



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 7, 2023 – 01:34 pm BST

PDB ID : 8BUI
Title : Structure of DDB1 bound to DRF-053-engaged CDK12-cyclin K
Authors : Kozicka, Z.; Kempf, G.; Petzold, G.; Thoma, N.H.
Deposited on : 2022-11-30
Resolution : 3.50 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35

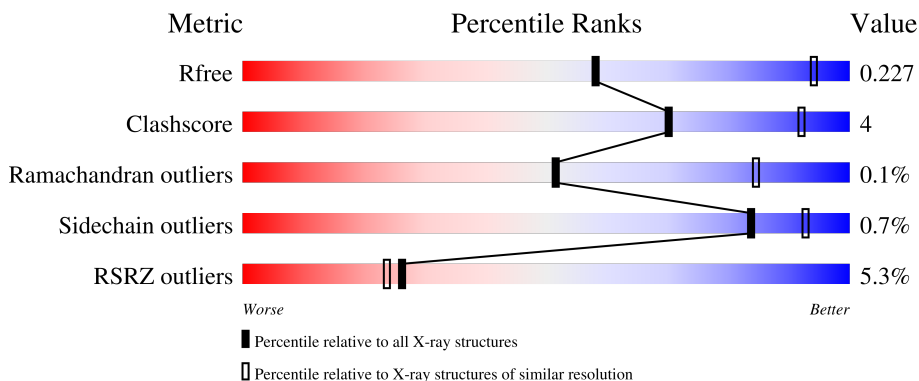
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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.



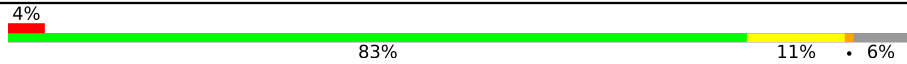

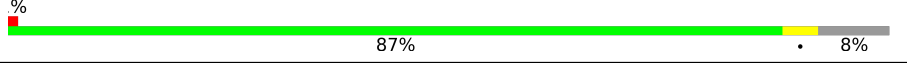
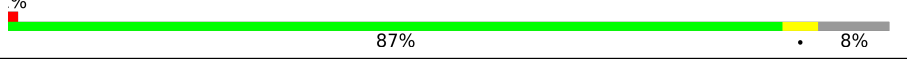
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1659 (3.60-3.40)
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)
RSRZ outliers	127900	1559 (3.60-3.40)

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	 6% 89% 9% .
1	D	840	 4% 88% 10% .
1	G	840	 7% 84% 15% .
2	B	344	 12% 85% 9% . 5%
2	E	344	 5% 85% 10% 6%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	H	344	 4% 83% 11% • 6%
3	C	271	 3% 87% • 8%
3	F	271	 % 87% • 8%
3	I	271	 % 87% • 8%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 67402 atoms, of which 33592 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	12936	4105	6449	1094	1252	36	6456	0	0
1	D	827	12957	4111	6462	1095	1253	36	6469	0	0
1	G	826	12940	4106	6454	1093	1251	36	6461	0	0

There are 30 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
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
G	-3	GLY	-	expression tag	UNP Q16531
G	-2	GLY	-	expression tag	UNP Q16531
G	-1	GLY	-	expression tag	UNP Q16531

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
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

- 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	327	5341	1706	2676	451	490	1	17	2676	0	0
2	E	325	5308	1695	2662	447	486	1	17	2662	0	0
2	H	324	5298	1692	2658	446	485	1	16	2658	0	0

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
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
			Total	C	H	N	O	S			
3	C	248	4111	1341	2048	346	363	13	2048	0	0

Continued on next page...

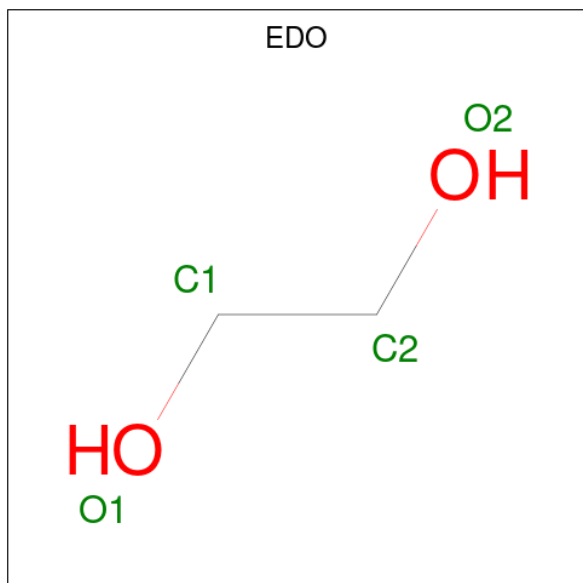
Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
3	F	248	4111	1341	2048	346	363	13	2048	0	0
3	I	248	4111	1341	2048	346	363	13	2048	0	0

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 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
4	A	1	10	2	6	2	6	0

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



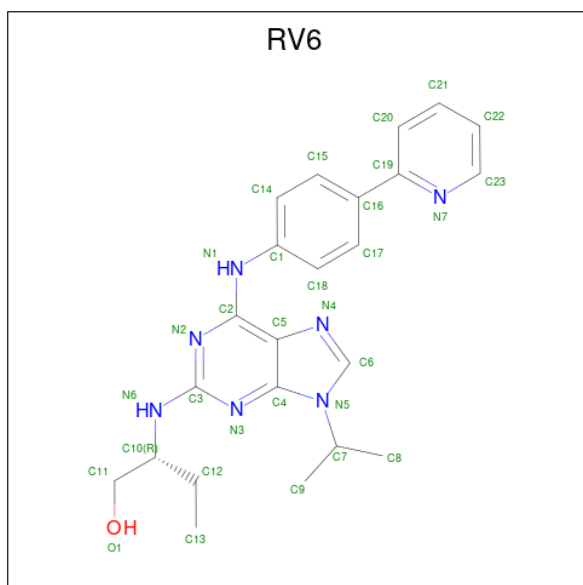
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total O S 5 4 1	0	0
5	A	1	Total O S 5 4 1	0	0
5	A	1	Total O S 5 4 1	0	0
5	B	1	Total O S 5 4 1	0	0
5	C	1	Total O S 5 4 1	0	0
5	C	1	Total O S 5 4 1	0	0
5	C	1	Total O S 5 4 1	0	0
5	D	1	Total O S 5 4 1	0	0
5	D	1	Total O S 5 4 1	0	0
5	D	1	Total O S 5 4 1	0	0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

Continued on next page...

Continued from previous page...

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

- Molecule 6 is (2 {R})-2-[[9-propan-2-yl-6-[(4-pyridin-2-ylphenyl)amino]purin-2-yl]amino]butan-1-ol (three-letter code: RV6) (formula: C₂₃H₂₇N₇O) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
6	B	1	Total	C	H	N	O	27	0
			58	23	27	7	1		
6	E	1	Total	C	H	N	O	27	0
			58	23	27	7	1		

Continued on next page...

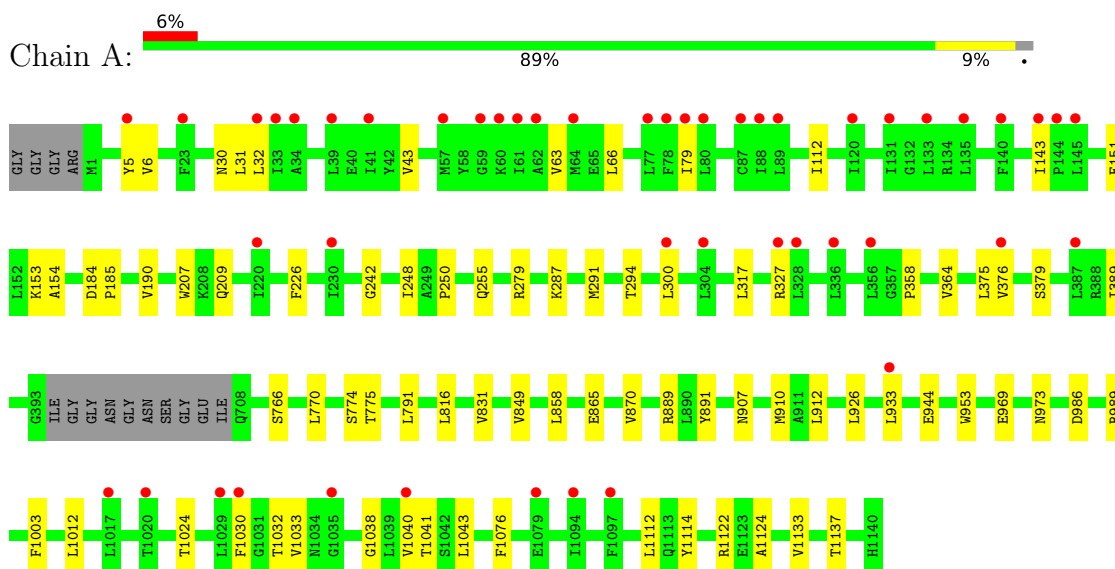
Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	N	O		
6	H	1	58	23	27	7	1	27	0

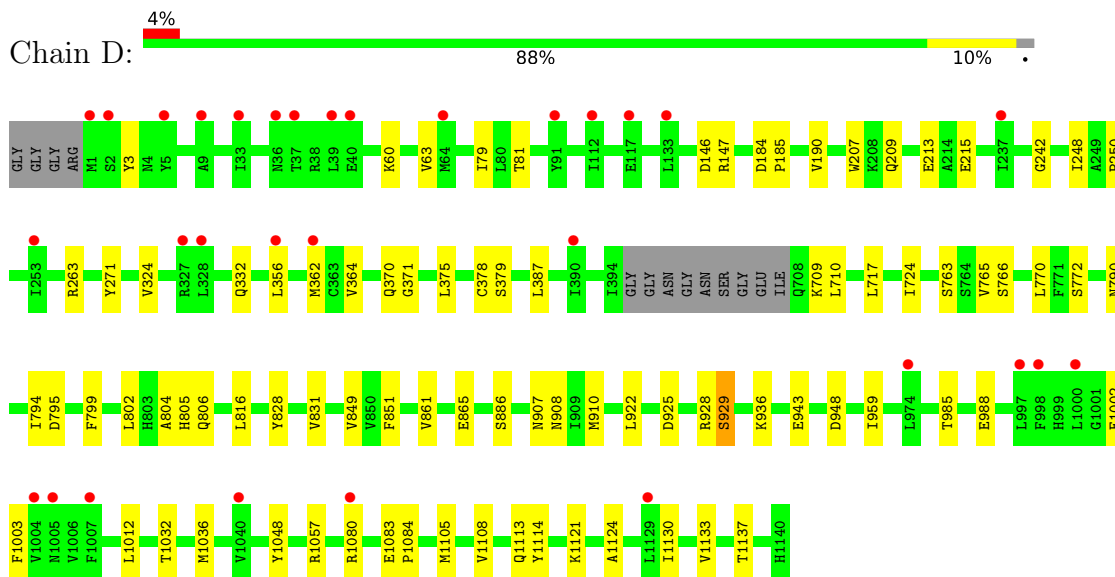
3 Residue-property plots [i](#)

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.

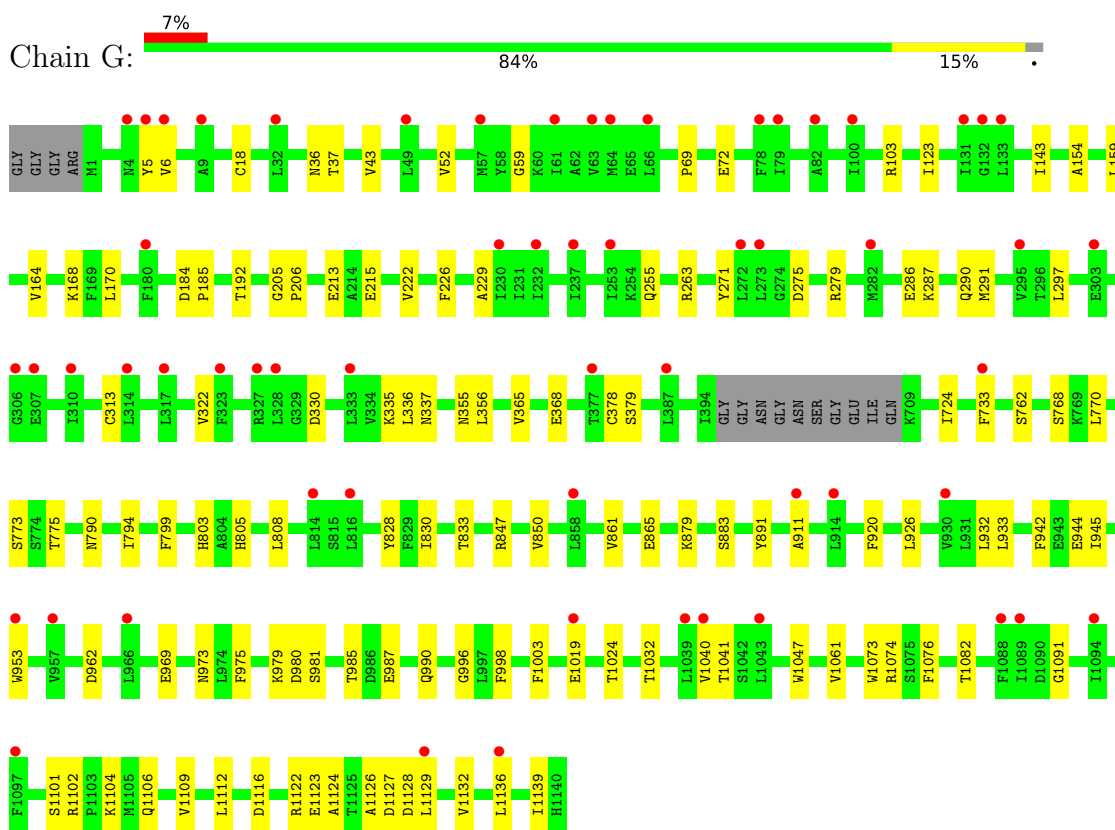
- Molecule 1: DNA damage-binding protein 1



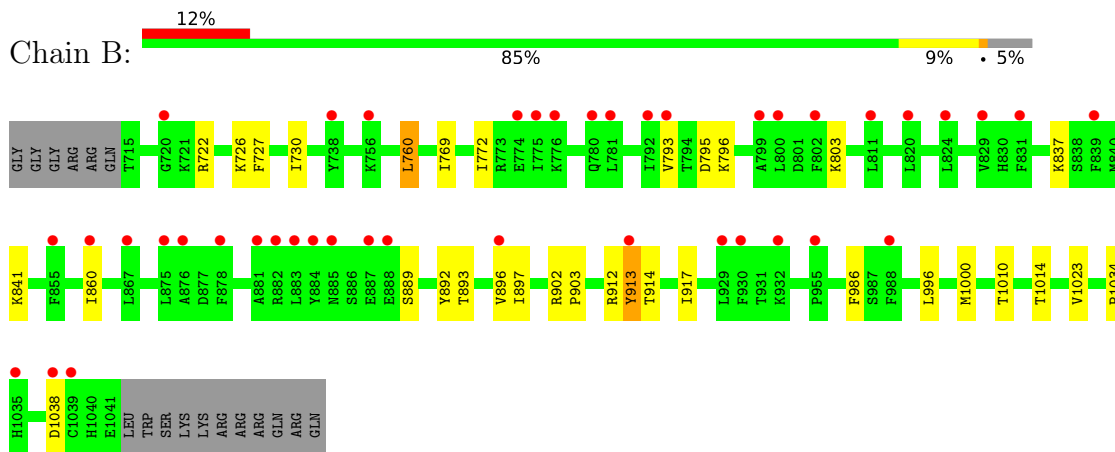
- Molecule 1: DNA damage-binding protein 1



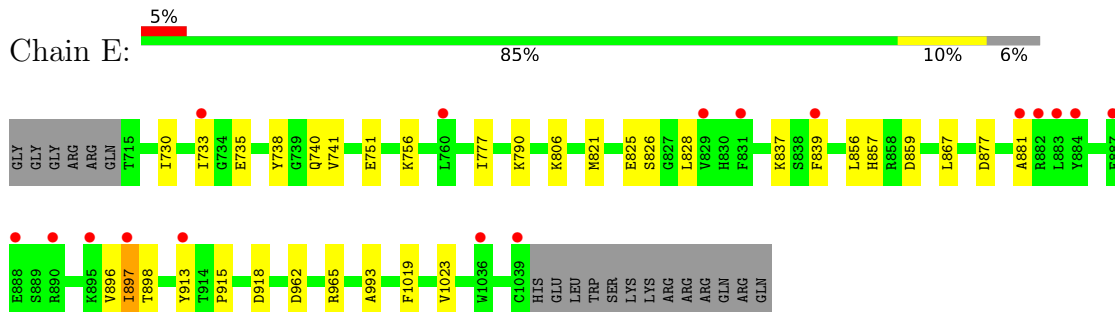
- Molecule 1: DNA damage-binding protein 1



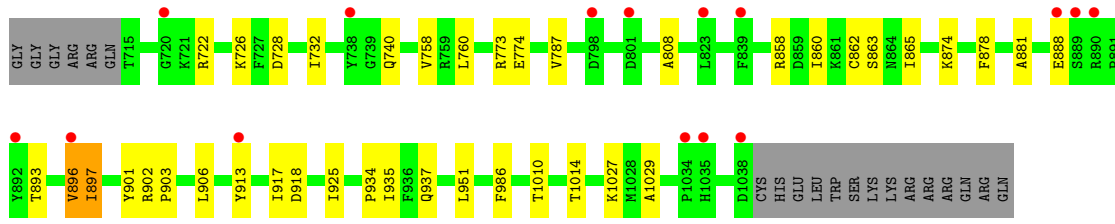
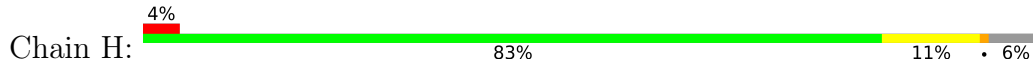
• Molecule 2: Cyclin-dependent kinase 12



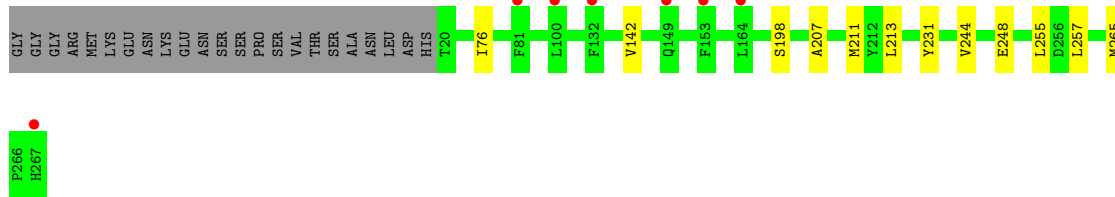
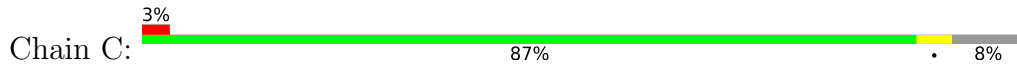
• Molecule 2: Cyclin-dependent kinase 12



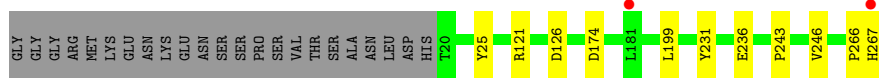
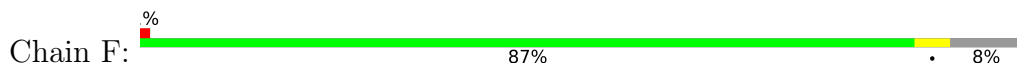
• Molecule 2: Cyclin-dependent kinase 12



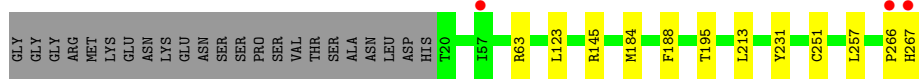
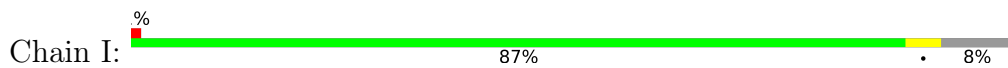
• Molecule 3: Cyclin-K



• Molecule 3: Cyclin-K



• Molecule 3: Cyclin-K



4 Data and refinement statistics

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	249.44Å 249.44Å 218.34Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	60.11 – 3.50 216.02 – 3.50	Depositor EDS
% Data completeness (in resolution range)	86.2 (60.11-3.50) 86.3 (216.02-3.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.45 (at 3.49Å)	Xtrriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.182 , 0.221 0.193 , 0.227	Depositor DCC
R_{free} test set	4212 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	157.8	Xtrriage
Anisotropy	0.004	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 131.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtrriage
Estimated twinning fraction	0.053 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	67402	wwPDB-VP
Average B, all atoms (Å ²)	188.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.74% 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: RV6, SO4, EDO, TPO

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	0.34	0/6604	0.63	2/8931 (0.0%)
1	D	0.32	0/6612	0.60	0/8942
1	G	0.34	0/6603	0.62	0/8930
2	B	0.34	0/2713	0.61	0/3657
2	E	0.33	0/2693	0.62	0/3630
2	H	0.35	0/2687	0.61	0/3622
3	C	0.31	0/2120	0.54	0/2868
3	F	0.33	0/2120	0.55	0/2868
3	I	0.31	0/2120	0.54	0/2868
All	All	0.33	0/34272	0.60	2/46316 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	291	MET	CB-CG-SD	-6.49	92.94	112.40
1	A	291	MET	CG-SD-CE	-6.21	90.27	100.20

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	6449	6451	41	1
1	D	6495	6462	6464	47	0
1	G	6486	6454	6456	77	1
2	B	2665	2676	2676	26	0
2	E	2646	2662	2662	18	0
2	H	2640	2658	2658	20	0
3	C	2063	2048	2048	8	0
3	F	2063	2048	2048	6	0
3	I	2063	2048	2048	7	0
4	A	4	6	6	0	0
5	A	15	0	0	0	0
5	B	5	0	0	0	0
5	C	15	0	0	0	0
5	D	20	0	0	0	0
5	F	15	0	0	1	0
5	G	15	0	0	0	0
5	H	5	0	0	0	0
5	I	15	0	0	0	0
6	B	31	27	0	0	0
6	E	31	27	0	0	0
6	H	31	27	0	0	0
All	All	33810	33592	33517	240	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 (240) 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:F:231:TYR:OH	3:F:236:GLU:OE1	1.95	0.84
2:B:897:ILE:HD12	2:B:903:PRO:HD3	1.72	0.70
2:H:902:ARG:HG2	2:H:903:PRO:HD2	1.74	0.69
2:H:862:CYS:HG	2:H:901:TYR:HH	1.38	0.69
1:G:1109:VAL:HG11	1:G:1126:ALA:HA	1.76	0.67
1:G:6:VAL:HG22	1:G:1040:VAL:HG22	1.77	0.65
2:B:889:SER:HB2	2:B:912:ARG:HG2	1.80	0.63
1:A:907:ASN:HB2	2:B:730:ILE:HG22	1.81	0.63
2:E:859:ASP:H	2:E:897:ILE:HD13	1.64	0.62
1:A:248:ILE:HD12	1:A:300:LEU:O	1.99	0.62
1:A:6:VAL:HG22	1:A:1040:VAL:HG22	1.82	0.61
1:G:365:VAL:HG11	1:G:733:PHE:HZ	1.65	0.61
1:D:1083:GLU:HG2	1:D:1084:PRO:HD2	1.82	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:912:LEU:HD11	1:A:926:LEU:HD23	1.81	0.60
2:B:803:LYS:HG3	3:C:142:VAL:HG21	1.82	0.60
2:H:787:VAL:HA	2:H:874:LYS:HD3	1.83	0.60
1:D:925:ASP:HB3	1:D:928:ARG:O	2.02	0.60
1:G:979:LYS:O	1:G:981:SER:N	2.34	0.60
2:H:1010:THR:O	2:H:1014:THR:HG23	2.01	0.59
2:B:903:PRO:HG3	2:B:917:ILE:HB	1.83	0.59
1:A:816:LEU:HD13	1:A:831:VAL:HG22	1.84	0.59
2:B:902:ARG:HG2	2:B:903:PRO:HD2	1.86	0.58
1:D:1114:TYR:HB2	1:D:1124:ALA:HB2	1.86	0.58
1:G:365:VAL:HG11	1:G:733:PHE:CZ	2.39	0.58
1:G:773:SER:O	1:G:775:THR:N	2.34	0.58
1:G:1124:ALA:HB1	1:G:1128:ASP:HB2	1.84	0.57
2:E:741:VAL:HG13	2:E:756:LYS:HG2	1.86	0.57
1:G:770:LEU:HD21	1:G:865:GLU:HB2	1.86	0.57
1:A:190:VAL:O	1:A:209:GLN:HA	2.05	0.57
3:F:243:PRO:HG2	3:F:246:VAL:HG23	1.86	0.57
1:G:773:SER:C	1:G:775:THR:H	2.08	0.56
1:G:43:VAL:HG23	1:G:52:VAL:HG21	1.86	0.56
1:A:364:VAL:HG22	1:A:375:LEU:HD13	1.88	0.56
1:A:933:LEU:HD23	1:A:944:GLU:HA	1.88	0.55
1:D:770:LEU:HD13	1:D:865:GLU:HB2	1.89	0.55
1:A:775:THR:HG22	1:A:775:THR:O	2.07	0.54
1:A:207:TRP:HB3	1:A:242:GLY:HA2	1.89	0.54
1:G:1106:GLN:HA	1:G:1109:VAL:HG22	1.89	0.54
2:E:751:GLU:OE1	2:E:790:LYS:NZ	2.39	0.54
1:D:709:LYS:HG2	1:D:710:LEU:N	2.23	0.54
1:A:248:ILE:HG12	1:A:250:PRO:HD3	1.89	0.54
1:A:5:TYR:HB3	1:A:1041:THR:HG23	1.90	0.53
2:E:777:ILE:HD13	2:E:881:ALA:HB3	1.90	0.53
1:A:63:VAL:O	1:A:79:ILE:HA	2.09	0.53
2:B:897:ILE:HB	2:B:902:ARG:HG3	1.90	0.53
3:C:76:ILE:CD1	3:C:198:SER:HB3	2.39	0.53
2:E:839:PHE:HE2	2:E:867:LEU:HD21	1.73	0.53
1:D:929:SER:OG	1:D:948:ASP:O	2.27	0.52
1:A:1003:PHE:O	1:A:1032:THR:HA	2.10	0.52
1:G:1109:VAL:HG12	1:G:1129:LEU:HD12	1.92	0.52
1:D:370:GLN:HG2	1:D:371:GLY:H	1.74	0.52
1:G:170:LEU:HD11	1:G:229:ALA:HB2	1.91	0.52
2:H:773:ARG:HD3	2:H:881:ALA:O	2.10	0.51
2:H:1027:LYS:HE2	2:H:1029:ALA:HB2	1.92	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:765:VAL:HG22	1:D:806:GLN:HB3	1.91	0.51
2:E:735:GLU:HG3	2:E:740:GLN:HG2	1.93	0.51
1:A:184:ASP:HB2	1:A:185:PRO:CD	2.41	0.51
1:A:207:TRP:CB	1:A:242:GLY:HA2	2.40	0.51
2:H:722:ARG:HE	2:H:726:LYS:HG3	1.75	0.51
1:D:60:LYS:O	1:D:81:THR:HA	2.11	0.51
2:H:897:ILE:HD12	2:H:903:PRO:HD3	1.91	0.51
2:E:821:MET:HG2	2:E:825:GLU:HG3	1.94	0.50
1:G:833:THR:OG1	1:G:847:ARG:HB2	2.11	0.50
1:A:1133:VAL:O	1:A:1137:THR:HG23	2.12	0.50
2:B:1010:THR:O	2:B:1014:THR:HG23	2.12	0.50
2:E:856:LEU:HD11	2:E:915:PRO:HG3	1.93	0.50
1:D:324:VAL:HB	1:D:332:GLN:HB2	1.93	0.49
1:D:828:TYR:CE1	1:D:861:VAL:HG21	2.48	0.49
1:G:59:GLY:HA2	1:G:1073:TRP:CE3	2.47	0.49
3:C:265:MET:SD	3:C:265:MET:N	2.85	0.49
1:D:1003:PHE:O	1:D:1032:THR:HA	2.13	0.49
2:B:722:ARG:HE	2:B:726:LYS:HG3	1.77	0.49
2:B:896:VAL:HG23	2:B:897:ILE:HG13	1.94	0.49
1:G:794:ILE:HG22	1:G:799:PHE:HA	1.95	0.49
1:G:1116:ASP:HB3	1:G:1122:ARG:HH21	1.77	0.49
1:G:184:ASP:HB2	1:G:185:PRO:CD	2.43	0.49
1:A:358:PRO:O	1:A:379:SER:HA	2.13	0.48
2:B:841:LYS:HD2	2:B:1023:VAL:HB	1.94	0.48
3:C:76:ILE:HD12	3:C:198:SER:HB3	1.95	0.48
3:I:195:THR:CG2	3:I:257:LEU:HD11	2.43	0.48
1:G:72:GLU:OE2	1:G:103:ARG:NH2	2.47	0.48
1:G:768:SER:HB3	1:G:808:LEU:HD11	1.95	0.48
1:G:985:THR:HG22	1:G:987:GLU:H	1.77	0.48
1:A:953:TRP:O	1:A:969:GLU:HA	2.14	0.48
1:D:375:LEU:HB2	1:D:1012:LEU:HD21	1.96	0.48
2:B:760:LEU:HD23	2:B:760:LEU:H	1.79	0.47
1:G:356:LEU:O	1:G:379:SER:HB3	2.14	0.47
1:D:378:CYS:SG	1:D:724:ILE:HB	2.55	0.47
2:B:727:PHE:HE2	2:B:793:VAL:HG11	1.79	0.47
1:G:883:SER:HB2	1:G:911:ALA:HB3	1.96	0.47
1:A:907:ASN:HB2	2:B:730:ILE:CG2	2.44	0.47
1:D:1080:ARG:HG3	2:E:825:GLU:HA	1.97	0.47
3:F:121:ARG:NH2	3:F:126:ASP:OD1	2.38	0.47
1:A:255:GLN:HB2	1:A:279:ARG:HH22	1.80	0.47
1:A:986:ASP:HA	1:A:989:ARG:HE	1.80	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:969:GLU:HG2	1:G:973:ASN:HB2	1.97	0.47
1:D:356:LEU:O	1:D:379:SER:HB3	2.15	0.47
1:D:816:LEU:HD13	1:D:831:VAL:HG22	1.97	0.47
1:G:192:THR:O	1:G:205:GLY:HA3	2.14	0.47
1:G:255:GLN:OE1	1:G:279:ARG:NH1	2.47	0.47
1:G:1112:LEU:O	1:G:1123:GLU:HG3	2.15	0.47
1:A:1112:LEU:HD23	1:A:1124:ALA:HB3	1.97	0.47
1:G:953:TRP:O	1:G:969:GLU:HA	2.15	0.46
1:G:5:TYR:HB3	1:G:1041:THR:HG23	1.97	0.46
1:G:1047:TRP:CZ3	1:G:1132:VAL:HG13	2.50	0.46
2:H:951:LEU:HD21	2:H:986:PHE:HE2	1.81	0.46
1:D:207:TRP:HB3	1:D:242:GLY:HA2	1.96	0.46
1:D:795:ASP:HB2	1:D:802:LEU:HD11	1.96	0.46
1:G:1047:TRP:HZ3	1:G:1132:VAL:HG13	1.79	0.46
1:G:43:VAL:HG23	1:G:52:VAL:CG2	2.46	0.46
2:H:858:ARG:HD2	2:H:896:VAL:HG21	1.98	0.46
2:E:837:LYS:HB3	2:E:1023:VAL:HG21	1.98	0.46
1:G:143:ILE:HG12	1:G:154:ALA:HB2	1.98	0.46
2:H:906:LEU:HD21	2:H:913:TYR:HB3	1.97	0.46
1:A:770:LEU:HD13	1:A:865:GLU:HB2	1.98	0.46
1:G:987:GLU:HA	2:H:740:GLN:NE2	2.30	0.46
1:G:998:PHE:CZ	1:G:1074:ARG:HD2	2.51	0.46
2:B:722:ARG:HB3	2:B:793:VAL:HG12	1.98	0.46
1:G:1003:PHE:O	1:G:1032:THR:HA	2.15	0.46
1:D:1083:GLU:CG	1:D:1084:PRO:HD2	2.47	0.45
3:I:195:THR:HG21	3:I:257:LEU:HD11	1.98	0.45
2:B:803:LYS:HA	3:C:142:VAL:HG11	1.98	0.45
1:G:828:TYR:HE1	1:G:861:VAL:HG21	1.81	0.45
1:G:790:ASN:HA	1:G:805:HIS:O	2.16	0.45
1:G:830:ILE:HG12	1:G:850:VAL:HG13	1.98	0.45
1:A:31:LEU:HD22	1:A:317:LEU:HD21	1.98	0.45
2:E:857:HIS:O	2:E:918:ASP:OD1	2.35	0.45
1:G:59:GLY:HA2	1:G:1073:TRP:CZ3	2.52	0.45
1:A:889:ARG:HD2	1:A:891:TYR:CZ	2.52	0.45
1:A:151:GLU:OE1	1:A:153:LYS:HE2	2.17	0.45
3:C:244:VAL:HG12	3:C:248:GLU:HG2	1.98	0.45
1:D:1002:GLU:HG3	1:D:1036:MET:SD	2.57	0.45
1:G:945:ILE:O	1:G:990:GLN:HA	2.17	0.44
1:G:1061:VAL:HG11	1:G:1104:LYS:HB3	1.99	0.44
1:A:30:ASN:ND2	1:A:43:VAL:HG22	2.33	0.44
2:E:993:ALA:HB2	2:E:1019:PHE:CE1	2.52	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:791:LEU:HD23	1:A:858:LEU:HD21	1.99	0.44
1:D:190:VAL:O	1:D:209:GLN:HA	2.17	0.44
1:A:1024:THR:HG22	1:A:1043:LEU:HD21	2.00	0.44
1:G:222:VAL:HG12	1:G:226:PHE:HB2	2.00	0.44
2:H:758:VAL:O	2:H:808:ALA:HB1	2.18	0.44
1:G:275:ASP:C	1:G:275:ASP:OD1	2.55	0.44
1:G:226:PHE:HZ	1:G:287:LYS:HG2	1.82	0.44
2:H:774:GLU:HG3	2:H:878:PHE:HB2	1.99	0.44
2:H:865:ILE:HD11	2:H:925:ILE:HD13	1.98	0.44
1:D:63:VAL:O	1:D:79:ILE:HA	2.17	0.44
1:D:922:LEU:HD22	1:D:959:ILE:HG12	2.00	0.44
1:D:936:LYS:HD3	1:D:943:GLU:OE1	2.18	0.44
2:H:934:PRO:HB2	2:H:937:GLN:HG3	2.00	0.44
1:D:146:ASP:OD1	1:D:147:ARG:N	2.51	0.44
1:G:36:ASN:O	1:G:37:THR:OG1	2.24	0.44
1:G:159:LEU:HD21	1:G:164:VAL:HG21	2.00	0.44
1:G:170:LEU:HD12	1:G:170:LEU:HA	1.90	0.43
1:G:378:CYS:SG	1:G:724:ILE:HB	2.57	0.43
2:H:935:ILE:HD12	2:H:986:PHE:HZ	1.83	0.43
1:D:794:ILE:HG22	1:D:799:PHE:HA	1.99	0.43
1:G:1102:ARG:NH2	1:G:1127:ASP:OD1	2.51	0.43
2:B:913:TYR:HB2	2:B:917:ILE:HD13	2.00	0.43
1:G:830:ILE:HG23	1:G:850:VAL:HG22	1.99	0.43
3:I:184:MET:HG2	3:I:188:PHE:CE2	2.53	0.43
1:G:879:LYS:HB3	1:G:891:TYR:O	2.18	0.43
3:C:213:LEU:HD11	3:C:255:LEU:HD11	2.01	0.43
1:D:907:ASN:HB2	2:E:730:ILE:HG22	2.00	0.43
1:G:1136:LEU:O	1:G:1139:ILE:HG12	2.19	0.43
1:D:213:GLU:HG2	1:D:215:GLU:H	1.82	0.43
2:E:733:ILE:HD11	2:E:741:VAL:HG12	1.99	0.43
1:G:926:LEU:O	1:G:953:TRP:HA	2.18	0.43
1:A:143:ILE:HG12	1:A:154:ALA:HB2	2.01	0.43
1:A:226:PHE:HZ	1:A:287:LYS:HG2	1.83	0.43
1:A:1114:TYR:HB2	1:A:1122:ARG:HD3	2.00	0.43
2:B:914:THR:O	2:B:917:ILE:HG12	2.18	0.43
1:D:364:VAL:HG22	1:D:375:LEU:HD13	2.00	0.43
1:A:774:SER:O	1:A:775:THR:HB	2.18	0.43
1:A:1003:PHE:HB3	1:A:1033:VAL:HG23	2.01	0.43
1:D:763:SER:HA	1:D:804:ALA:O	2.19	0.43
1:D:248:ILE:HG12	1:D:250:PRO:HD3	2.01	0.43
2:H:760:LEU:HD11	3:I:145:ARG:NH2	2.34	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:1057:ARG:HD3	1:D:1108:VAL:O	2.19	0.42
1:G:192:THR:OG1	1:G:206:PRO:HD2	2.18	0.42
1:G:330:ASP:HA	1:G:355:ASN:HB3	2.00	0.42
1:G:828:TYR:CE1	1:G:861:VAL:HG21	2.55	0.42
1:D:1105:MET:SD	1:D:1130:ILE:HD11	2.59	0.42
1:G:18:CYS:SG	1:G:313:CYS:SG	3.15	0.42
3:I:213:LEU:HB2	3:I:251:CYS:SG	2.60	0.42
1:A:1030:PHE:CZ	1:A:1038:GLY:HA3	2.54	0.42
1:G:933:LEU:HD22	1:G:942:PHE:HB3	2.01	0.42
1:G:975:PHE:HA	1:G:996:GLY:O	2.19	0.42
2:B:892:TYR:HB3	2:B:913:TYR:CE2	2.54	0.42
2:B:897:ILE:HD12	2:B:903:PRO:CD	2.46	0.42
1:G:920:PHE:HB3	1:G:932:LEU:HD11	2.02	0.42
1:D:1113:GLN:HG2	1:D:1121:LYS:HB2	2.01	0.42
1:G:213:GLU:HG2	1:G:215:GLU:H	1.84	0.42
3:I:266:PRO:O	3:I:267:HIS:C	2.58	0.42
2:B:996:LEU:O	2:B:1000:MET:HG3	2.20	0.42
1:D:3:TYR:HB3	1:D:1048:TYR:HB2	2.02	0.42
2:E:839:PHE:CE2	2:E:867:LEU:HD21	2.52	0.42
1:G:286:GLU:O	1:G:297:LEU:HD12	2.20	0.42
1:A:112:ILE:HD13	2:B:986:PHE:CE2	2.55	0.41
1:G:773:SER:C	1:G:775:THR:N	2.73	0.41
2:E:826:SER:CB	2:E:828:LEU:HD12	2.50	0.41
1:D:387:LEU:HG	1:D:717:LEU:HD11	2.02	0.41
1:D:709:LYS:CG	1:D:710:LEU:N	2.83	0.41
1:D:985:THR:HB	1:D:988:GLU:HB2	2.02	0.41
2:E:962:ASP:HB3	2:E:965:ARG:HD2	2.02	0.41
1:G:263:ARG:HA	1:G:271:TYR:CD2	2.55	0.41
2:B:795:ASP:O	2:B:796:LYS:C	2.58	0.41
2:B:1034:PRO:HB2	2:B:1038:ASP:OD2	2.20	0.41
1:D:263:ARG:HA	1:D:271:TYR:CD2	2.56	0.41
1:D:1133:VAL:O	1:D:1137:THR:HG23	2.20	0.41
1:G:1076:PHE:O	1:G:1082:THR:HA	2.21	0.41
1:A:973:ASN:HB3	1:A:1076:PHE:CE1	2.56	0.41
1:G:6:VAL:O	1:G:1091:GLY:N	2.45	0.41
1:G:335:LYS:HE2	1:G:337:ASN:OD1	2.20	0.41
1:G:762:SER:O	1:G:803:HIS:HA	2.20	0.41
1:G:290:GLN:O	1:G:291:MET:HB2	2.20	0.41
1:G:322:VAL:HG21	1:G:336:LEU:HD11	2.02	0.41
1:G:944:GLU:OE1	2:H:732:ILE:HG22	2.21	0.41
3:C:207:ALA:O	3:C:211:MET:HG3	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:69:PRO:HG2	1:G:72:GLU:HG3	2.02	0.41
1:A:32:LEU:HD13	1:A:66:LEU:HD11	2.03	0.41
1:D:790:ASN:HA	1:D:805:HIS:O	2.21	0.41
1:D:886:SER:HB2	1:D:908:ASN:O	2.21	0.41
3:F:25:TYR:HA	3:F:199:LEU:O	2.21	0.41
3:F:174:ASP:HB2	5:F:301:SO4:O2	2.21	0.41
1:G:123:ILE:HG21	1:G:168:LYS:HA	2.02	0.41
1:G:275:ASP:OD2	1:G:279:ARG:HB2	2.21	0.41
3:I:63:ARG:HE	3:I:123:LEU:HD21	1.86	0.41
1:D:910:MET:O	1:D:925:ASP:HA	2.21	0.41
2:H:917:ILE:HG13	2:H:918:ASP:N	2.36	0.41
1:A:375:LEU:HB2	1:A:1012:LEU:HD21	2.03	0.40
2:B:769:ILE:HA	2:B:772:ILE:HB	2.03	0.40
1:D:184:ASP:HB2	1:D:185:PRO:CD	2.51	0.40
1:D:849:VAL:HG11	1:D:851:PHE:CZ	2.56	0.40
1:D:362:MET:SD	1:D:375:LEU:HD21	2.61	0.40
3:F:266:PRO:O	3:F:267:HIS:C	2.59	0.40
1:A:376:VAL:HG13	1:A:389:ILE:HD13	2.02	0.40
2:E:806:LYS:HD3	2:E:806:LYS:HA	1.98	0.40
1:G:1101:SER:OG	1:G:1104:LYS:HG2	2.21	0.40
2:B:837:LYS:HB3	2:B:1023:VAL:HG21	2.02	0.40
1:G:1024:THR:HG21	1:G:1139:ILE:HD13	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)
1:A:1114:TYR:OH	1:G:291:MET:O[2_565]	2.15	0.05

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%)	803 (98%)	19 (2%)	0	100	100
1	D	823/840 (98%)	803 (98%)	18 (2%)	2 (0%)	47	81
1	G	822/840 (98%)	801 (97%)	20 (2%)	1 (0%)	51	84
2	B	324/344 (94%)	313 (97%)	11 (3%)	0	100	100
2	E	322/344 (94%)	315 (98%)	6 (2%)	1 (0%)	41	75
2	H	321/344 (93%)	310 (97%)	11 (3%)	0	100	100
3	C	246/271 (91%)	243 (99%)	3 (1%)	0	100	100
3	F	246/271 (91%)	244 (99%)	2 (1%)	0	100	100
3	I	246/271 (91%)	243 (99%)	3 (1%)	0	100	100
All	All	4172/4365 (96%)	4075 (98%)	93 (2%)	4 (0%)	51	84

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	929	SER
2	E	877	ASP
1	G	980	ASP
1	D	772	SER

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%)	81	91
1	D	722/728 (99%)	721 (100%)	1 (0%)	93	98
1	G	721/728 (99%)	718 (100%)	3 (0%)	91	96
2	B	294/308 (96%)	291 (99%)	3 (1%)	76	88
2	E	292/308 (95%)	287 (98%)	5 (2%)	60	82
2	H	291/308 (94%)	285 (98%)	6 (2%)	53	79
3	C	223/242 (92%)	221 (99%)	2 (1%)	78	90
3	F	223/242 (92%)	223 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	I	223/242 (92%)	222 (100%)	1 (0%)	91	96
All	All	3710/3834 (97%)	3683 (99%)	27 (1%)	84	93

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	294	THR
1	A	327	ARG
1	A	766	SER
1	A	849	VAL
1	A	870	VAL
1	A	910	MET
2	B	760	LEU
2	B	860	ILE
2	B	913	TYR
3	C	231	TYR
3	C	257	LEU
1	D	766	SER
2	E	738	TYR
2	E	896	VAL
2	E	897	ILE
2	E	898	THR
2	E	913	TYR
1	G	368	GLU
1	G	962	ASP
1	G	1019	GLU
2	H	728	ASP
2	H	860	ILE
2	H	863	SER
2	H	888	GLU
2	H	896	VAL
2	H	897	ILE
3	I	231	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	372	GLN
1	D	908	ASN
1	G	240	HIS
1	G	905	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	G	908	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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	E	893	2	8,10,11	1.25	0	10,14,16	1.00	0
2	TPO	H	893	2	8,10,11	1.84	2 (25%)	10,14,16	1.46	2 (20%)
2	TPO	B	893	2	8,10,11	1.11	0	10,14,16	1.25	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	E	893	2	-	1/9/11/13	-
2	TPO	H	893	2	-	1/9/11/13	-
2	TPO	B	893	2	-	0/9/11/13	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	893	TPO	P-O1P	3.42	1.61	1.50
2	H	893	TPO	CB-CA	2.18	1.58	1.53

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	893	TPO	P-OG1-CB	-2.63	115.25	123.21
2	H	893	TPO	P-OG1-CB	-2.44	115.84	123.21
2	H	893	TPO	CG2-CB-CA	-2.43	108.38	113.16

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	E	893	TPO	CB-OG1-P-O3P
2	H	893	TPO	CB-OG1-P-O2P

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

25 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	$\# Z > 2$
5	SO4	C	303	-	4,4,4	0.16	0	6,6,6	0.08	0
6	RV6	H	1101	-	31,34,34	0.56	0	37,47,47	0.97	3 (8%)
5	SO4	I	301	-	4,4,4	0.13	0	6,6,6	0.08	0
6	RV6	E	1101	-	31,34,34	0.60	1 (3%)	37,47,47	1.20	3 (8%)
5	SO4	D	1202	-	4,4,4	0.13	0	6,6,6	0.15	0
5	SO4	F	303	-	4,4,4	0.14	0	6,6,6	0.21	0
5	SO4	G	1202	-	4,4,4	0.15	0	6,6,6	0.15	0
6	RV6	B	1101	-	31,34,34	0.56	0	37,47,47	1.32	4 (10%)
5	SO4	C	302	-	4,4,4	0.13	0	6,6,6	0.22	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	SO4	D	1201	-	4,4,4	0.15	0	6,6,6	0.06	0
5	SO4	C	301	-	4,4,4	0.14	0	6,6,6	0.15	0
5	SO4	F	302	-	4,4,4	0.16	0	6,6,6	0.12	0
5	SO4	I	303	-	4,4,4	0.13	0	6,6,6	0.09	0
5	SO4	G	1203	-	4,4,4	0.16	0	6,6,6	0.14	0
5	SO4	A	1204	-	4,4,4	0.16	0	6,6,6	0.11	0
5	SO4	F	301	-	4,4,4	0.11	0	6,6,6	0.24	0
5	SO4	A	1203	-	4,4,4	0.17	0	6,6,6	0.07	0
5	SO4	D	1203	-	4,4,4	0.18	0	6,6,6	0.16	0
5	SO4	A	1202	-	4,4,4	0.14	0	6,6,6	0.13	0
5	SO4	H	1102	-	4,4,4	0.18	0	6,6,6	0.13	0
5	SO4	G	1201	-	4,4,4	0.13	0	6,6,6	0.21	0
5	SO4	B	1102	-	4,4,4	0.12	0	6,6,6	0.13	0
5	SO4	D	1204	-	4,4,4	0.14	0	6,6,6	0.10	0
5	SO4	I	302	-	4,4,4	0.14	0	6,6,6	0.18	0
4	EDO	A	1201	-	3,3,3	0.56	0	2,2,2	0.47	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
6	RV6	E	1101	-	-	9/20/20/20	0/4/4/4
6	RV6	B	1101	-	-	9/20/20/20	0/4/4/4
4	EDO	A	1201	-	-	0/1/1/1	-
6	RV6	H	1101	-	-	10/20/20/20	0/4/4/4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	E	1101	RV6	C2-N2	2.14	1.35	1.32

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	1101	RV6	N1-C2-N2	4.82	123.18	118.66
6	E	1101	RV6	N1-C2-N2	4.31	122.71	118.66
6	E	1101	RV6	C5-C2-N2	-3.52	117.88	120.81
6	B	1101	RV6	C6-N5-C7	3.42	128.78	125.42
6	B	1101	RV6	C5-C2-N2	-3.29	118.08	120.81

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	H	1101	RV6	C5-C2-N2	-3.19	118.16	120.81
6	E	1101	RV6	C6-N5-C7	2.70	128.06	125.42
6	H	1101	RV6	C6-N5-C7	2.43	127.80	125.42
6	H	1101	RV6	N1-C2-N2	2.41	120.92	118.66
6	B	1101	RV6	C3-N3-C4	-2.07	112.92	115.28

There are no chirality outliers.

All (28) torsion outliers are listed below:

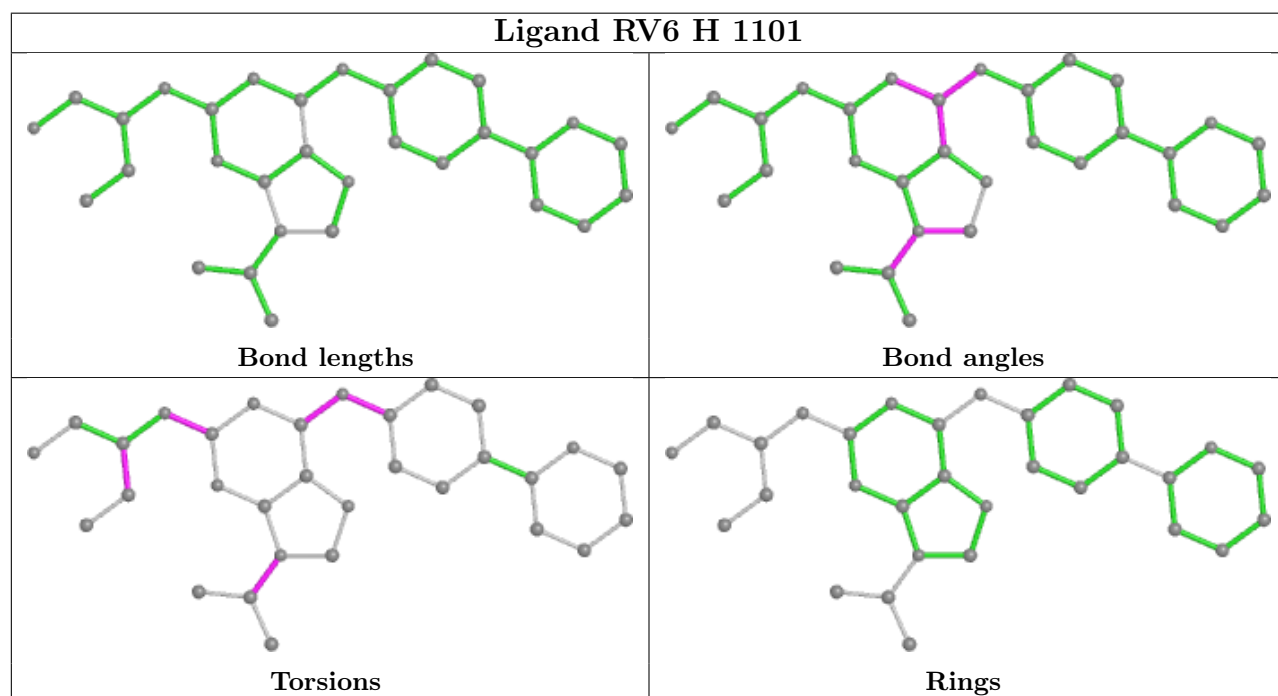
Mol	Chain	Res	Type	Atoms
6	B	1101	RV6	N2-C3-N6-C10
6	B	1101	RV6	N3-C3-N6-C10
6	B	1101	RV6	C5-C2-N1-C1
6	B	1101	RV6	N2-C2-N1-C1
6	B	1101	RV6	C9-C7-N5-C4
6	B	1101	RV6	C9-C7-N5-C6
6	E	1101	RV6	N2-C3-N6-C10
6	E	1101	RV6	N3-C3-N6-C10
6	E	1101	RV6	C5-C2-N1-C1
6	E	1101	RV6	N2-C2-N1-C1
6	E	1101	RV6	C9-C7-N5-C4
6	E	1101	RV6	C9-C7-N5-C6
6	H	1101	RV6	N2-C3-N6-C10
6	H	1101	RV6	N3-C3-N6-C10
6	H	1101	RV6	C5-C2-N1-C1
6	H	1101	RV6	N2-C2-N1-C1
6	H	1101	RV6	C11-C10-C12-C13
6	H	1101	RV6	C9-C7-N5-C4
6	H	1101	RV6	C9-C7-N5-C6
6	B	1101	RV6	C14-C1-N1-C2
6	E	1101	RV6	C14-C1-N1-C2
6	E	1101	RV6	C18-C1-N1-C2
6	H	1101	RV6	C14-C1-N1-C2
6	B	1101	RV6	C18-C1-N1-C2
6	H	1101	RV6	C18-C1-N1-C2
6	H	1101	RV6	C8-C7-N5-C6
6	B	1101	RV6	C8-C7-N5-C6
6	E	1101	RV6	C8-C7-N5-C6

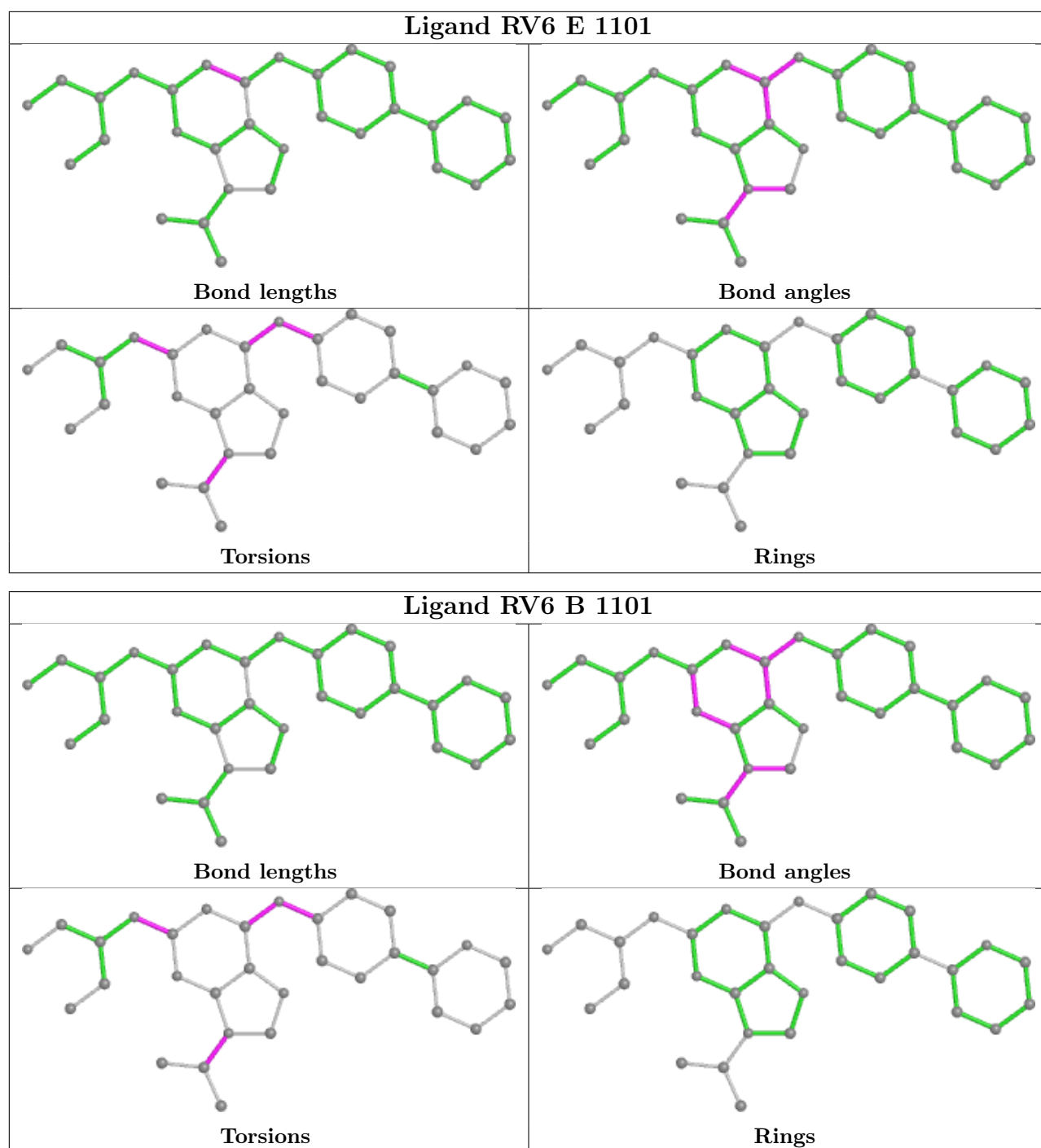
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	F	301	SO4	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 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	826/840 (98%)	0.36	48 (5%) 23 20	124, 171, 248, 331	1 (0%)
1	D	827/840 (98%)	0.30	31 (3%) 41 37	117, 163, 241, 298	1 (0%)
1	G	826/840 (98%)	0.37	59 (7%) 16 15	129, 175, 252, 344	1 (0%)
2	B	326/344 (94%)	0.64	42 (12%) 3 4	149, 187, 256, 282	0
2	E	324/344 (94%)	0.52	17 (5%) 27 24	126, 169, 247, 359	0
2	H	323/344 (93%)	0.48	15 (4%) 32 28	116, 150, 218, 304	0
3	C	248/271 (91%)	0.34	7 (2%) 53 47	134, 170, 216, 276	0
3	F	248/271 (91%)	0.39	2 (0%) 86 81	110, 138, 184, 256	0
3	I	248/271 (91%)	0.41	3 (1%) 79 73	116, 143, 192, 263	0
All	All	4196/4365 (96%)	0.40	224 (5%) 26 24	110, 167, 245, 359	3 (0%)

All (224) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	1039	CYS	5.5
2	B	884	TYR	5.2
2	B	876	ALA	4.9
2	B	720	GLY	4.8
2	E	882	ARG	4.8
2	B	883	LEU	4.1
2	B	1035	HIS	4.1
2	E	890	ARG	3.9
1	A	1097	PHE	3.9
3	I	267	HIS	3.8
2	B	896	VAL	3.8
2	E	913	TYR	3.8
1	G	131	ILE	3.7
2	H	1038	ASP	3.7
1	A	61	ILE	3.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	G	911	ALA	3.5
3	F	267	HIS	3.5
1	G	1040	VAL	3.4
1	A	327	ARG	3.4
2	E	895	LYS	3.4
2	B	811	LEU	3.4
1	A	1017	LEU	3.4
1	G	295	VAL	3.3
1	A	39	LEU	3.3
1	G	1088	PHE	3.3
1	A	60	LYS	3.2
2	B	839	PHE	3.2
2	B	885	ASN	3.2
2	B	932	LYS	3.1
2	B	756	LYS	3.1
1	A	131	ILE	3.1
1	D	39	LEU	3.1
2	E	829	VAL	3.1
2	H	890	ARG	3.1
2	B	1039	CYS	3.1
1	G	49	LEU	3.0
2	B	800	LEU	3.0
2	E	883	LEU	3.0
2	E	831	PHE	3.0
1	A	1079	GLU	3.0
2	B	878	PHE	3.0
1	A	62	ALA	3.0
1	D	64	MET	3.0
3	C	149	GLN	3.0
2	B	875	LEU	2.9
2	H	1035	HIS	2.9
2	B	802	PHE	2.9
2	E	839	PHE	2.9
1	G	307	GLU	2.9
2	H	798	ASP	2.9
1	A	328	LEU	2.8
2	E	888	GLU	2.8
1	A	1035	GLY	2.8
1	G	306	GLY	2.8
2	E	881	ALA	2.8
1	G	1043	LEU	2.8
2	B	855	PHE	2.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	G	132	GLY	2.8
1	G	957	VAL	2.8
2	E	1036	TRP	2.8
1	A	32	LEU	2.8
2	H	896	VAL	2.8
1	D	974	LEU	2.8
2	B	775	ILE	2.7
2	B	860	ILE	2.7
1	G	133	LEU	2.7
1	D	1007	PHE	2.7
1	G	914	LEU	2.7
1	G	5	TYR	2.7
2	B	1038	ASP	2.7
1	A	145	LEU	2.7
1	A	34	ALA	2.7
1	A	77	LEU	2.7
2	E	884	TYR	2.7
1	G	61	ILE	2.7
1	A	23	PHE	2.7
1	G	310	ILE	2.6
1	G	303	GLU	2.6
1	A	120	ILE	2.6
3	C	267	HIS	2.6
1	G	317	LEU	2.6
1	G	9	ALA	2.6
2	B	887	GLU	2.5
2	B	882	ARG	2.5
1	A	356	LEU	2.5
1	D	91	TYR	2.5
1	G	1089	ILE	2.5
2	B	867	LEU	2.5
1	D	33	ILE	2.5
1	D	1005	ASN	2.5
2	B	829	VAL	2.5
1	A	57	MET	2.5
1	D	37	THR	2.5
1	G	64	MET	2.5
1	G	273	LEU	2.5
1	G	1136	LEU	2.5
2	B	913	TYR	2.5
1	A	133	LEU	2.5
1	G	328	LEU	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	G	57	MET	2.5
1	D	5	TYR	2.5
1	A	1029	LEU	2.5
1	A	33	ILE	2.5
1	A	143	ILE	2.5
1	A	41	ILE	2.5
2	H	913	TYR	2.4
2	H	720	GLY	2.4
1	A	59	GLY	2.4
1	G	816	LEU	2.4
1	G	230	ILE	2.4
1	G	253	ILE	2.4
1	G	327	ARG	2.4
2	E	760	LEU	2.4
2	B	831	PHE	2.4
3	C	153	PHE	2.4
1	D	1129	LEU	2.4
2	H	892	TYR	2.4
1	G	79	ILE	2.4
1	D	1040	VAL	2.3
1	G	858	LEU	2.3
1	A	1030	PHE	2.3
1	A	336	LEU	2.3
1	D	328	LEU	2.3
2	B	780	GLN	2.3
1	G	953	TRP	2.3
1	G	100	ILE	2.3
1	G	314	LEU	2.3
1	G	966	LEU	2.3
1	G	377	THR	2.3
1	D	36	ASN	2.3
1	G	930	VAL	2.3
3	C	81	PHE	2.3
1	G	232	ILE	2.3
1	A	87	CYS	2.3
1	G	1039	LEU	2.3
2	B	930	PHE	2.3
2	E	733	ILE	2.3
3	I	57	ILE	2.3
3	F	181	LEU	2.3
1	A	64	MET	2.3
2	H	839	PHE	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
2	B	988	PHE	2.3
1	A	144	PRO	2.3
2	B	793	VAL	2.3
1	A	1020	THR	2.3
1	G	66	LEU	2.3
1	G	1094	ILE	2.3
1	A	304	LEU	2.3
1	G	237	ILE	2.3
1	D	998	PHE	2.3
1	G	323	PHE	2.2
1	D	2	SER	2.2
1	D	356	LEU	2.2
1	D	1000	LEU	2.2
2	B	799	ALA	2.2
1	A	135	LEU	2.2
1	G	82	ALA	2.2
2	H	823	LEU	2.2
2	B	774	GLU	2.2
1	A	80	LEU	2.2
1	A	933	LEU	2.2
1	A	1040	VAL	2.2
1	D	1080	ARG	2.2
1	D	253	ILE	2.2
2	B	792	ILE	2.2
1	G	4	ASN	2.2
2	B	820	LEU	2.2
1	G	1129	LEU	2.2
2	B	929	LEU	2.2
3	C	132	PHE	2.2
3	C	164	LEU	2.2
1	G	180	PHE	2.2
2	B	881	ALA	2.2
1	D	133	LEU	2.2
1	G	387	LEU	2.2
3	C	100	LEU	2.1
1	G	1097	PHE	2.1
2	H	738	TYR	2.1
2	B	888	GLU	2.1
1	A	387	LEU	2.1
1	A	140	PHE	2.1
1	D	390	ILE	2.1
2	B	738	TYR	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
3	I	266	PRO	2.1
1	D	117	GLU	2.1
1	A	89	LEU	2.1
1	A	230	ILE	2.1
1	D	237	ILE	2.1
2	B	776	LYS	2.1
1	D	40	GLU	2.1
1	A	220	ILE	2.1
1	A	79	ILE	2.1
2	H	1034	PRO	2.1
1	A	376	VAL	2.1
1	G	333	LEU	2.1
2	B	824	LEU	2.1
1	G	32	LEU	2.1
1	G	63	VAL	2.1
1	G	814	LEU	2.1
1	G	78	PHE	2.1
1	A	88	ILE	2.0
1	D	327	ARG	2.0
2	H	801	ASP	2.0
1	D	1004	VAL	2.0
1	G	6	VAL	2.0
1	D	1	MET	2.0
1	D	9	ALA	2.0
2	E	887	GLU	2.0
1	A	1094	ILE	2.0
2	B	955	PRO	2.0
1	G	272	LEU	2.0
1	A	78	PHE	2.0
1	A	300	LEU	2.0
1	G	733	PHE	2.0
1	G	1019	GLU	2.0
2	H	888	GLU	2.0
1	D	362	MET	2.0
2	E	897	ILE	2.0
1	D	997	LEU	2.0
2	H	889	SER	2.0
2	B	781	LEU	2.0
1	D	112	ILE	2.0
1	A	5	TYR	2.0
1	G	282	MET	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
2	TPO	E	893	11/12	0.64	0.23	229,265,326,330	5
2	TPO	B	893	11/12	0.79	0.17	220,243,295,306	6
2	TPO	H	893	11/12	0.79	0.25	164,202,252,266	6

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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.

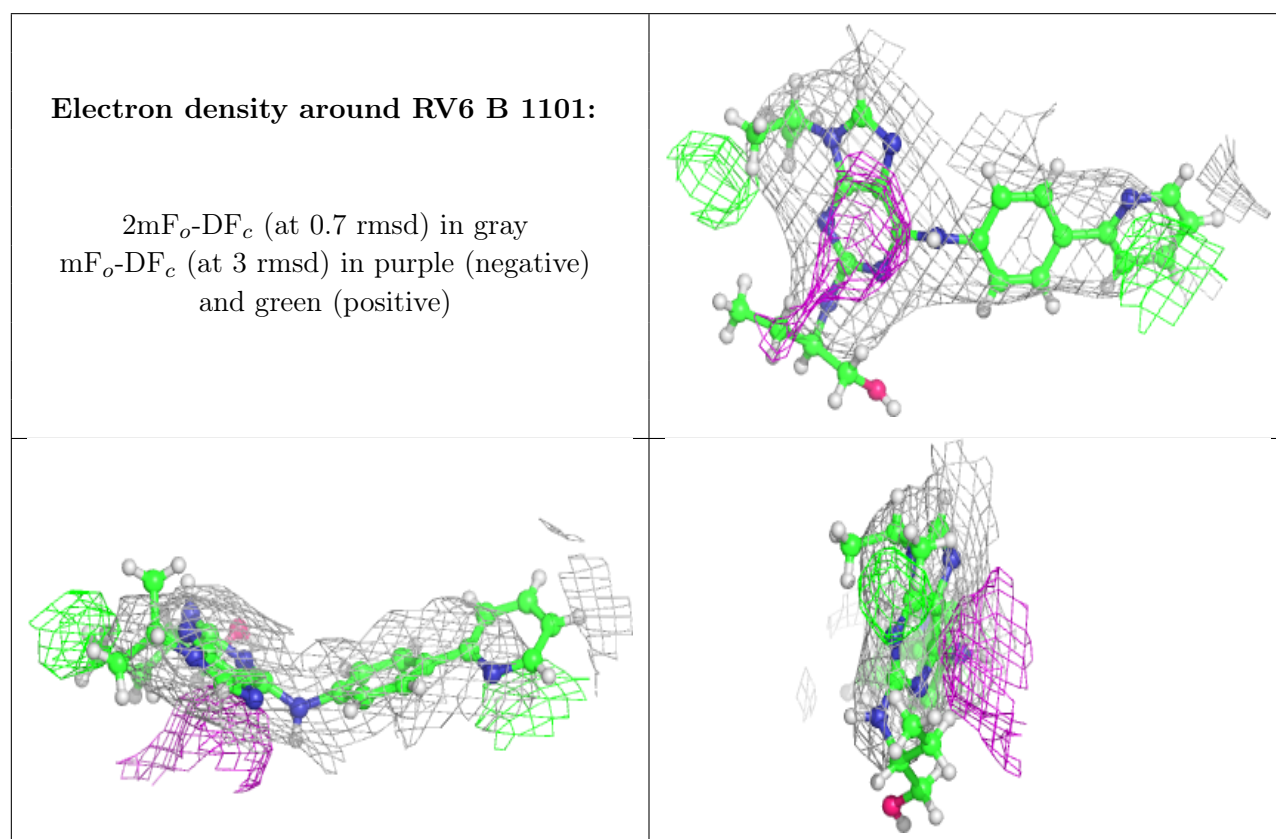
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	SO4	F	302	5/5	0.63	0.22	186,196,207,252	0
5	SO4	G	1203	5/5	0.67	0.18	151,205,227,264	0
5	SO4	D	1203	5/5	0.68	0.17	184,185,231,262	0
4	EDO	A	1201	4/4	0.70	0.28	130,157,171,179	6
5	SO4	G	1202	5/5	0.72	0.16	183,185,207,245	0
5	SO4	D	1204	5/5	0.72	0.27	172,187,207,248	0
5	SO4	A	1203	5/5	0.73	0.23	161,173,182,224	0
5	SO4	C	302	5/5	0.75	0.16	186,202,219,261	0
5	SO4	G	1201	5/5	0.77	0.18	165,178,200,218	0
5	SO4	C	303	5/5	0.80	0.14	175,190,197,241	0
5	SO4	D	1202	5/5	0.81	0.23	165,179,196,238	0
5	SO4	B	1102	5/5	0.82	0.14	190,197,210,251	0
5	SO4	I	302	5/5	0.82	0.17	174,186,197,235	0
5	SO4	I	303	5/5	0.82	0.21	143,151,167,179	0
5	SO4	F	301	5/5	0.84	0.21	169,174,213,233	0
5	SO4	I	301	5/5	0.84	0.16	176,183,197,230	0
5	SO4	C	301	5/5	0.85	0.23	155,168,195,210	0
5	SO4	A	1204	5/5	0.86	0.11	206,211,227,272	0
5	SO4	D	1201	5/5	0.87	0.16	165,167,186,207	0

Continued on next page...

Continued from previous page...

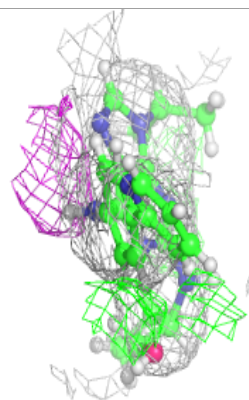
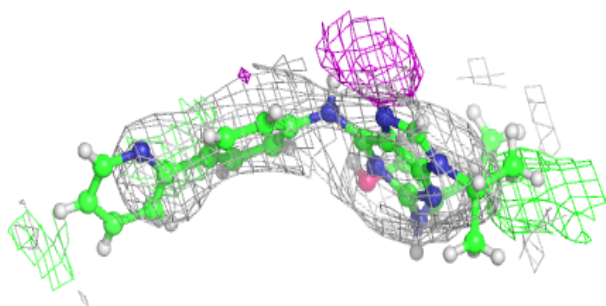
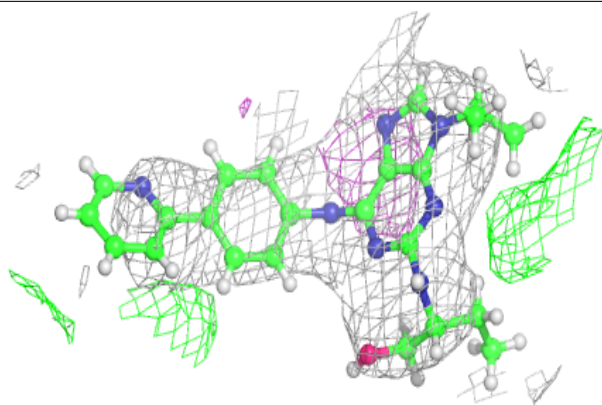
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
6	RV6	B	1101	31/31	0.87	0.58	127,166,227,246	27
6	RV6	H	1101	31/31	0.87	0.54	119,157,218,250	27
5	SO4	H	1102	5/5	0.88	0.12	191,194,202,247	0
6	RV6	E	1101	31/31	0.89	0.66	110,165,215,245	27
5	SO4	F	303	5/5	0.89	0.21	142,144,174,184	0
5	SO4	A	1202	5/5	0.93	0.15	163,173,193,212	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.

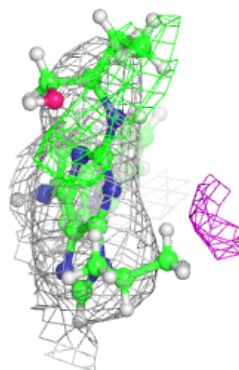
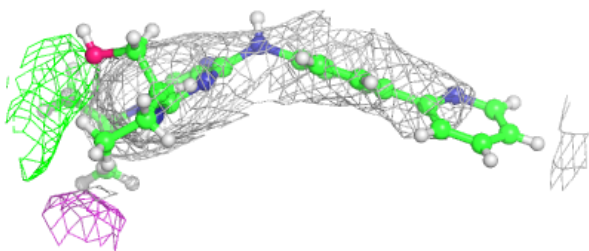
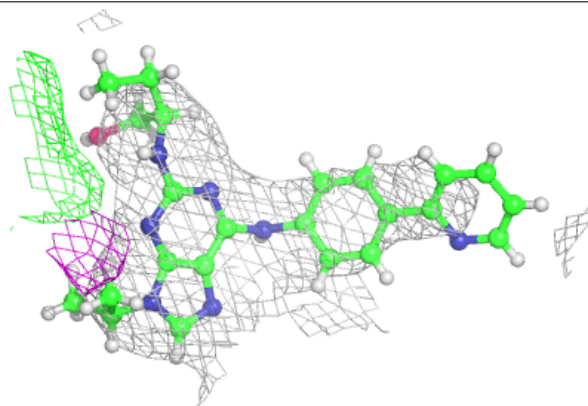


Electron density around RV6 H 1101:

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

**Electron density around RV6 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.