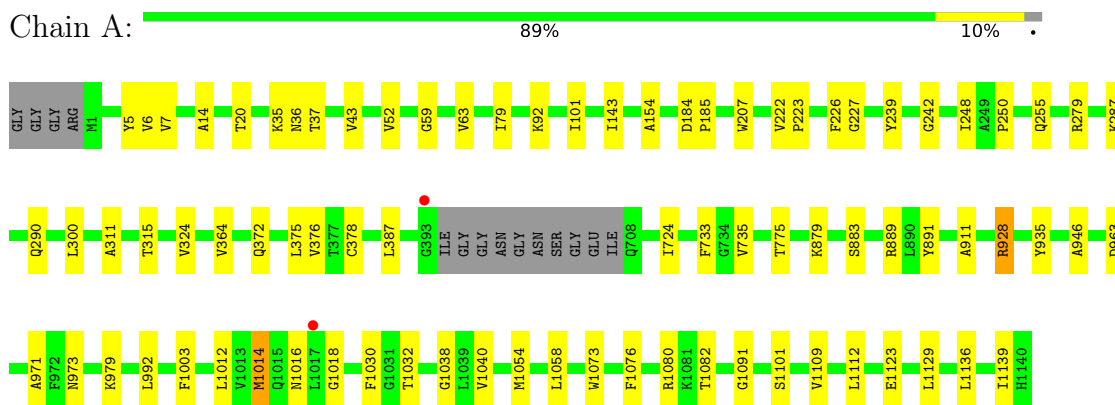


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
5	B	1	Total 44	C 18	H 19	N 3	O 3	S 1	19	0
5	E	1	Total 44	C 18	H 19	N 3	O 3	S 1	19	0
5	H	1	Total 44	C 18	H 19	N 3	O 3	S 1	19	0

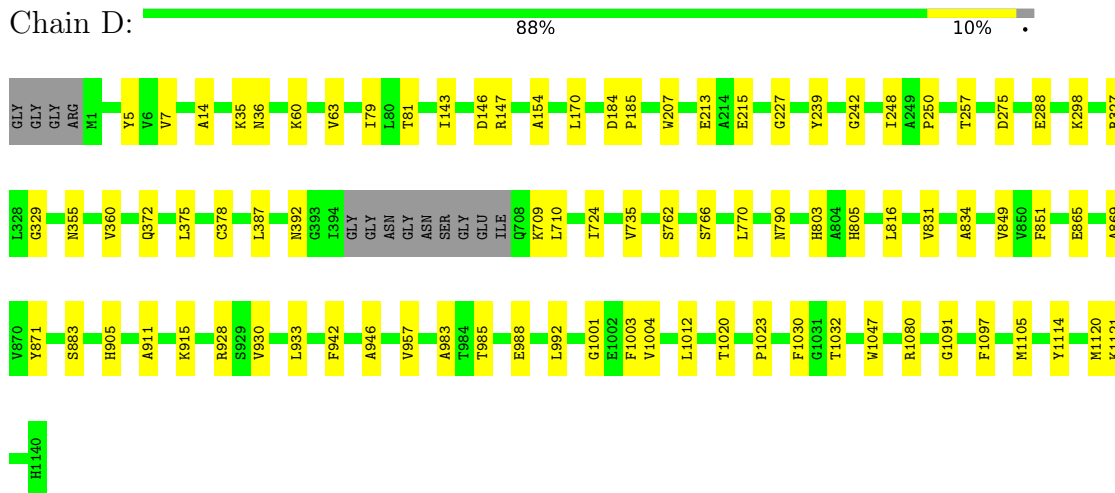
3 Residue-property plots

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.

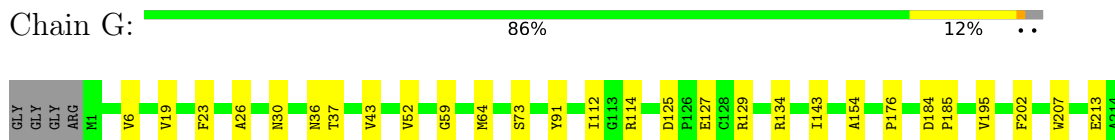
- Molecule 1: DNA damage-binding protein 1

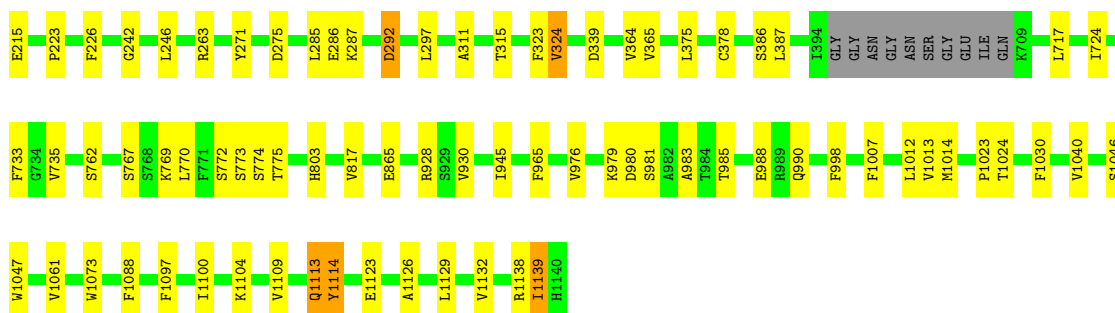


- Molecule 1: DNA damage-binding protein 1

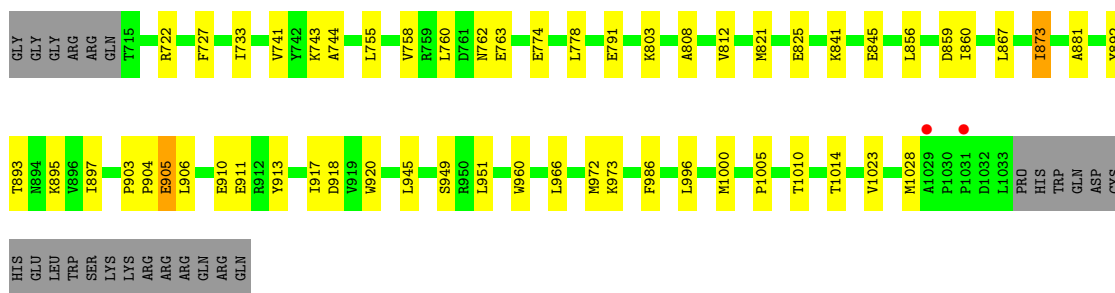
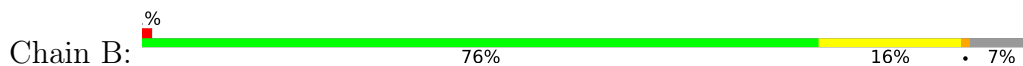


- Molecule 1: DNA damage-binding protein 1

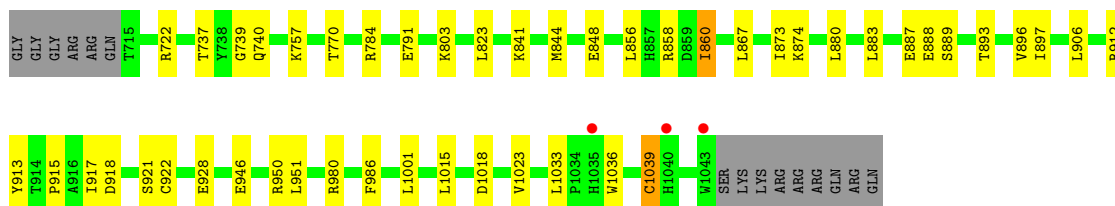
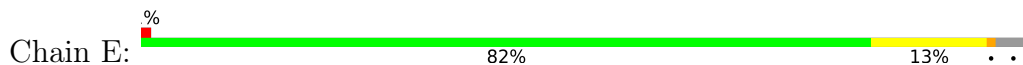




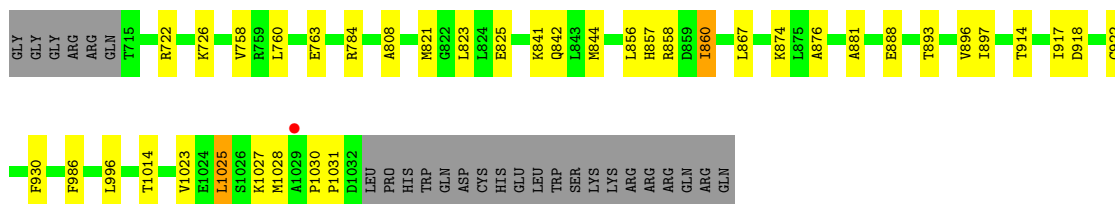
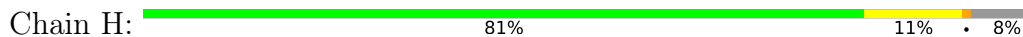
- Molecule 2: Cyclin-dependent kinase 12



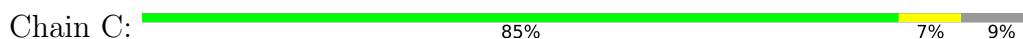
- Molecule 2: Cyclin-dependent kinase 12



- Molecule 2: Cyclin-dependent kinase 12



- Molecule 3: Cyclin-K





HIS

- Molecule 3: Cyclin-K

Chain F: 84% 7% 8%



L255

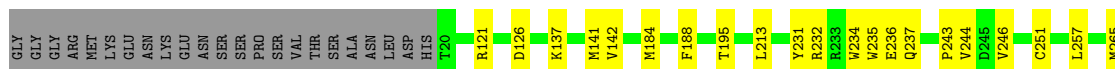
M265

P266

H267

- Molecule 3: Cyclin-K

Chain I: 83% 8% 9%



P266

HIS

4 Data and refinement statistics i

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	249.62Å 249.62Å 220.67Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	60.33 – 3.30 60.33 – 3.30	Depositor EDS
% Data completeness (in resolution range)	84.5 (60.33-3.30) 84.7 (60.33-3.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.53 (at 3.33Å)	Xtrriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.184 , 0.220 0.195 , 0.229	Depositor DCC
R_{free} test set	5043 reflections (4.23%)	wwPDB-VP
Wilson B-factor (Å ²)	135.3	Xtrriage
Anisotropy	0.006	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 110.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtrriage
Estimated twinning fraction	0.034 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	67286	wwPDB-VP
Average B, all atoms (Å ²)	156.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.59% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, TPO, RW6

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	0.24	0/6604	0.52	0/8931
1	D	0.23	0/6612	0.49	0/8942
1	G	0.28	1/6603 (0.0%)	0.51	0/8930
2	B	0.27	0/2635	0.54	2/3549 (0.1%)
2	E	0.24	0/2737	0.49	0/3691
2	H	0.27	0/2627	0.53	1/3538 (0.0%)
3	C	0.23	0/2109	0.47	0/2853
3	F	0.25	0/2120	0.48	0/2868
3	I	0.23	0/2109	0.46	0/2853
All	All	0.25	1/34156 (0.0%)	0.50	3/46155 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	324	VAL	C-N	9.40	1.38	1.33

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	895	LYS	CA-C-N	-5.78	117.31	122.97
2	B	895	LYS	C-N-CA	-5.78	117.31	122.97
2	H	876	ALA	N-CA-C	5.70	122.94	110.80

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	6487	6450	6451	42	0
1	D	6495	6462	6464	45	0
1	G	6486	6454	6456	62	0
2	B	2592	2622	2622	33	0
2	E	2687	2697	2697	24	1
2	H	2584	2611	2611	23	0
3	C	2053	2039	2041	10	0
3	F	2063	2048	2048	12	0
3	I	2053	2041	2041	10	1
4	A	40	0	0	0	0
4	B	10	0	0	0	0
4	C	10	0	0	0	0
4	D	45	0	0	0	0
4	E	20	0	0	0	0
4	F	20	0	0	0	0
4	G	45	0	0	1	0
4	H	30	0	0	0	0
4	I	10	0	0	0	0
5	B	25	19	0	2	0
5	E	25	19	0	0	0
5	H	25	19	0	0	0
All	All	33805	33481	33431	253	1

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 4.

All (253) 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)
3:C:121:ARG:NH2	3:C:126:ASP:OD1	1.86	1.08
3:F:231:TYR:OH	3:F:236:GLU:OE1	1.98	0.81
1:A:227:GLY:O	1:A:239:TYR:OH	2.01	0.79
1:G:285:LEU:HB3	1:G:297:LEU:HD11	1.72	0.71
1:G:1114:TYR:HA	1:G:1123:GLU:HA	1.73	0.70
1:G:983:ALA:HB1	1:G:988:GLU:OE1	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:773:SER:O	1:G:775:THR:N	2.27	0.67
1:G:979:LYS:O	1:G:981:SER:N	2.28	0.67
3:F:121:ARG:NH2	3:F:126:ASP:OD1	2.23	0.63
1:G:364:VAL:HG22	1:G:375:LEU:HD13	1.79	0.63
1:G:226:PHE:CZ	1:G:287:LYS:HG2	2.34	0.63
1:G:1047:TRP:HZ3	1:G:1132:VAL:HG13	1.64	0.62
1:G:773:SER:C	1:G:775:THR:H	2.07	0.61
2:E:844:MET:HE1	2:E:922:CYS:SG	2.40	0.61
1:G:226:PHE:CE1	1:G:287:LYS:HG2	2.34	0.61
2:H:841:LYS:HD2	2:H:1023:VAL:HB	1.82	0.61
2:B:906:LEU:HD21	2:B:913:TYR:CD1	2.36	0.60
1:A:1112:LEU:O	1:A:1123:GLU:HA	2.02	0.59
1:D:329:GLY:O	1:D:355:ASN:ND2	2.35	0.59
1:A:1109:VAL:HG12	1:A:1129:LEU:HD12	1.83	0.59
1:D:207:TRP:HB3	1:D:242:GLY:HA2	1.85	0.59
3:I:195:THR:CG2	3:I:257:LEU:HD11	2.33	0.59
1:A:775:THR:HG22	1:A:775:THR:O	2.03	0.59
2:E:823:LEU:HD12	2:E:867:LEU:HD23	1.84	0.59
1:G:1109:VAL:HG11	1:G:1126:ALA:HA	1.86	0.58
2:E:844:MET:HE2	2:E:844:MET:HA	1.86	0.57
1:A:889:ARG:HD2	1:A:891:TYR:CZ	2.40	0.57
1:D:816:LEU:HD13	1:D:831:VAL:HG22	1.86	0.57
1:A:59:GLY:HA2	1:A:1073:TRP:CZ3	2.40	0.57
2:B:905:GLU:HA	2:B:960:TRP:HH2	1.69	0.56
1:G:292:ASP:OD1	1:G:292:ASP:N	2.39	0.56
1:G:43:VAL:HG23	1:G:52:VAL:HG21	1.86	0.56
1:D:387:LEU:HD11	1:D:735:VAL:HG21	1.88	0.56
1:A:207:TRP:HB3	1:A:242:GLY:HA2	1.87	0.56
2:E:841:LYS:HD2	2:E:1023:VAL:HB	1.89	0.55
2:B:841:LYS:HD2	2:B:1023:VAL:HB	1.88	0.55
1:G:1023:PRO:HB3	1:G:1047:TRP:CE2	2.42	0.55
1:A:372:GLN:HG3	1:A:1014:MET:HG2	1.89	0.55
1:A:248:ILE:HG12	1:A:250:PRO:HD3	1.88	0.55
1:A:1054:MET:HE2	1:A:1058:LEU:HD11	1.90	0.54
3:F:79:HIS:HB3	3:F:199:LEU:HD11	1.88	0.54
2:B:1010:THR:O	2:B:1014:THR:HG23	2.08	0.54
2:E:1036:TRP:HA	2:E:1039:CYS:HB3	1.89	0.54
1:D:288:GLU:HB2	1:D:298:LYS:HB2	1.89	0.53
1:G:387:LEU:HD11	1:G:735:VAL:HG21	1.90	0.53
1:G:770:LEU:HD21	1:G:865:GLU:HB2	1.90	0.53
1:D:213:GLU:HG2	1:D:215:GLU:H	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:7:VAL:HG12	1:A:1091:GLY:HA3	1.91	0.53
1:G:387:LEU:HG	1:G:717:LEU:HD11	1.89	0.53
1:A:226:PHE:CE2	1:A:287:LYS:HG2	2.44	0.52
2:B:910:GLU:O	2:B:911:GLU:HB3	2.09	0.52
1:D:871:TYR:HE1	2:E:1036:TRP:HZ3	1.56	0.52
2:E:739:GLY:HA3	2:E:757:LYS:O	2.09	0.52
1:D:834:ALA:HB2	1:D:869:ALA:HA	1.90	0.52
1:G:767:SER:N	4:G:1205:SO4:O1	2.43	0.52
2:E:951:LEU:HD21	2:E:986:PHE:HE2	1.75	0.51
3:I:231:TYR:OH	3:I:236:GLU:OE1	2.22	0.51
1:D:1080:ARG:NH1	2:E:928:GLU:OE2	2.44	0.51
2:H:760:LEU:HD12	2:H:760:LEU:N	2.26	0.51
2:B:951:LEU:HD21	2:B:986:PHE:HE2	1.76	0.51
1:A:311:ALA:HB2	1:A:324:VAL:HG13	1.92	0.51
1:D:227:GLY:O	1:D:239:TYR:OH	2.22	0.51
1:D:378:CYS:SG	1:D:724:ILE:HB	2.51	0.50
1:A:1003:PHE:O	1:A:1032:THR:HA	2.12	0.50
1:A:255:GLN:HB2	1:A:279:ARG:HH22	1.77	0.50
2:B:917:ILE:HG13	2:B:918:ASP:N	2.26	0.50
1:D:770:LEU:HD13	1:D:865:GLU:HB2	1.94	0.50
1:D:983:ALA:HB3	1:D:988:GLU:HG3	1.93	0.50
1:G:311:ALA:HB2	1:G:324:VAL:HG13	1.94	0.50
2:E:858:ARG:NE	2:E:880:LEU:O	2.45	0.50
2:H:722:ARG:HE	2:H:726:LYS:HG3	1.77	0.50
2:E:906:LEU:HD21	2:E:913:TYR:CD2	2.47	0.50
3:F:138:GLU:O	3:F:142:VAL:HG13	2.11	0.50
1:D:709:LYS:HG2	1:D:710:LEU:N	2.27	0.49
1:G:19:VAL:HG22	1:G:64:MET:HE3	1.94	0.49
3:C:76:ILE:CD1	3:C:198:SER:HB3	2.42	0.49
1:G:1113:GLN:HG2	1:G:1114:TYR:H	1.78	0.49
2:E:867:LEU:HD13	2:E:873:ILE:CD1	2.42	0.49
2:H:842:GLN:HG3	2:H:1025:LEU:HD11	1.94	0.49
1:A:928:ARG:HG2	5:B:1101:RW6:C18	2.43	0.49
2:E:856:LEU:HD11	2:E:915:PRO:HG3	1.95	0.49
1:D:7:VAL:HG12	1:D:1091:GLY:HA3	1.94	0.49
1:A:946:ALA:HB1	1:A:992:LEU:HG	1.93	0.48
1:D:375:LEU:HB2	1:D:1012:LEU:HD21	1.95	0.48
1:A:36:ASN:O	1:A:37:THR:OG1	2.28	0.48
1:D:946:ALA:HB1	1:D:992:LEU:HG	1.95	0.48
1:G:6:VAL:HG22	1:G:1040:VAL:HG22	1.95	0.48
1:G:246:LEU:HD12	1:G:297:LEU:HD23	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:774:GLU:HG2	2:B:778:LEU:HD12	1.96	0.48
1:G:378:CYS:SG	1:G:724:ILE:HB	2.53	0.48
1:A:387:LEU:HD11	1:A:735:VAL:HG21	1.94	0.48
2:E:803:LYS:HG3	3:F:142:VAL:HG11	1.96	0.48
3:I:184:MET:HG3	3:I:266:PRO:HB2	1.95	0.47
1:G:114:ARG:HD3	2:H:930:PHE:O	2.14	0.47
1:A:14:ALA:O	1:A:35:LYS:HG2	2.15	0.47
1:A:43:VAL:HG23	1:A:52:VAL:HG11	1.97	0.47
1:G:143:ILE:HG12	1:G:154:ALA:HB2	1.97	0.47
1:G:1061:VAL:HG11	1:G:1104:LYS:HB3	1.97	0.47
3:I:234:TRP:O	3:I:237:GLN:HG2	2.15	0.47
3:I:243:PRO:HG2	3:I:246:VAL:HG23	1.95	0.47
3:C:27:ASP:OD1	3:C:28:LYS:N	2.48	0.47
2:E:946:GLU:O	2:E:950:ARG:HG2	2.14	0.47
1:G:1024:THR:HG21	1:G:1139:ILE:HD13	1.97	0.47
2:B:803:LYS:HG3	3:C:142:VAL:HG21	1.97	0.47
1:D:146:ASP:OD1	1:D:147:ARG:N	2.48	0.47
2:B:867:LEU:HG	2:B:873:ILE:HG13	1.95	0.47
1:G:762:SER:O	1:G:803:HIS:HA	2.15	0.47
1:G:36:ASN:O	1:G:37:THR:OG1	2.24	0.46
1:G:184:ASP:HB2	1:G:185:PRO:CD	2.45	0.46
1:D:60:LYS:O	1:D:81:THR:HA	2.15	0.46
2:H:758:VAL:O	2:H:808:ALA:HB1	2.15	0.46
3:C:132:PHE:O	3:C:139:GLU:HG3	2.16	0.46
1:D:63:VAL:O	1:D:79:ILE:HA	2.15	0.46
1:G:207:TRP:HB3	1:G:242:GLY:HA2	1.97	0.46
1:G:1014:MET:HE2	1:G:1014:MET:HB2	1.86	0.46
1:D:849:VAL:HG11	1:D:851:PHE:CZ	2.50	0.46
1:D:1120:MET:HG2	1:D:1121:LYS:H	1.80	0.46
1:D:372:GLN:NE2	1:D:392:ASN:O	2.48	0.46
1:G:59:GLY:HA2	1:G:1073:TRP:CE3	2.51	0.46
1:G:1113:GLN:HG2	1:G:1114:TYR:N	2.30	0.46
2:H:844:MET:HA	2:H:844:MET:HE2	1.96	0.46
1:D:1097:PHE:O	1:D:1105:MET:HE2	2.15	0.46
2:E:867:LEU:HD13	2:E:873:ILE:HD13	1.98	0.46
1:A:184:ASP:HB2	1:A:185:PRO:CD	2.46	0.46
2:B:758:VAL:O	2:B:808:ALA:HB1	2.16	0.46
1:G:30:ASN:ND2	1:G:43:VAL:HG22	2.31	0.45
1:G:365:VAL:HG11	1:G:733:PHE:CZ	2.51	0.45
2:H:917:ILE:HG13	2:H:918:ASP:N	2.31	0.45
1:A:879:LYS:NZ	1:A:935:TYR:OH	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:234:TRP:O	3:C:237:GLN:HG2	2.16	0.45
3:F:25:TYR:OH	3:F:203:PRO:HD3	2.16	0.45
1:D:915:LYS:HE3	1:D:957:VAL:O	2.17	0.45
1:G:195:VAL:HG22	1:G:202:PHE:HE1	1.82	0.45
1:D:1003:PHE:O	1:D:1032:THR:HA	2.17	0.45
2:H:858:ARG:HG2	2:H:917:ILE:HD11	1.98	0.45
1:A:5:TYR:CE2	1:A:7:VAL:HG13	2.53	0.44
1:A:248:ILE:HD12	1:A:300:LEU:O	2.17	0.44
1:A:1080:ARG:HD3	2:B:825:GLU:HA	1.99	0.44
2:E:722:ARG:NH1	2:E:791:GLU:OE2	2.50	0.44
3:C:76:ILE:HD12	3:C:198:SER:HB3	1.99	0.44
2:E:980:ARG:NH2	2:E:1001:LEU:O	2.46	0.44
1:D:14:ALA:HB1	1:D:327:ARG:HG3	2.00	0.44
1:D:35:LYS:O	1:D:36:ASN:C	2.60	0.44
1:D:1023:PRO:HB3	1:D:1047:TRP:CZ2	2.53	0.44
1:G:315:THR:HG22	1:G:323:PHE:HB3	2.00	0.44
1:A:92:LYS:HD2	1:A:101:ILE:HD11	1.99	0.44
2:E:917:ILE:HG13	2:E:918:ASP:N	2.32	0.44
1:D:985:THR:HB	1:D:988:GLU:HG2	1.99	0.43
1:G:59:GLY:HA2	1:G:1073:TRP:CZ3	2.53	0.43
1:G:1007:PHE:CD1	1:G:1030:PHE:HB3	2.53	0.43
2:H:856:LEU:O	2:H:881:ALA:HA	2.18	0.43
2:H:1027:LYS:O	2:H:1028:MET:C	2.61	0.43
2:B:904:PRO:HD3	2:B:920:TRP:CE2	2.53	0.43
3:F:255:LEU:HD22	3:F:265:MET:HG2	2.00	0.43
2:B:960:TRP:CD1	2:B:960:TRP:C	2.96	0.43
3:C:165:LEU:O	3:C:169:LYS:HG3	2.18	0.43
1:D:36:ASN:ND2	1:D:1001:GLY:O	2.51	0.43
2:B:905:GLU:OE1	2:B:1005:PRO:HB3	2.18	0.43
1:G:1013:VAL:HG11	1:G:1138:ARG:O	2.19	0.43
1:G:134:ARG:C	1:G:134:ARG:HD2	2.44	0.43
1:G:127:GLU:HB2	1:G:129:ARG:HG3	2.00	0.43
2:B:903:PRO:HG3	2:B:917:ILE:HG22	2.00	0.43
2:H:844:MET:HE1	2:H:922:CYS:SG	2.59	0.43
3:F:184:MET:HE3	3:F:184:MET:HB2	1.90	0.43
2:E:860:ILE:HB	2:E:921:SER:CB	2.49	0.42
1:D:7:VAL:CG1	1:D:1091:GLY:HA3	2.50	0.42
2:E:889:SER:HB2	2:E:912:ARG:HD3	2.02	0.42
1:G:286:GLU:O	1:G:297:LEU:HD12	2.19	0.42
2:H:888:GLU:O	2:H:888:GLU:HG3	2.19	0.42
1:A:6:VAL:HG22	1:A:1040:VAL:HG22	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:834:ALA:HB2	1:D:869:ALA:CB	2.50	0.42
1:G:365:VAL:HG11	1:G:733:PHE:CE2	2.55	0.42
2:B:722:ARG:NH1	2:B:791:GLU:OE2	2.53	0.42
2:B:803:LYS:HG3	3:C:142:VAL:HG11	2.01	0.42
3:C:207:ALA:O	3:C:210:VAL:HG22	2.19	0.42
1:D:933:LEU:HD22	1:D:942:PHE:HB3	2.01	0.42
2:H:914:THR:O	2:H:917:ILE:HG12	2.18	0.42
1:A:378:CYS:SG	1:A:724:ILE:HB	2.60	0.42
1:A:1016:ASN:C	1:A:1018:GLY:H	2.27	0.42
2:B:727:PHE:HB3	2:B:744:ALA:HB1	2.02	0.42
1:D:5:TYR:CE2	1:D:7:VAL:HG13	2.55	0.42
1:G:125:ASP:OD2	1:G:176:PRO:HB3	2.18	0.42
2:B:733:ILE:HG23	2:B:743:LYS:HB2	2.01	0.42
2:H:763:GLU:O	2:H:763:GLU:CD	2.62	0.42
1:D:905:HIS:CG	1:D:933:LEU:HD11	2.55	0.42
1:G:375:LEU:HB2	1:G:1012:LEU:HD21	2.02	0.42
2:B:841:LYS:O	2:B:845:GLU:HB2	2.19	0.42
2:B:903:PRO:HB2	2:B:905:GLU:HG3	2.02	0.42
1:D:248:ILE:HG12	1:D:250:PRO:HD3	2.02	0.42
2:B:821:MET:HE2	2:B:821:MET:HB3	1.87	0.41
2:B:906:LEU:HD23	2:B:906:LEU:HA	1.79	0.41
1:D:790:ASN:HA	1:D:805:HIS:O	2.20	0.41
3:F:61:GLY:HA3	3:F:71:LEU:CD2	2.50	0.41
3:F:202:GLU:OE1	3:F:202:GLU:N	2.48	0.41
1:G:965:PHE:O	1:G:976:VAL:HA	2.20	0.41
2:B:856:LEU:O	2:B:881:ALA:HA	2.20	0.41
2:B:945:LEU:HD22	2:B:972:MET:HE2	2.02	0.41
2:E:784:ARG:O	2:E:874:LYS:HE2	2.19	0.41
2:E:848:GLU:OE1	2:E:1015:LEU:HD12	2.20	0.41
1:D:883:SER:HB2	1:D:911:ALA:HB3	2.02	0.41
1:G:223:PRO:HD3	1:G:271:TYR:OH	2.19	0.41
1:G:945:ILE:O	1:G:990:GLN:HA	2.20	0.41
2:H:722:ARG:HH21	2:H:726:LYS:HB3	1.85	0.41
1:A:883:SER:HB2	1:A:911:ALA:HB3	2.02	0.41
2:B:892:TYR:O	2:B:911:GLU:HG3	2.21	0.41
1:D:257:THR:O	1:D:275:ASP:HB2	2.20	0.41
3:F:125:ASN:OD1	3:F:125:ASN:C	2.64	0.41
2:H:784:ARG:O	2:H:874:LYS:HE2	2.19	0.41
3:I:235:TRP:HZ2	3:I:244:VAL:HG22	1.85	0.41
1:A:222:VAL:HA	1:A:223:PRO:HD3	1.88	0.41
1:D:1004:VAL:HG13	1:D:1030:PHE:HB2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:112:ILE:HD13	2:H:986:PHE:CE2	2.56	0.41
1:G:769:LYS:O	1:G:772:SER:HB3	2.21	0.41
1:G:1097:PHE:O	1:G:1100:ILE:HG12	2.21	0.41
2:H:823:LEU:HD12	2:H:867:LEU:HD21	2.03	0.41
1:A:63:VAL:O	1:A:79:ILE:HA	2.21	0.41
1:G:26:ALA:HB2	1:G:73:SER:O	2.21	0.41
1:G:1109:VAL:HG12	1:G:1129:LEU:HD12	2.01	0.41
2:H:1030:PRO:HA	2:H:1031:PRO:HD3	1.90	0.41
3:I:213:LEU:HB2	3:I:251:CYS:SG	2.60	0.41
1:A:971:ALA:HB3	1:A:973:ASN:HD22	1.86	0.41
1:A:1030:PHE:CZ	1:A:1038:GLY:HA3	2.56	0.41
2:B:859:ASP:OD1	2:B:859:ASP:N	2.54	0.41
1:D:143:ILE:HG12	1:D:154:ALA:HB2	2.02	0.41
1:D:170:LEU:HD23	1:D:170:LEU:HA	1.86	0.41
1:G:263:ARG:HA	1:G:271:TYR:CD2	2.55	0.41
2:H:857:HIS:ND1	2:H:860:ILE:HG12	2.36	0.41
2:B:762:ASN:O	2:B:763:GLU:HB3	2.21	0.41
1:A:1076:PHE:O	1:A:1082:THR:HA	2.21	0.40
2:B:755:LEU:HD22	2:B:812:VAL:HG22	2.03	0.40
2:B:996:LEU:O	2:B:1000:MET:HG3	2.21	0.40
1:G:275:ASP:OD1	1:G:275:ASP:C	2.64	0.40
1:A:376:VAL:HG21	1:A:733:PHE:CZ	2.57	0.40
1:A:1136:LEU:O	1:A:1139:ILE:HG12	2.21	0.40
2:B:741:VAL:HG21	5:B:1101:RW6:C11	2.51	0.40
1:D:184:ASP:HB2	1:D:185:PRO:CD	2.51	0.40
1:D:762:SER:HB3	1:D:803:HIS:ND1	2.35	0.40
1:G:23:PHE:CE2	1:G:91:TYR:HB2	2.57	0.40
3:I:121:ARG:NH2	3:I:126:ASP:OD1	2.45	0.40
1:A:143:ILE:HG12	1:A:154:ALA:HB2	2.04	0.40
1:A:963:ASP:OD1	1:A:979:LYS:HE3	2.21	0.40
2:H:821:MET:HG2	2:H:825:GLU:HG3	2.03	0.40
3:I:184:MET:HG2	3:I:188:PHE:CE2	2.57	0.40
1:A:364:VAL:HG22	1:A:375:LEU:HD13	2.04	0.40
1:A:375:LEU:HB2	1:A:1012:LEU:HD21	2.04	0.40
2:B:945:LEU:O	2:B:949:SER:OG	2.27	0.40
2:E:887:GLU:O	2:E:888:GLU:C	2.65	0.40
3:F:233:ARG:HB3	3:F:236:GLU:HG3	2.02	0.40
1:G:213:GLU:HG2	1:G:215:GLU:H	1.86	0.40
1:G:998:PHE:HB2	1:G:1088:PHE:CG	2.57	0.40
3:I:137:LYS:HE3	3:I:141:MET:HE2	2.03	0.40
1:G:226:PHE:HZ	1:G:287:LYS:HG2	1.84	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:996:LEU:HD11	2:H:1014:THR:HG22	2.03	0.40

All (1) 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)
2:E:1018:ASP:OD2	3:I:232:ARG:HE[5_554]	1.53	0.07

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	822/840 (98%)	794 (97%)	28 (3%)	0	100	100
1	D	823/840 (98%)	802 (97%)	21 (3%)	0	100	100
1	G	822/840 (98%)	798 (97%)	21 (3%)	3 (0%)	30	60
2	B	316/344 (92%)	306 (97%)	10 (3%)	0	100	100
2	E	326/344 (95%)	316 (97%)	10 (3%)	0	100	100
2	H	315/344 (92%)	308 (98%)	7 (2%)	0	100	100
3	C	245/271 (90%)	244 (100%)	1 (0%)	0	100	100
3	F	246/271 (91%)	243 (99%)	3 (1%)	0	100	100
3	I	245/271 (90%)	242 (99%)	3 (1%)	0	100	100
All	All	4160/4365 (95%)	4053 (97%)	104 (2%)	3 (0%)	48	75

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	1113	GLN
1	G	774	SER
1	G	980	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	721/728 (99%)	715 (99%)	6 (1%)	73	79
1	D	722/728 (99%)	716 (99%)	6 (1%)	73	79
1	G	721/728 (99%)	711 (99%)	10 (1%)	59	73
2	B	286/308 (93%)	278 (97%)	8 (3%)	38	62
2	E	296/308 (96%)	287 (97%)	9 (3%)	36	61
2	H	285/308 (92%)	281 (99%)	4 (1%)	59	73
3	C	222/242 (92%)	219 (99%)	3 (1%)	59	73
3	F	223/242 (92%)	219 (98%)	4 (2%)	51	70
3	I	222/242 (92%)	220 (99%)	2 (1%)	70	78
All	All	3698/3834 (96%)	3646 (99%)	52 (1%)	59	73

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

Mol	Chain	Res	Type
1	A	20	THR
1	A	290	GLN
1	A	315	THR
1	A	928	ARG
1	A	1014	MET
1	A	1101	SER
2	B	760	LEU
2	B	860	ILE
2	B	873	ILE
2	B	897	ILE
2	B	905	GLU
2	B	966	LEU
2	B	973	LYS
2	B	1028	MET
3	C	146	ILE
3	C	257	LEU
3	C	265	MET
1	D	360	VAL

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Mol	Chain	Res	Type
1	D	766	SER
1	D	928	ARG
1	D	930	VAL
1	D	1020	THR
1	D	1114	TYR
2	E	737	THR
2	E	740	GLN
2	E	770	THR
2	E	860	ILE
2	E	883	LEU
2	E	896	VAL
2	E	897	ILE
2	E	1033	LEU
2	E	1039	CYS
3	F	76	ILE
3	F	162	GLN
3	F	198	SER
3	F	265	MET
1	G	292	ASP
1	G	339	ASP
1	G	386	SER
1	G	817	VAL
1	G	928	ARG
1	G	930	VAL
1	G	985	THR
1	G	1046	SER
1	G	1114	TYR
1	G	1139	ILE
2	H	860	ILE
2	H	896	VAL
2	H	897	ILE
2	H	1025	LEU
3	I	142	VAL
3	I	265	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (48) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	4	ASN
1	A	105	HIS
1	A	186	GLN
1	A	234	GLN

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Mol	Chain	Res	Type
1	A	255	GLN
1	A	711	HIS
1	A	778	HIS
1	A	790	ASN
1	A	970	ASN
1	A	1034	ASN
1	A	1113	GLN
2	B	780	GLN
2	B	999	HIS
3	C	37	GLN
3	C	156	GLN
1	D	4	ASN
1	D	85	ASN
1	D	105	HIS
1	D	778	HIS
1	D	952	ASN
1	D	970	ASN
1	D	978	GLN
2	E	780	GLN
2	E	797	GLN
2	E	818	HIS
2	E	851	HIS
2	E	977	GLN
3	F	149	GLN
3	F	200	GLN
3	F	253	GLN
1	G	4	ASN
1	G	189	HIS
1	G	234	GLN
1	G	240	HIS
1	G	370	GLN
1	G	711	HIS
1	G	778	HIS
1	G	905	HIS
1	G	908	ASN
1	G	970	ASN
1	G	990	GLN
1	G	1015	GLN
1	G	1140	HIS
2	H	740	GLN
2	H	797	GLN
2	H	999	HIS

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Mol	Chain	Res	Type
3	I	156	GLN
3	I	252	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

3 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
2	TPO	B	893	2	8,10,11	1.70	1 (12%)	10,14,16	1.43	2 (20%)
2	TPO	H	893	2	8,10,11	1.48	1 (12%)	10,14,16	1.51	2 (20%)
2	TPO	E	893	2	8,10,11	1.31	0	10,14,16	1.17	1 (10%)

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	TPO	B	893	2	-	0/9/11/13	-
2	TPO	H	893	2	-	0/9/11/13	-
2	TPO	E	893	2	-	1/9/11/13	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	893	TPO	P-O1P	3.59	1.61	1.50
2	H	893	TPO	P-OG1	2.49	1.63	1.59

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	893	TPO	P-OG1-CB	-3.36	114.20	123.33
2	E	893	TPO	P-OG1-CB	-2.99	115.21	123.33
2	H	893	TPO	P-OG1-CB	-2.88	115.50	123.33
2	H	893	TPO	CG2-CB-CA	-2.54	108.31	113.26
2	B	893	TPO	O-C-CA	-2.00	119.62	124.77

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	893	TPO	CB-OG1-P-O3P

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](#)

49 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	SO4	D	1203	-	4,4,4	0.34	0	6,6,6	0.12	0
4	SO4	A	1202	-	4,4,4	0.37	0	6,6,6	0.10	0
4	SO4	A	1207	-	4,4,4	0.34	0	6,6,6	0.08	0
4	SO4	G	1202	-	4,4,4	0.35	0	6,6,6	0.08	0
4	SO4	A	1206	-	4,4,4	0.36	0	6,6,6	0.08	0
4	SO4	D	1201	-	4,4,4	0.30	0	6,6,6	0.09	0
4	SO4	F	303	-	4,4,4	0.34	0	6,6,6	0.10	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	SO4	G	1207	-	4,4,4	0.35	0	6,6,6	0.09	0
4	SO4	D	1206	-	4,4,4	0.33	0	6,6,6	0.07	0
4	SO4	E	1102	-	4,4,4	0.34	0	6,6,6	0.08	0
4	SO4	H	1103	-	4,4,4	0.39	0	6,6,6	0.11	0
4	SO4	A	1205	-	4,4,4	0.35	0	6,6,6	0.10	0
4	SO4	G	1208	-	4,4,4	0.35	0	6,6,6	0.14	0
4	SO4	A	1204	-	4,4,4	0.34	0	6,6,6	0.09	0
4	SO4	F	304	-	4,4,4	0.39	0	6,6,6	0.13	0
4	SO4	G	1205	-	4,4,4	0.33	0	6,6,6	0.08	0
4	SO4	C	301	-	4,4,4	0.29	0	6,6,6	0.08	0
4	SO4	A	1208	-	4,4,4	0.34	0	6,6,6	0.07	0
4	SO4	H	1105	-	4,4,4	0.34	0	6,6,6	0.08	0
4	SO4	F	302	-	4,4,4	0.29	0	6,6,6	0.08	0
5	RW6	E	1101	-	26,28,28	0.72	0	36,40,40	0.89	1 (2%)
4	SO4	D	1202	-	4,4,4	0.34	0	6,6,6	0.07	0
5	RW6	B	1101	-	26,28,28	0.75	0	36,40,40	0.69	0
4	SO4	H	1104	-	4,4,4	0.35	0	6,6,6	0.10	0
4	SO4	H	1107	-	4,4,4	0.39	0	6,6,6	0.08	0
4	SO4	D	1207	-	4,4,4	0.34	0	6,6,6	0.09	0
4	SO4	G	1201	-	4,4,4	0.31	0	6,6,6	0.10	0
4	SO4	G	1203	-	4,4,4	0.30	0	6,6,6	0.07	0
4	SO4	G	1209	-	4,4,4	0.33	0	6,6,6	0.06	0
4	SO4	D	1205	-	4,4,4	0.36	0	6,6,6	0.09	0
4	SO4	I	302	-	4,4,4	0.28	0	6,6,6	0.09	0
4	SO4	B	1102	-	4,4,4	0.34	0	6,6,6	0.10	0
4	SO4	D	1208	-	4,4,4	0.36	0	6,6,6	0.10	0
4	SO4	E	1104	-	4,4,4	0.33	0	6,6,6	0.04	0
4	SO4	E	1105	-	4,4,4	0.34	0	6,6,6	0.10	0
4	SO4	A	1201	-	4,4,4	0.31	0	6,6,6	0.08	0
4	SO4	B	1103	-	4,4,4	0.32	0	6,6,6	0.07	0
4	SO4	G	1204	-	4,4,4	0.36	0	6,6,6	0.10	0
4	SO4	G	1206	-	4,4,4	0.32	0	6,6,6	0.10	0
5	RW6	H	1101	-	26,28,28	0.72	0	36,40,40	0.85	1 (2%)
4	SO4	I	301	-	4,4,4	0.37	0	6,6,6	0.08	0
4	SO4	E	1103	-	4,4,4	0.31	0	6,6,6	0.05	0
4	SO4	A	1203	-	4,4,4	0.35	0	6,6,6	0.10	0
4	SO4	D	1209	-	4,4,4	0.36	0	6,6,6	0.08	0
4	SO4	F	301	-	4,4,4	0.32	0	6,6,6	0.08	0
4	SO4	H	1106	-	4,4,4	0.33	0	6,6,6	0.09	0
4	SO4	H	1102	-	4,4,4	0.33	0	6,6,6	0.09	0
4	SO4	C	302	-	4,4,4	0.37	0	6,6,6	0.05	0
4	SO4	D	1204	-	4,4,4	0.34	0	6,6,6	0.07	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	RW6	E	1101	-	-	2/6/17/17	0/4/4/4
5	RW6	B	1101	-	-	4/6/17/17	0/4/4/4
5	RW6	H	1101	-	-	2/6/17/17	0/4/4/4

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	1101	RW6	C2-N1-C1	-3.03	122.15	123.90
5	H	1101	RW6	C2-N1-C1	-2.99	122.17	123.90

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	1101	RW6	C1-C3-N3-C13
5	B	1101	RW6	C1-C3-N3-C14
5	E	1101	RW6	C1-C3-N3-C14
5	H	1101	RW6	C1-C3-N3-C13
5	H	1101	RW6	C1-C3-N3-C14
5	B	1101	RW6	C6-C7-O3-C11
5	B	1101	RW6	C8-C7-O3-C11
5	E	1101	RW6	C1-C3-N3-C13

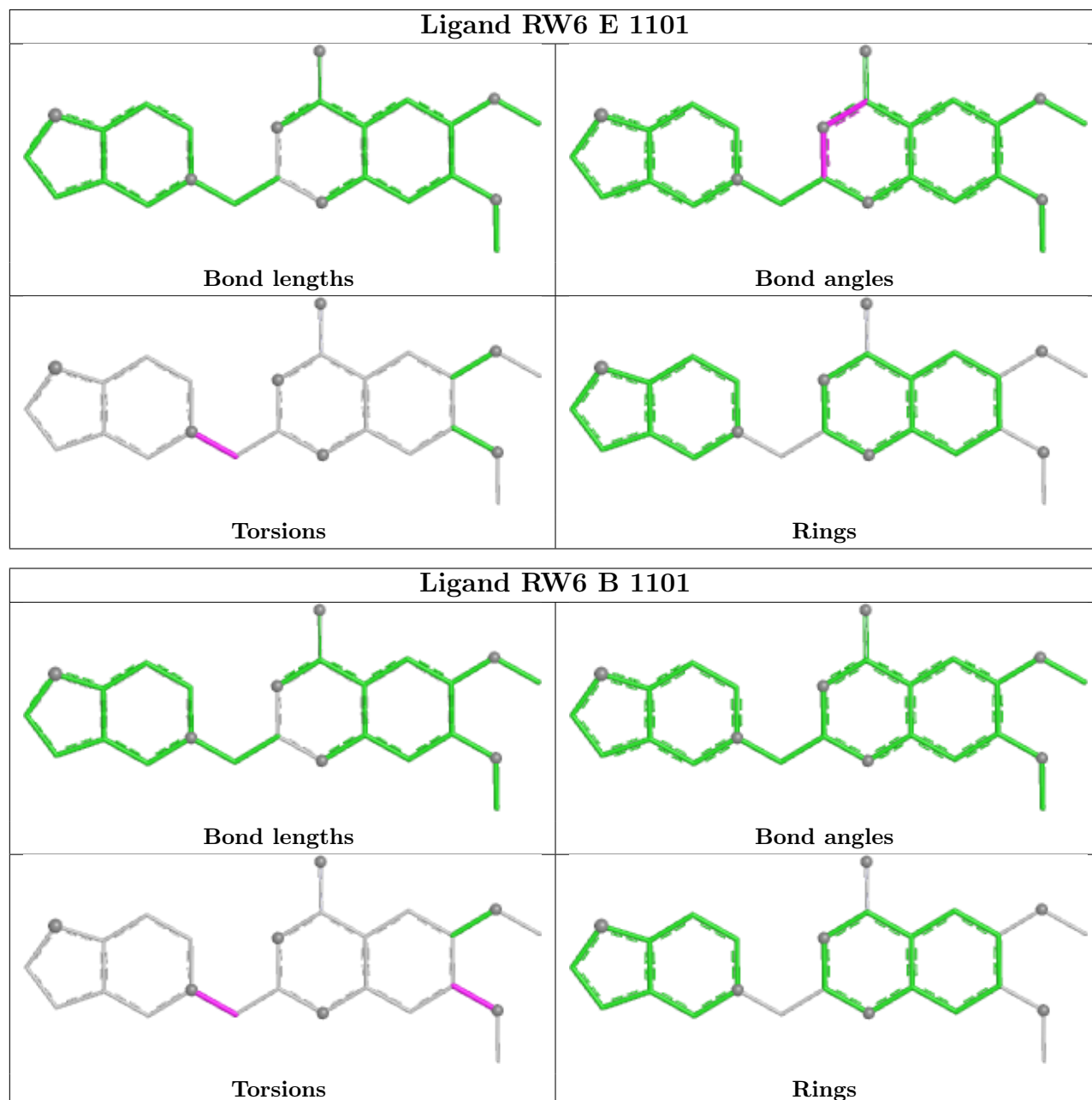
There are no ring outliers.

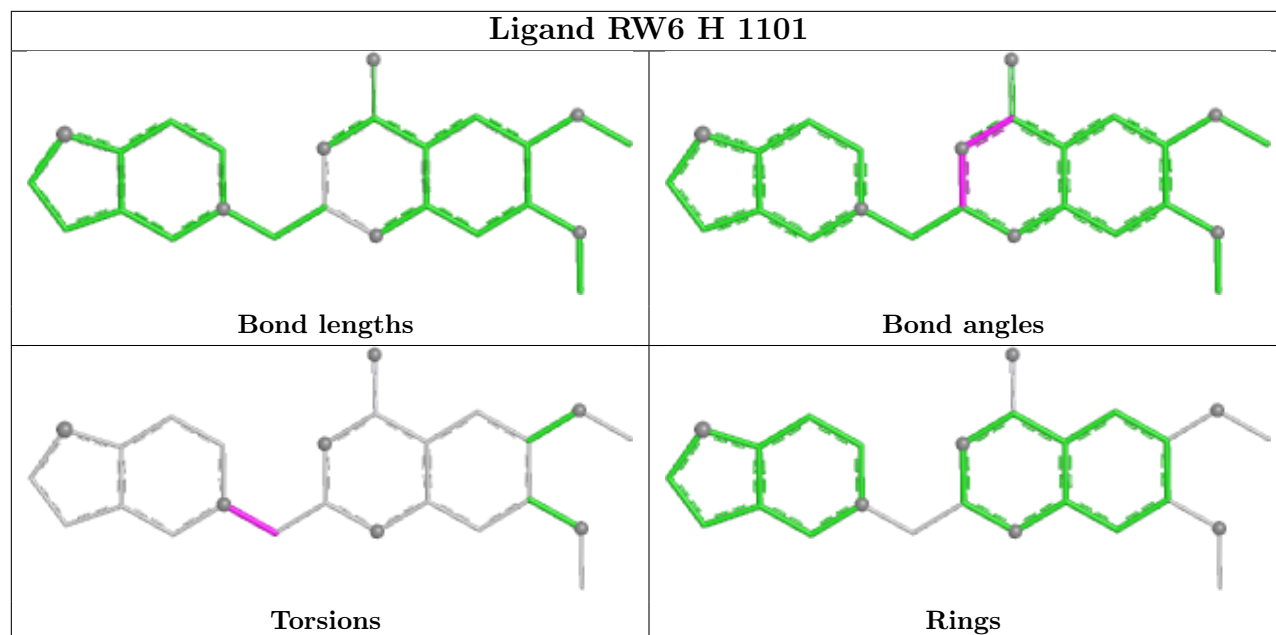
2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	G	1205	SO4	1	0
5	B	1101	RW6	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 [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	826/840 (98%)	-0.59	2 (0%) 91 86	43, 72, 122, 197	0
1	D	822/840 (97%)	-0.67	0 100 100	42, 71, 114, 161	0
1	G	826/840 (98%)	-0.60	0 100 100	43, 71, 118, 193	0
2	B	315/344 (91%)	-0.48	2 (0%) 85 73	49, 75, 113, 154	0
2	E	328/344 (95%)	-0.40	3 (0%) 81 65	45, 73, 126, 176	0
2	H	317/344 (92%)	-0.47	1 (0%) 90 82	38, 62, 104, 177	0
3	C	247/271 (91%)	-0.67	0 100 100	46, 68, 109, 146	0
3	F	248/271 (91%)	-0.75	0 100 100	37, 58, 96, 159	0
3	I	247/271 (91%)	-0.74	0 100 100	40, 62, 101, 157	0
All	All	4176/4365 (95%)	-0.60	8 (0%) 91 86	37, 69, 115, 197	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	1031	PRO	3.9
2	E	1035	HIS	3.8
2	E	1040	HIS	3.7
2	E	1043	TRP	3.0
1	A	1017	LEU	2.3
2	B	1029	ALA	2.3
1	A	393	GLY	2.3
2	H	1029	ALA	2.1

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(\AA^2)	Q<0.9
2	TPO	B	893	11/12	0.79	0.11	190,211,255,259	6
2	TPO	E	893	11/12	0.81	0.10	196,207,249,249	6
2	TPO	H	893	11/12	0.92	0.09	142,153,187,190	6

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(\AA^2)	Q<0.9
4	SO4	H	1103	5/5	0.50	0.08	167,167,177,212	0
4	SO4	B	1103	5/5	0.51	0.08	163,164,175,199	0
4	SO4	H	1105	5/5	0.55	0.09	154,154,162,192	0
4	SO4	G	1208	5/5	0.60	0.22	148,151,165,175	0
4	SO4	A	1208	5/5	0.60	0.09	163,165,171,199	0
4	SO4	G	1204	5/5	0.60	0.08	154,158,169,197	0
4	SO4	H	1107	5/5	0.60	0.08	156,159,176,201	0
4	SO4	F	303	5/5	0.61	0.07	158,161,166,197	0
4	SO4	D	1205	5/5	0.63	0.08	157,161,171,196	0
4	SO4	E	1103	5/5	0.63	0.07	157,158,164,191	0
4	SO4	D	1209	5/5	0.66	0.07	164,166,170,194	0
4	SO4	D	1202	5/5	0.66	0.07	144,158,169,194	0
4	SO4	I	301	5/5	0.66	0.07	160,160,163,189	0
4	SO4	D	1207	5/5	0.69	0.07	143,150,166,189	0
4	SO4	G	1202	5/5	0.70	0.13	149,153,161,182	0
4	SO4	G	1209	5/5	0.70	0.21	148,152,163,181	0
4	SO4	E	1104	5/5	0.72	0.07	174,175,180,205	0
4	SO4	B	1102	5/5	0.72	0.07	172,172,180,203	0
4	SO4	E	1105	5/5	0.74	0.06	170,174,177,202	0
4	SO4	C	302	5/5	0.74	0.07	161,165,167,194	0
4	SO4	H	1102	5/5	0.75	0.06	168,170,173,198	0
4	SO4	F	304	5/5	0.76	0.09	156,165,179,202	0
4	SO4	H	1104	5/5	0.78	0.12	142,152,159,183	0
4	SO4	G	1207	5/5	0.78	0.15	144,148,153,177	0

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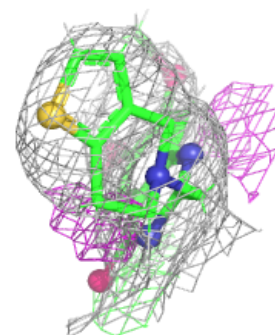
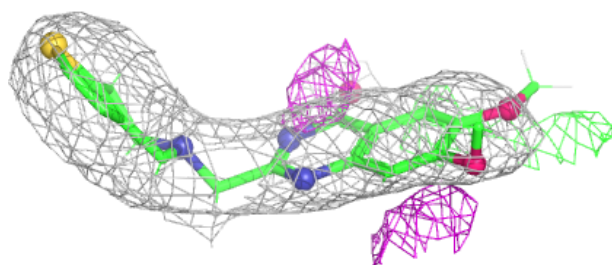
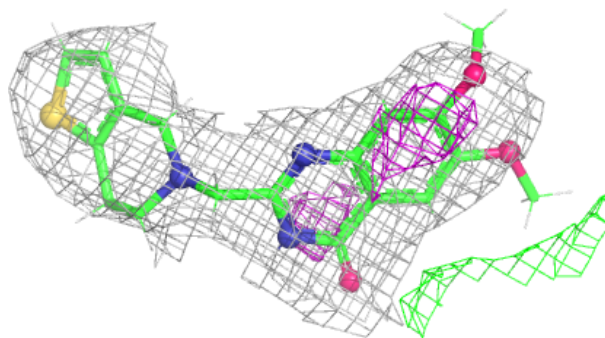
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	SO4	A	1205	5/5	0.79	0.14	140,143,161,183	0
4	SO4	E	1102	5/5	0.79	0.07	152,167,170,195	0
4	SO4	A	1204	5/5	0.80	0.07	178,178,180,200	0
4	SO4	F	301	5/5	0.81	0.13	153,153,160,181	0
4	SO4	G	1206	5/5	0.82	0.06	172,174,179,203	0
4	SO4	H	1106	5/5	0.86	0.15	145,147,156,178	0
4	SO4	A	1207	5/5	0.86	0.12	153,156,161,182	0
4	SO4	A	1206	5/5	0.86	0.06	162,164,169,194	0
4	SO4	I	302	5/5	0.86	0.11	118,130,143,150	0
4	SO4	D	1208	5/5	0.87	0.05	163,165,165,190	0
4	SO4	G	1203	5/5	0.88	0.11	144,151,155,171	0
4	SO4	G	1201	5/5	0.90	0.16	136,136,146,149	0
4	SO4	D	1203	5/5	0.90	0.14	138,152,154,179	0
4	SO4	D	1206	5/5	0.90	0.10	138,138,146,171	0
4	SO4	D	1204	5/5	0.90	0.10	146,151,163,185	0
5	RW6	B	1101	25/25	0.90	0.11	110,134,161,169	19
4	SO4	A	1202	5/5	0.91	0.06	141,142,143,165	0
4	SO4	C	301	5/5	0.92	0.06	135,139,150,159	0
4	SO4	G	1205	5/5	0.92	0.11	142,157,159,175	0
4	SO4	D	1201	5/5	0.92	0.08	144,148,152,162	0
5	RW6	E	1101	25/25	0.92	0.12	112,139,166,174	19
4	SO4	F	302	5/5	0.93	0.09	113,121,138,139	0
4	SO4	A	1201	5/5	0.93	0.07	148,148,164,169	0
4	SO4	A	1203	5/5	0.94	0.13	131,141,154,169	0
5	RW6	H	1101	25/25	0.95	0.10	111,134,161,201	19

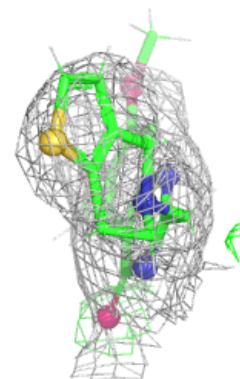
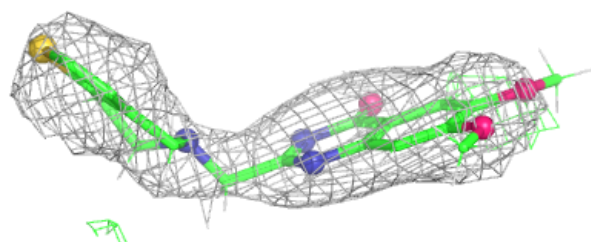
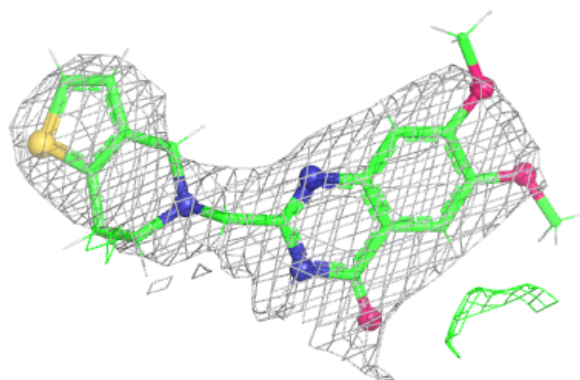
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

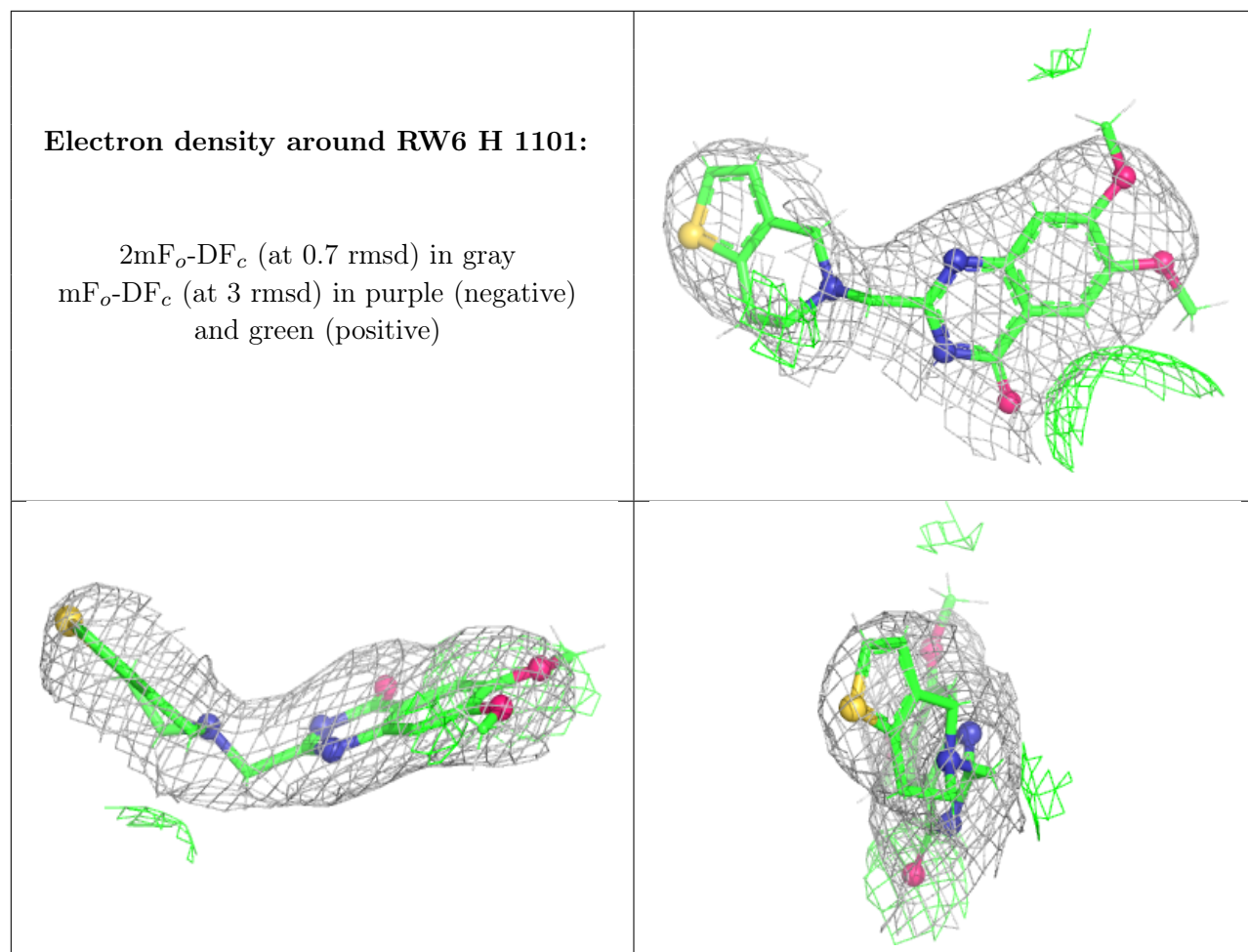
Electron density around RW6 B 1101:

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

**Electron density around RW6 E 1101:**

$2mF_o-DF_c$ (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.