



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 7, 2023 – 01:32 pm BST

PDB ID : 8BUD
Title : Structure of DDB1 bound to Z7-engaged CDK12-cyclin K
Authors : Kozicka, Z.; Kempf, G.; Petzold, G.; Thoma, N.H.
Deposited on : 2022-11-30
Resolution : 3.20 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

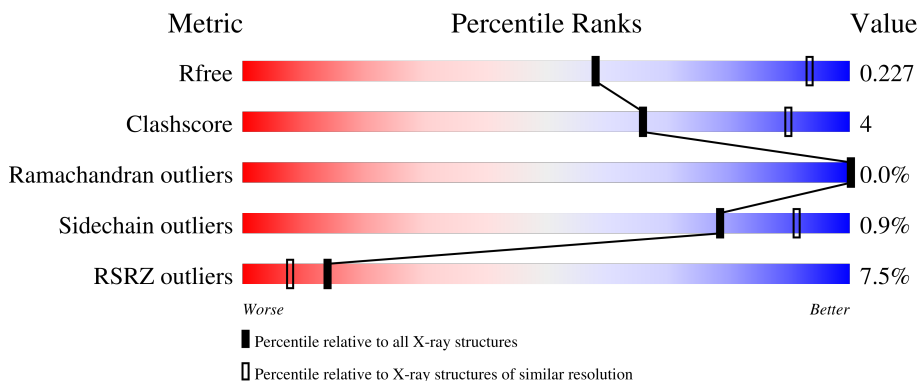
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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.



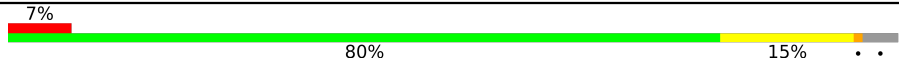
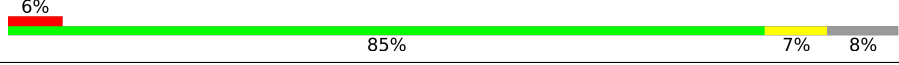
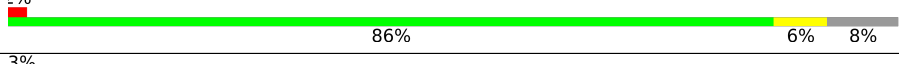
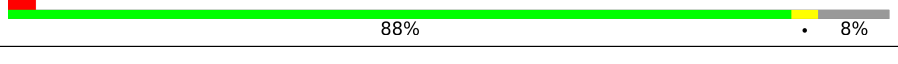
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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	 9% 87% 11%
1	D	840	 5% 88% 11%
1	G	840	 8% 85% 14%
2	B	344	 12% 84% 11%
2	E	344	 9% 82% 13%

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Mol	Chain	Length	Quality of chain
2	H	344	 <p>7% 80% 15% . .</p>
3	C	271	 <p>6% 85% 7% 8%</p>
3	F	271	 <p>2% 86% 6% 8%</p>
3	I	271	 <p>3% 88% . 8%</p>

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 67623 atoms, of which 33641 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	12938	4105	6451	1094	1252	36	6451	0	0
1	D	827	12957	4111	6462	1095	1253	36	6462	0	0
1	G	826	12941	4106	6455	1093	1251	36	6455	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	329	Total	C	H	N	O	P	S	2697	0	0
			5384	1723	2697	454	492	1	17			
2	E	329	Total	C	H	N	O	P	S	2697	0	0
			5384	1723	2697	454	492	1	17			
2	H	329	Total	C	H	N	O	P	S	2696	0	0
			5383	1723	2696	454	492	1	17			

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	248	Total	C	H	N	O	S	2048	0	0
			4111	1341	2048	346	363	13			
3	F	248	Total	C	H	N	O	S	2048	0	0
			4111	1341	2048	346	363	13			
3	I	248	Total	C	H	N	O	S	2048	0	0
			4111	1341	2048	346	363	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 (three-letter code: SO4) (formula: O₄S).



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

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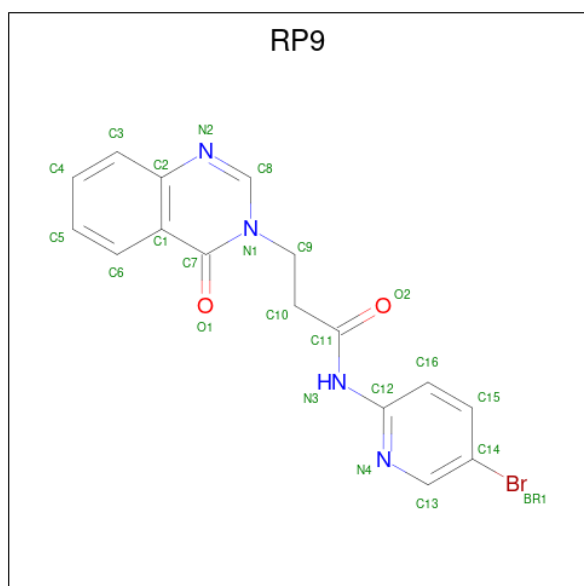
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
4	D	1	5	4	1	0	0
4	D	1	5	4	1	0	0
4	D	1	5	4	1	0	0
4	D	1	5	4	1	0	0
4	D	1	5	4	1	0	0
4	D	1	5	4	1	0	0
4	E	1	5	4	1	0	0
4	F	1	5	4	1	0	0
4	F	1	5	4	1	0	0
4	F	1	5	4	1	0	0
4	F	1	5	4	1	0	0
4	F	1	5	4	1	0	0
4	G	1	5	4	1	0	0
4	G	1	5	4	1	0	0
4	G	1	5	4	1	0	0
4	G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

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

- Molecule 5 is {N}-(5-bromanylpyridin-2-yl)-3-(4-oxidanylidenequinazolin-3-yl)propanamide (three-letter code: RP9) (formula: C₁₆H₁₃BrN₄O₂) (labeled as "Ligand of Interest" by depositor).

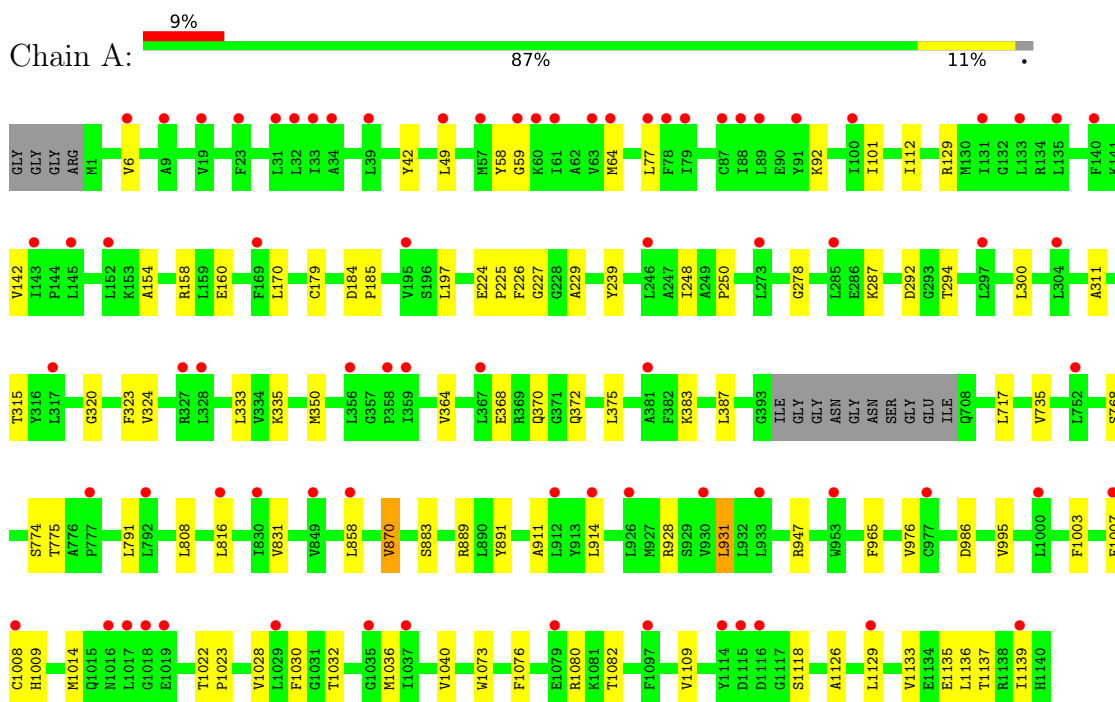


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
5	B	1	Total	Br	C	H	N	O	13	0
			36	1	16	13	4	2		
5	D	1	Total	Br	C	H	N	O	13	0
			36	1	16	13	4	2		
5	H	1	Total	Br	C	H	N	O	13	0
			36	1	16	13	4	2		

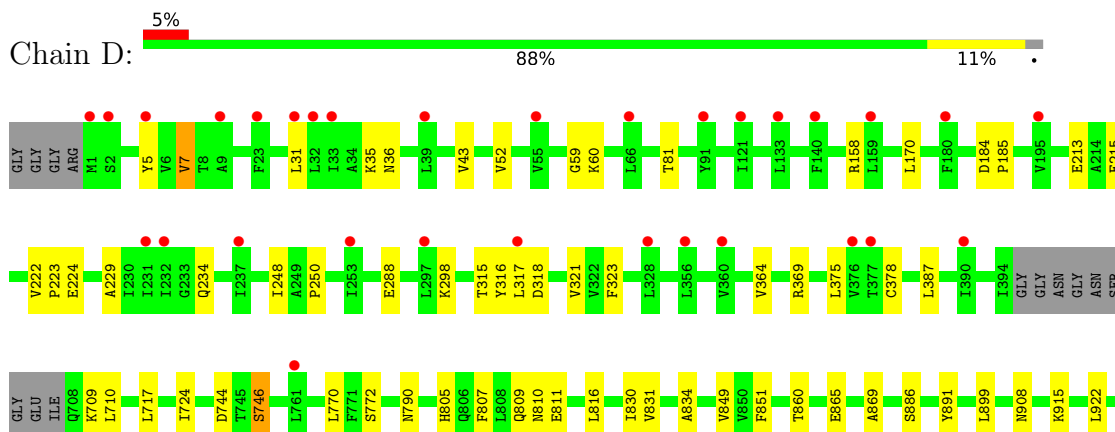
3 Residue-property plots [i](#)

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

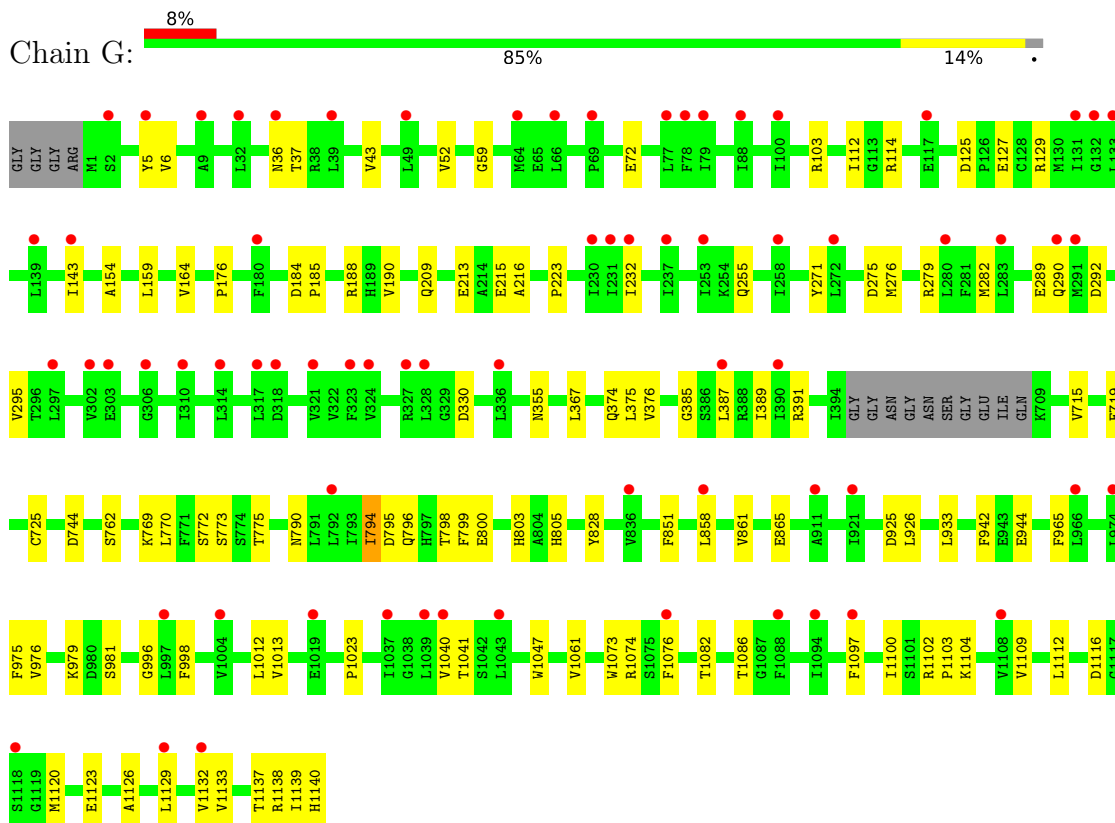


- Molecule 1: DNA damage-binding protein 1

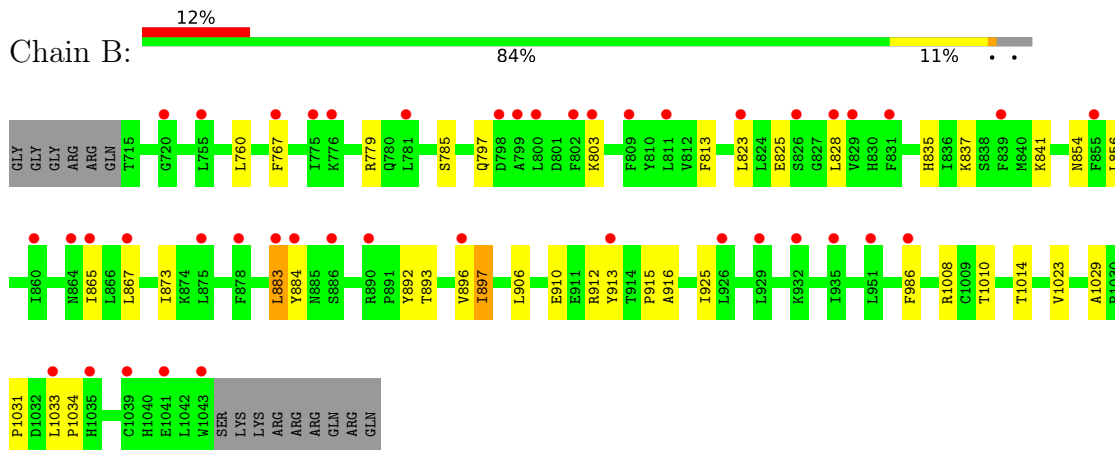




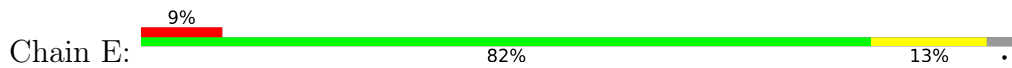
- Molecule 1: DNA damage-binding protein 1

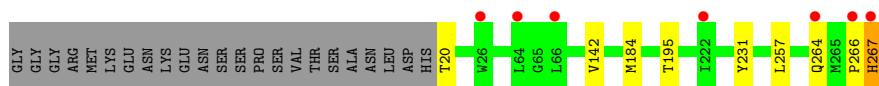


- Molecule 2: Cyclin-dependent kinase 12



- Molecule 2: Cyclin-dependent kinase 12





4 Data and refinement statistics i

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	249.63Å 249.63Å 218.22Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	60.35 – 3.20 216.18 – 3.20	Depositor EDS
% Data completeness (in resolution range)	96.3 (60.35-3.20) 82.6 (216.18-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.51 (at 3.19Å)	Xtrriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.189 , 0.220 0.200 , 0.227	Depositor DCC
R_{free} test set	5242 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	128.1	Xtrriage
Anisotropy	0.000	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 90.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	0.029 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	67623	wwPDB-VP
Average B, all atoms (Å ²)	151.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.60% 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, RP9

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	0.35	0/6604	0.64	1/8931 (0.0%)
1	D	0.35	0/6612	0.61	0/8942
1	G	0.36	0/6603	0.63	0/8930
2	B	0.37	0/2737	0.63	0/3691
2	E	0.36	0/2737	0.61	0/3691
2	H	0.39	0/2737	0.62	0/3691
3	C	0.35	0/2120	0.54	0/2868
3	F	0.38	0/2120	0.59	0/2868
3	I	0.36	0/2120	0.56	0/2868
All	All	0.36	0/34390	0.61	1/46480 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	931	LEU	CA-CB-CG	5.19	127.25	115.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6487	6451	6453	56	3

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	6495	6462	6464	52	0
1	G	6486	6455	6456	67	3
2	B	2687	2697	2696	24	0
2	E	2687	2697	2697	29	0
2	H	2687	2696	2696	34	0
3	C	2063	2048	2048	10	0
3	F	2063	2048	2048	10	0
3	I	2063	2048	2048	4	0
4	A	25	0	0	0	0
4	B	10	0	0	0	0
4	C	15	0	0	0	0
4	D	50	0	0	1	0
4	E	5	0	0	0	0
4	F	20	0	0	0	0
4	G	35	0	0	0	0
4	H	20	0	0	0	0
4	I	15	0	0	0	0
5	B	23	13	0	1	0
5	D	23	13	0	0	0
5	H	23	13	0	0	0
All	All	33982	33641	33606	271	3

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 (271) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:1109:VAL:HG12	1:G:1129:LEU:HD12	1.64	0.80
1:D:315:THR:HG22	1:D:323:PHE:HB3	1.70	0.73
2:H:828:LEU:O	2:H:1034:PRO:HD2	1.94	0.68
1:G:1109:VAL:HG11	1:G:1126:ALA:HA	1.80	0.64
1:G:1047:TRP:HZ3	1:G:1132:VAL:HG13	1.61	0.63
1:G:925:ASP:OD1	1:G:926:LEU:N	2.31	0.62
2:E:856:LEU:HD11	2:E:915:PRO:HG3	1.81	0.62
1:G:773:SER:O	1:G:775:THR:N	2.31	0.60
1:D:317:LEU:HB2	1:D:321:VAL:HG13	1.83	0.60
1:G:289:GLU:HG2	1:G:295:VAL:HG22	1.83	0.60
1:G:1013:VAL:HG11	1:G:1138:ARG:O	2.02	0.60
2:H:906:LEU:HD21	2:H:913:TYR:CD2	2.36	0.60
2:B:910:GLU:HG3	2:B:912:ARG:H	1.66	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:223:PRO:HD3	1:G:271:TYR:OH	2.02	0.59
1:A:775:THR:HG22	1:A:775:THR:O	2.03	0.58
1:G:773:SER:C	1:G:775:THR:H	2.06	0.58
1:D:5:TYR:HB2	1:D:1043:LEU:HD11	1.86	0.58
1:G:43:VAL:HG23	1:G:52:VAL:HG21	1.84	0.58
1:A:931:LEU:HD23	1:A:947:ARG:HB2	1.86	0.57
1:D:43:VAL:HG23	1:D:52:VAL:HG11	1.86	0.57
1:D:709:LYS:HG2	1:D:710:LEU:N	2.19	0.56
1:G:1023:PRO:HB3	1:G:1047:TRP:CE2	2.41	0.56
1:D:816:LEU:HD13	1:D:831:VAL:HG22	1.87	0.55
1:D:213:GLU:HG2	1:D:215:GLU:H	1.71	0.55
3:F:79:HIS:HB3	3:F:199:LEU:HD11	1.86	0.55
3:F:243:PRO:HG2	3:F:246:VAL:HG23	1.88	0.55
1:D:7:VAL:HG13	1:D:1091:GLY:HA3	1.87	0.55
1:A:889:ARG:HD2	1:A:891:TYR:CZ	2.42	0.55
1:A:6:VAL:HG22	1:A:1040:VAL:HG22	1.88	0.54
1:G:770:LEU:HD21	1:G:865:GLU:HB2	1.88	0.54
1:A:368:GLU:HB2	1:A:370:GLN:HG3	1.90	0.54
2:H:1010:THR:O	2:H:1014:THR:HG23	2.08	0.54
1:A:292:ASP:HB3	1:A:294:THR:HG22	1.89	0.54
2:B:803:LYS:HG3	3:C:142:VAL:HG21	1.90	0.54
1:A:227:GLY:O	1:A:239:TYR:OH	2.15	0.54
1:A:248:ILE:HG12	1:A:250:PRO:HD3	1.89	0.54
2:E:758:VAL:O	2:E:808:ALA:HB1	2.07	0.54
2:H:917:ILE:HG13	2:H:918:ASP:N	2.23	0.54
1:A:372:GLN:HG2	1:A:1014:MET:HB2	1.91	0.53
2:E:799:ALA:HB1	2:E:804:LYS:HE3	1.90	0.53
1:G:769:LYS:O	1:G:772:SER:HB3	2.09	0.53
1:A:59:GLY:HA2	1:A:1073:TRP:CZ3	2.44	0.53
1:A:816:LEU:HD13	1:A:831:VAL:HG22	1.92	0.52
1:G:72:GLU:OE2	1:G:103:ARG:NH2	2.43	0.52
1:G:1047:TRP:CZ3	1:G:1132:VAL:HG13	2.43	0.52
1:D:158:ARG:HD2	2:E:987:SER:HB2	1.92	0.52
1:G:255:GLN:OE1	1:G:279:ARG:NH1	2.42	0.52
2:H:856:LEU:HD22	2:H:915:PRO:HA	1.92	0.52
2:E:1036:TRP:O	2:E:1037:GLN:HB2	2.09	0.52
2:B:1010:THR:O	2:B:1014:THR:HG23	2.10	0.52
2:E:835:HIS:HD2	2:E:1029:ALA:HB1	1.75	0.52
2:B:841:LYS:HD2	2:B:1023:VAL:HB	1.91	0.51
1:G:184:ASP:HB2	1:G:185:PRO:CD	2.41	0.51
1:D:31:LEU:HD22	1:D:317:LEU:HD21	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:127:GLU:HB2	1:G:129:ARG:HG3	1.92	0.51
2:B:823:LEU:HD11	2:B:867:LEU:HD22	1.94	0.50
1:G:933:LEU:HD22	1:G:942:PHE:HB3	1.93	0.50
2:H:858:ARG:NH1	2:H:893:TPO:O1P	2.43	0.50
2:H:823:LEU:HB3	2:H:829:VAL:CG1	2.42	0.50
1:A:387:LEU:HD11	1:A:735:VAL:HG21	1.93	0.50
1:G:5:TYR:HB3	1:G:1041:THR:HG23	1.94	0.50
2:B:906:LEU:HD21	2:B:913:TYR:HB3	1.92	0.50
1:G:1061:VAL:HG11	1:G:1104:LYS:HB3	1.93	0.50
1:G:59:GLY:HA2	1:G:1073:TRP:CE3	2.47	0.49
2:B:779:ARG:HB3	3:C:21:LYS:HE2	1.94	0.49
1:G:828:TYR:CE1	1:G:861:VAL:HG21	2.47	0.49
2:E:867:LEU:HD13	2:E:873:ILE:CD1	2.42	0.49
1:A:870:VAL:O	1:A:870:VAL:HG22	2.11	0.49
1:D:364:VAL:HG23	1:D:1008:CYS:SG	2.53	0.49
1:D:790:ASN:HA	1:D:805:HIS:O	2.11	0.49
1:G:367:LEU:HD22	1:G:796:GLN:HG3	1.94	0.49
1:A:1009:HIS:CE1	1:A:1028:VAL:HG22	2.47	0.49
2:H:722:ARG:HE	2:H:726:LYS:HG3	1.78	0.49
2:E:867:LEU:HD21	2:E:1031:PRO:HG3	1.95	0.49
3:I:266:PRO:O	3:I:267:HIS:C	2.51	0.49
1:D:316:TYR:CE2	1:D:318:ASP:HA	2.48	0.49
1:D:860:THR:HG21	4:D:1204:SO4:O4	2.13	0.49
1:G:1097:PHE:O	1:G:1100:ILE:HG12	2.12	0.49
1:G:188:ARG:NH1	1:G:216:ALA:O	2.44	0.49
3:I:195:THR:CG2	3:I:257:LEU:HD11	2.42	0.49
1:G:975:PHE:HA	1:G:996:GLY:O	2.13	0.49
1:D:387:LEU:HG	1:D:717:LEU:HD11	1.95	0.48
1:A:64:MET:HG3	1:A:77:LEU:HD11	1.95	0.48
2:E:844:MET:HE3	2:E:922:CYS:HB3	1.95	0.48
1:G:998:PHE:CZ	1:G:1074:ARG:HD2	2.49	0.48
1:A:248:ILE:HD12	1:A:300:LEU:O	2.14	0.48
3:C:76:ILE:CD1	3:C:198:SER:HB3	2.43	0.48
2:H:928:GLU:O	2:H:932:LYS:N	2.43	0.48
1:G:36:ASN:O	1:G:37:THR:OG1	2.21	0.48
2:H:800:LEU:HD12	2:H:800:LEU:H	1.79	0.48
1:D:60:LYS:O	1:D:81:THR:HA	2.14	0.48
2:B:892:TYR:HB3	2:B:913:TYR:CZ	2.48	0.47
2:H:773:ARG:HD3	2:H:881:ALA:O	2.14	0.47
2:H:858:ARG:NE	2:H:880:LEU:O	2.46	0.47
3:C:265:MET:SD	3:C:265:MET:N	2.86	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:813:PHE:CB	5:B:1101:RP9:BR1	3.18	0.47
1:G:851:PHE:HB3	1:G:858:LEU:HD22	1.97	0.47
2:H:823:LEU:HB3	2:H:829:VAL:HG13	1.96	0.47
2:H:938:ALA:HB2	2:H:947:LEU:HD12	1.97	0.47
1:D:849:VAL:HG11	1:D:851:PHE:CZ	2.49	0.47
1:G:387:LEU:HB2	1:G:715:VAL:HB	1.97	0.47
1:A:184:ASP:HB2	1:A:185:PRO:CD	2.45	0.47
1:A:1007:PHE:CD1	1:A:1030:PHE:HB3	2.50	0.47
1:D:288:GLU:HB2	1:D:298:LYS:HB2	1.98	0.46
2:E:906:LEU:HD21	2:E:913:TYR:CD2	2.51	0.46
2:B:1031:PRO:HG2	2:B:1033:LEU:HD12	1.98	0.46
3:C:213:LEU:HD11	3:C:255:LEU:HD11	1.97	0.46
1:G:790:ASN:HA	1:G:805:HIS:O	2.16	0.46
1:G:376:VAL:HG13	1:G:389:ILE:HD13	1.97	0.46
1:G:213:GLU:HG2	1:G:215:GLU:H	1.80	0.46
1:A:170:LEU:HD21	1:A:229:ALA:HB2	1.97	0.46
2:E:803:LYS:HG3	3:F:142:VAL:HG21	1.97	0.46
2:E:828:LEU:O	2:E:1034:PRO:HD2	2.15	0.46
1:G:374:GLN:HG3	1:G:391:ARG:HB3	1.98	0.46
2:H:800:LEU:HD12	2:H:800:LEU:N	2.30	0.45
1:A:142:VAL:O	1:A:154:ALA:HB1	2.17	0.45
1:G:276:MET:O	1:G:276:MET:HG3	2.16	0.45
1:G:798:THR:HG23	1:G:800:GLU:H	1.81	0.45
2:B:910:GLU:C	2:B:912:ARG:H	2.18	0.45
2:E:722:ARG:NH1	2:E:791:GLU:OE2	2.49	0.45
2:E:784:ARG:O	2:E:874:LYS:HE2	2.16	0.45
2:H:896:VAL:HG13	2:H:897:ILE:HG12	1.99	0.45
1:A:112:ILE:HD13	2:B:986:PHE:CE2	2.51	0.45
1:A:370:GLN:C	1:A:372:GLN:H	2.19	0.45
2:E:867:LEU:HD13	2:E:873:ILE:HD13	1.99	0.45
1:G:59:GLY:HA2	1:G:1073:TRP:CZ3	2.51	0.45
1:G:794:ILE:HG22	1:G:799:PHE:HA	1.97	0.45
1:D:744:ASP:OD1	1:D:746:SER:HB3	2.16	0.45
2:H:865:ILE:HD11	2:H:925:ILE:HD13	1.99	0.45
1:G:125:ASP:OD2	1:G:176:PRO:HB3	2.17	0.45
1:D:891:TYR:HB3	1:D:899:LEU:HD22	1.98	0.45
1:G:6:VAL:HG22	1:G:1040:VAL:HG22	1.98	0.45
2:H:867:LEU:HD13	2:H:873:ILE:CD1	2.47	0.45
1:A:1022:THR:HB	1:A:1023:PRO:HD2	1.99	0.45
2:B:884:TYR:CZ	2:B:915:PRO:HD3	2.51	0.45
2:B:896:VAL:HG13	2:B:897:ILE:HG12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:170:LEU:HD21	1:D:229:ALA:HB2	1.98	0.45
1:D:936:LYS:HD3	1:D:943:GLU:OE1	2.17	0.45
2:E:779:ARG:HB3	3:F:21:LYS:HE2	1.99	0.45
1:D:364:VAL:HG22	1:D:375:LEU:HD13	2.00	0.44
3:F:222:ILE:HD12	3:F:234:TRP:CZ2	2.52	0.44
1:G:762:SER:O	1:G:803:HIS:HA	2.17	0.44
2:H:841:LYS:HD2	2:H:1023:VAL:HB	1.99	0.44
1:A:158:ARG:NH1	1:A:160:GLU:HG2	2.33	0.44
1:D:915:LYS:HE3	1:D:957:VAL:O	2.18	0.44
1:D:998:PHE:CZ	1:D:1074:ARG:HD2	2.52	0.44
2:H:905:GLU:HA	2:H:960:TRP:HH2	1.82	0.44
3:C:239:VAL:HG12	3:C:242:VAL:HG23	1.99	0.44
1:D:1109:VAL:HG12	1:D:1129:LEU:HD12	2.00	0.44
1:A:1022:THR:HG22	1:A:1135:GLU:HG3	1.98	0.44
1:D:378:CYS:SG	1:D:724:ILE:HB	2.58	0.44
1:G:1112:LEU:O	1:G:1123:GLU:HA	2.18	0.44
3:I:184:MET:HG3	3:I:266:PRO:HB2	1.98	0.44
1:D:248:ILE:HG12	1:D:250:PRO:HD3	2.00	0.44
1:G:114:ARG:HD3	2:H:930:PHE:O	2.18	0.44
1:G:1102:ARG:HB3	1:G:1103:PRO:HD3	2.00	0.44
1:A:768:SER:HB3	1:A:808:LEU:HD11	2.00	0.44
3:C:79:HIS:HB3	3:C:199:LEU:HD11	1.99	0.44
1:A:42:TYR:CD2	1:A:49:LEU:HB3	2.53	0.44
1:A:226:PHE:CE2	1:A:287:LYS:HG2	2.52	0.43
2:H:935:ILE:HD12	2:H:986:PHE:HZ	1.83	0.43
1:D:809:GLN:O	1:D:810:ASN:HB2	2.18	0.43
2:E:916:ALA:O	2:E:1008:ARG:NH1	2.51	0.43
3:F:223:GLN:H	3:F:223:GLN:HG3	1.54	0.43
1:G:773:SER:C	1:G:775:THR:N	2.70	0.43
2:H:902:ARG:HG2	2:H:903:PRO:HD2	2.00	0.43
2:B:856:LEU:HD21	2:B:884:TYR:HB2	2.01	0.43
1:G:112:ILE:HD13	2:H:986:PHE:CE2	2.53	0.43
1:A:1109:VAL:HG11	1:A:1126:ALA:HA	2.01	0.43
1:G:979:LYS:O	1:G:981:SER:N	2.42	0.43
1:A:58:TYR:HB3	1:A:1073:TRP:CB	2.49	0.43
1:D:184:ASP:HB2	1:D:185:PRO:CD	2.49	0.43
1:D:1007:PHE:CD1	1:D:1030:PHE:HB3	2.54	0.43
1:D:709:LYS:CG	1:D:710:LEU:N	2.81	0.43
1:D:927:MET:HB3	2:E:828:LEU:HD12	1.99	0.43
1:A:315:THR:HG22	1:A:323:PHE:HB3	2.01	0.43
2:E:993:ALA:HB2	2:E:1019:PHE:CE1	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:43:VAL:HG23	1:G:52:VAL:CG2	2.46	0.43
2:H:951:LEU:HD21	2:H:986:PHE:HE2	1.82	0.43
2:B:865:ILE:HD11	2:B:925:ILE:HD13	2.00	0.43
1:G:271:TYR:O	1:G:282:MET:HG3	2.18	0.43
3:I:195:THR:HG21	3:I:257:LEU:HD11	2.00	0.43
1:A:883:SER:HB3	1:A:914:LEU:HD11	2.01	0.43
1:A:1003:PHE:O	1:A:1032:THR:HA	2.19	0.43
2:B:854:ASN:O	2:B:883:LEU:HD22	2.19	0.43
2:E:762:ASN:OD1	2:E:763:GLU:N	2.51	0.43
1:A:1133:VAL:O	1:A:1137:THR:HG23	2.19	0.42
3:C:82:TYR:CE2	3:C:95:THR:HG21	2.54	0.42
1:D:1114:TYR:HB2	1:D:1124:ALA:HB2	2.01	0.42
1:G:996:GLY:HA2	1:G:1086:THR:O	2.19	0.42
1:A:364:VAL:HG23	1:A:1008:CYS:SG	2.59	0.42
1:D:816:LEU:HD12	1:D:830:ILE:O	2.19	0.42
1:D:1023:PRO:HB3	1:D:1047:TRP:CZ2	2.55	0.42
1:G:275:ASP:C	1:G:275:ASP:OD1	2.57	0.42
2:B:837:LYS:HB3	2:B:1023:VAL:HG21	2.00	0.42
1:D:1076:PHE:O	1:D:1082:THR:HA	2.18	0.42
1:G:1116:ASP:O	1:G:1120:MET:HB2	2.19	0.42
1:A:278:GLY:HA3	1:A:383:LYS:HE2	2.02	0.42
2:E:803:LYS:HA	3:F:142:VAL:CG1	2.50	0.42
1:D:222:VAL:HA	1:D:223:PRO:HD3	1.93	0.42
1:G:159:LEU:HD21	1:G:164:VAL:HG21	2.02	0.42
1:A:774:SER:O	1:A:775:THR:HB	2.19	0.42
1:A:1109:VAL:HG12	1:A:1129:LEU:HD12	2.00	0.42
1:D:770:LEU:HD13	1:D:865:GLU:HB2	2.02	0.42
2:H:966:LEU:HD23	2:H:966:LEU:HA	1.90	0.42
1:A:170:LEU:HD11	1:A:179:CYS:HB2	2.02	0.42
1:A:1076:PHE:O	1:A:1082:THR:HA	2.20	0.42
1:D:1126:ALA:O	1:D:1130:ILE:HG13	2.20	0.42
1:A:387:LEU:HG	1:A:717:LEU:HD11	2.02	0.42
1:A:1136:LEU:O	1:A:1139:ILE:HG12	2.20	0.42
1:D:927:MET:HB3	2:E:828:LEU:CD1	2.50	0.42
1:D:1057:ARG:HD3	1:D:1108:VAL:O	2.20	0.42
2:H:899:LEU:HD11	2:H:941:GLU:HA	2.02	0.42
2:B:828:LEU:O	2:B:1034:PRO:HD2	2.20	0.41
1:D:834:ALA:HB2	1:D:869:ALA:CB	2.49	0.41
2:E:857:HIS:O	2:E:858:ARG:HB2	2.20	0.41
2:H:787:VAL:HA	2:H:874:LYS:HD3	2.02	0.41
1:A:364:VAL:HG22	1:A:375:LEU:CD1	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:886:SER:HB3	1:D:908:ASN:O	2.20	0.41
1:D:1043:LEU:HD13	1:D:1051:LEU:HD12	2.02	0.41
2:E:762:ASN:HB2	2:E:764:LYS:HG3	2.03	0.41
2:H:1021:LYS:HB3	2:H:1021:LYS:HE3	1.85	0.41
1:A:333:LEU:O	1:A:350:MET:HB2	2.20	0.41
1:D:35:LYS:O	1:D:36:ASN:C	2.59	0.41
1:G:190:VAL:O	1:G:209:GLN:HA	2.21	0.41
1:A:311:ALA:HB2	1:A:324:VAL:HG13	2.02	0.41
1:A:1080:ARG:HD3	2:B:825:GLU:HA	2.02	0.41
1:D:59:GLY:HA2	1:D:1073:TRP:CZ3	2.55	0.41
1:G:376:VAL:HG13	1:G:389:ILE:CD1	2.51	0.41
1:G:944:GLU:OE1	2:H:732:ILE:HG22	2.20	0.41
3:F:266:PRO:O	3:F:267:HIS:C	2.58	0.41
1:G:965:PHE:O	1:G:976:VAL:HA	2.21	0.41
1:A:92:LYS:HD2	1:A:101:ILE:HD11	2.02	0.41
1:A:320:GLY:O	1:A:335:LYS:HA	2.20	0.41
2:E:858:ARG:O	2:E:897:ILE:HG12	2.20	0.41
1:A:224:GLU:N	1:A:225:PRO:CD	2.84	0.41
1:A:965:PHE:O	1:A:976:VAL:HA	2.20	0.41
1:D:213:GLU:OE2	1:D:234:GLN:N	2.45	0.41
1:G:143:ILE:HG12	1:G:154:ALA:HB2	2.03	0.41
1:G:375:LEU:HB2	1:G:1012:LEU:HD21	2.02	0.41
1:G:385:GLY:HA3	1:G:719:GLU:O	2.21	0.41
1:G:795:ASP:OD2	1:G:798:THR:HG22	2.21	0.41
2:H:724:VAL:O	2:H:724:VAL:HG22	2.21	0.41
3:C:222:ILE:HD12	3:C:234:TRP:CZ2	2.56	0.41
2:E:857:HIS:ND1	2:E:860:ILE:HG12	2.36	0.41
2:E:933:LYS:HE2	2:E:937:GLN:OE1	2.20	0.41
1:G:795:ASP:HB3	1:G:798:THR:HG22	2.02	0.41
1:A:158:ARG:HH12	1:A:160:GLU:HG2	1.86	0.41
1:G:1076:PHE:O	1:G:1082:THR:HA	2.21	0.41
1:G:1133:VAL:O	1:G:1137:THR:HG23	2.21	0.41
1:A:129:ARG:HH21	1:A:197:LEU:HD12	1.85	0.41
3:C:266:PRO:O	3:C:267:HIS:C	2.60	0.41
1:D:364:VAL:HG22	1:D:375:LEU:CD1	2.51	0.41
1:D:807:PHE:HB3	1:D:811:GLU:OE1	2.21	0.41
2:E:841:LYS:HD2	2:E:1023:VAL:HB	2.03	0.41
1:A:883:SER:HB2	1:A:911:ALA:HB3	2.03	0.40
2:B:835:HIS:ND1	2:B:1029:ALA:HB1	2.36	0.40
2:E:717:SER:HB2	3:F:22:PRO:HD3	2.02	0.40
3:F:38:LEU:HD12	1:G:744:ASP:HB3	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:785:SER:HA	2:B:873:ILE:O	2.21	0.40
1:D:922:LEU:HD11	1:D:930:VAL:CG1	2.51	0.40
2:H:885:ASN:HB3	2:H:888:GLU:HB3	2.03	0.40
1:A:775:THR:O	1:A:775:THR:CG2	2.70	0.40
1:A:791:LEU:HD23	1:A:858:LEU:HD21	2.04	0.40
2:B:760:LEU:HD21	2:B:767:PHE:HD1	1.87	0.40
2:B:916:ALA:O	2:B:1008:ARG:NH1	2.50	0.40
1:D:369:ARG:HD2	1:D:369:ARG:HA	1.87	0.40
2:H:762:ASN:HB2	2:H:764:LYS:HG3	2.02	0.40
1:A:928:ARG:HA	1:A:928:ARG:HD3	1.93	0.40
1:G:330:ASP:HA	1:G:355:ASN:HB3	2.03	0.40
2:H:716:GLU:H	2:H:716:GLU:CD	2.25	0.40

All (3) 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:1118:SER:N	1:G:292:ASP:OD2[2_565]	2.07	0.13
1:A:1118:SER:OG	1:G:290:GLN:OE1[2_565]	2.12	0.08
1:A:1118:SER:H	1:G:292:ASP:OD2[2_565]	1.54	0.06

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%)	796 (97%)	26 (3%)	0	100	100
1	D	823/840 (98%)	804 (98%)	18 (2%)	1 (0%)	51	83
1	G	822/840 (98%)	797 (97%)	25 (3%)	0	100	100
2	B	326/344 (95%)	318 (98%)	8 (2%)	0	100	100
2	E	326/344 (95%)	316 (97%)	10 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	H	326/344 (95%)	315 (97%)	11 (3%)	0	100	100
3	C	246/271 (91%)	244 (99%)	2 (1%)	0	100	100
3	F	246/271 (91%)	243 (99%)	3 (1%)	0	100	100
3	I	246/271 (91%)	244 (99%)	2 (1%)	0	100	100
All	All	4183/4365 (96%)	4077 (98%)	105 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
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%)	717 (99%)	4 (1%)	86	94
1	D	722/728 (99%)	718 (99%)	4 (1%)	86	94
1	G	721/728 (99%)	716 (99%)	5 (1%)	84	94
2	B	296/308 (96%)	293 (99%)	3 (1%)	76	90
2	E	296/308 (96%)	291 (98%)	5 (2%)	60	83
2	H	296/308 (96%)	292 (99%)	4 (1%)	67	86
3	C	223/242 (92%)	221 (99%)	2 (1%)	78	91
3	F	223/242 (92%)	221 (99%)	2 (1%)	78	91
3	I	223/242 (92%)	218 (98%)	5 (2%)	52	79
All	All	3721/3834 (97%)	3687 (99%)	34 (1%)	78	91

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	870	VAL
1	A	986	ASP

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Mol	Chain	Res	Type
1	A	995	VAL
1	A	1036	MET
2	B	797	GLN
2	B	883	LEU
2	B	897	ILE
3	C	231	TYR
3	C	257	LEU
1	D	7	VAL
1	D	224	GLU
1	D	746	SER
1	D	1086	THR
2	E	728	ASP
2	E	801	ASP
2	E	860	ILE
2	E	883	LEU
2	E	911	GLU
3	F	76	ILE
3	F	231	TYR
1	G	232	ILE
1	G	725	CYS
1	G	794	ILE
1	G	1139	ILE
1	G	1140	HIS
2	H	858	ARG
2	H	896	VAL
2	H	897	ILE
2	H	1006	SER
3	I	20	THR
3	I	142	VAL
3	I	231	TYR
3	I	264	GLN
3	I	267	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	1040	HIS
2	H	999	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	1.24	0	10,14,16	1.52	1 (10%)
2	TPO	E	893	2	8,10,11	1.31	1 (12%)	10,14,16	1.03	1 (10%)
2	TPO	H	893	2	8,10,11	2.05	3 (37%)	10,14,16	1.19	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. '-' means no outliers of that kind were identified.

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

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	893	TPO	P-O1P	3.82	1.62	1.50
2	H	893	TPO	P-OG1	2.59	1.64	1.59
2	E	893	TPO	P-O2P	2.11	1.63	1.54
2	H	893	TPO	P-O2P	2.08	1.62	1.54

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	893	TPO	P-OG1-CB	-3.62	112.26	123.21
2	E	893	TPO	P-OG1-CB	-2.29	116.30	123.21
2	H	893	TPO	CG2-CB-CA	-2.07	109.08	113.16

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	893	TPO	O-C-CA-CB
2	E	893	TPO	O-C-CA-CB
2	H	893	TPO	O-C-CA-CB

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	H	893	TPO	1	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

42 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	1207	-	4,4,4	0.25	0	6,6,6	0.07	0
4	SO4	H	1102	-	4,4,4	0.20	0	6,6,6	0.16	0
4	SO4	A	1201	-	4,4,4	0.21	0	6,6,6	0.14	0
4	SO4	B	1103	-	4,4,4	0.20	0	6,6,6	0.06	0
4	SO4	G	1202	-	4,4,4	0.18	0	6,6,6	0.08	0
4	SO4	H	1105	-	4,4,4	0.18	0	6,6,6	0.08	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	RP9	B	1101	-	25,25,25	0.76	0	33,34,34	0.98	1 (3%)
4	SO4	D	1206	-	4,4,4	0.30	0	6,6,6	0.13	0
4	SO4	B	1102	-	4,4,4	0.22	0	6,6,6	0.10	0
4	SO4	G	1201	-	4,4,4	0.15	0	6,6,6	0.09	0
4	SO4	G	1205	-	4,4,4	0.19	0	6,6,6	0.08	0
4	SO4	C	301	-	4,4,4	0.19	0	6,6,6	0.12	0
4	SO4	C	303	-	4,4,4	0.19	0	6,6,6	0.10	0
4	SO4	D	1208	-	4,4,4	0.19	0	6,6,6	0.08	0
4	SO4	C	302	-	4,4,4	0.23	0	6,6,6	0.12	0
4	SO4	D	1211	-	4,4,4	0.20	0	6,6,6	0.04	0
4	SO4	D	1205	-	4,4,4	0.21	0	6,6,6	0.06	0
4	SO4	H	1104	-	4,4,4	0.17	0	6,6,6	0.06	0
4	SO4	D	1203	-	4,4,4	0.16	0	6,6,6	0.10	0
4	SO4	G	1203	-	4,4,4	0.17	0	6,6,6	0.14	0
4	SO4	I	302	-	4,4,4	0.16	0	6,6,6	0.08	0
4	SO4	D	1204	-	4,4,4	0.16	0	6,6,6	0.19	0
4	SO4	D	1209	-	4,4,4	0.21	0	6,6,6	0.05	0
5	RP9	D	1201	-	25,25,25	0.71	0	33,34,34	1.00	2 (6%)
4	SO4	A	1202	-	4,4,4	0.20	0	6,6,6	0.09	0
4	SO4	E	1101	-	4,4,4	0.18	0	6,6,6	0.08	0
4	SO4	H	1103	-	4,4,4	0.25	0	6,6,6	0.08	0
4	SO4	F	301	-	4,4,4	0.19	0	6,6,6	0.10	0
4	SO4	F	302	-	4,4,4	0.20	0	6,6,6	0.08	0
4	SO4	G	1204	-	4,4,4	0.20	0	6,6,6	0.09	0
4	SO4	F	304	-	4,4,4	0.17	0	6,6,6	0.13	0
5	RP9	H	1101	-	25,25,25	0.77	0	33,34,34	1.06	2 (6%)
4	SO4	D	1210	-	4,4,4	0.19	0	6,6,6	0.07	0
4	SO4	G	1207	-	4,4,4	0.22	0	6,6,6	0.04	0
4	SO4	G	1206	-	4,4,4	0.24	0	6,6,6	0.08	0
4	SO4	D	1202	-	4,4,4	0.24	0	6,6,6	0.08	0
4	SO4	A	1203	-	4,4,4	0.22	0	6,6,6	0.08	0
4	SO4	I	301	-	4,4,4	0.18	0	6,6,6	0.09	0
4	SO4	A	1204	-	4,4,4	0.19	0	6,6,6	0.05	0
4	SO4	A	1205	-	4,4,4	0.15	0	6,6,6	0.13	0
4	SO4	I	303	-	4,4,4	0.20	0	6,6,6	0.10	0
4	SO4	F	303	-	4,4,4	0.17	0	6,6,6	0.15	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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	RP9	H	1101	-	-	2/9/9/9	0/3/3/3
5	RP9	D	1201	-	-	2/9/9/9	0/3/3/3
5	RP9	B	1101	-	-	2/9/9/9	0/3/3/3

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	1201	RP9	C9-N1-C8	3.17	122.47	119.20
5	B	1101	RP9	C9-N1-C8	3.07	122.37	119.20
5	H	1101	RP9	C9-N1-C8	3.06	122.35	119.20
5	H	1101	RP9	C10-C9-N1	2.36	114.98	111.92
5	D	1201	RP9	C1-C7-N1	2.05	115.00	113.80

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	1101	RP9	C10-C9-N1-C8
5	D	1201	RP9	C10-C9-N1-C8
5	H	1101	RP9	C10-C9-N1-C8
5	B	1101	RP9	C10-C9-N1-C7
5	D	1201	RP9	C10-C9-N1-C7
5	H	1101	RP9	C10-C9-N1-C7

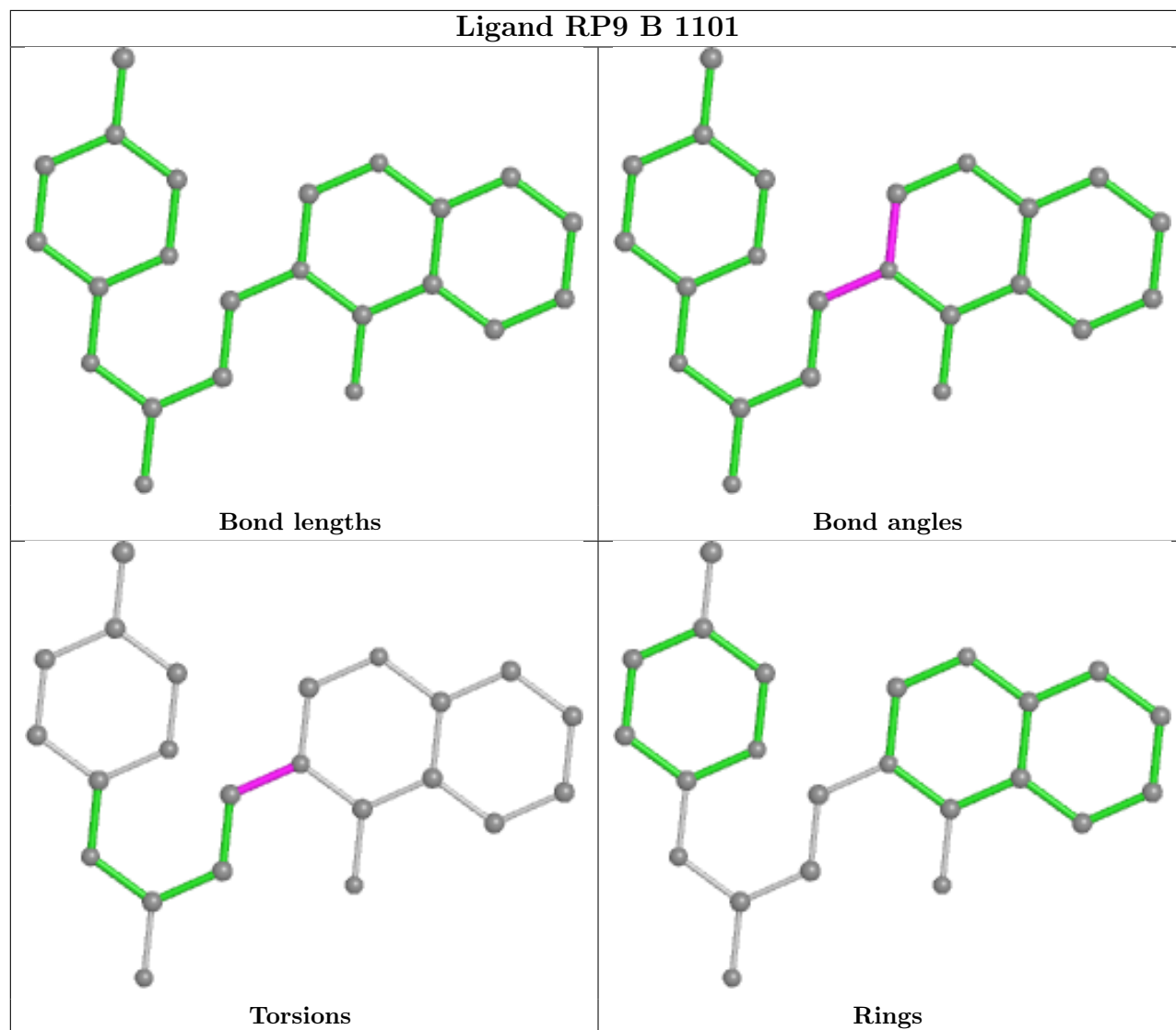
There are no ring outliers.

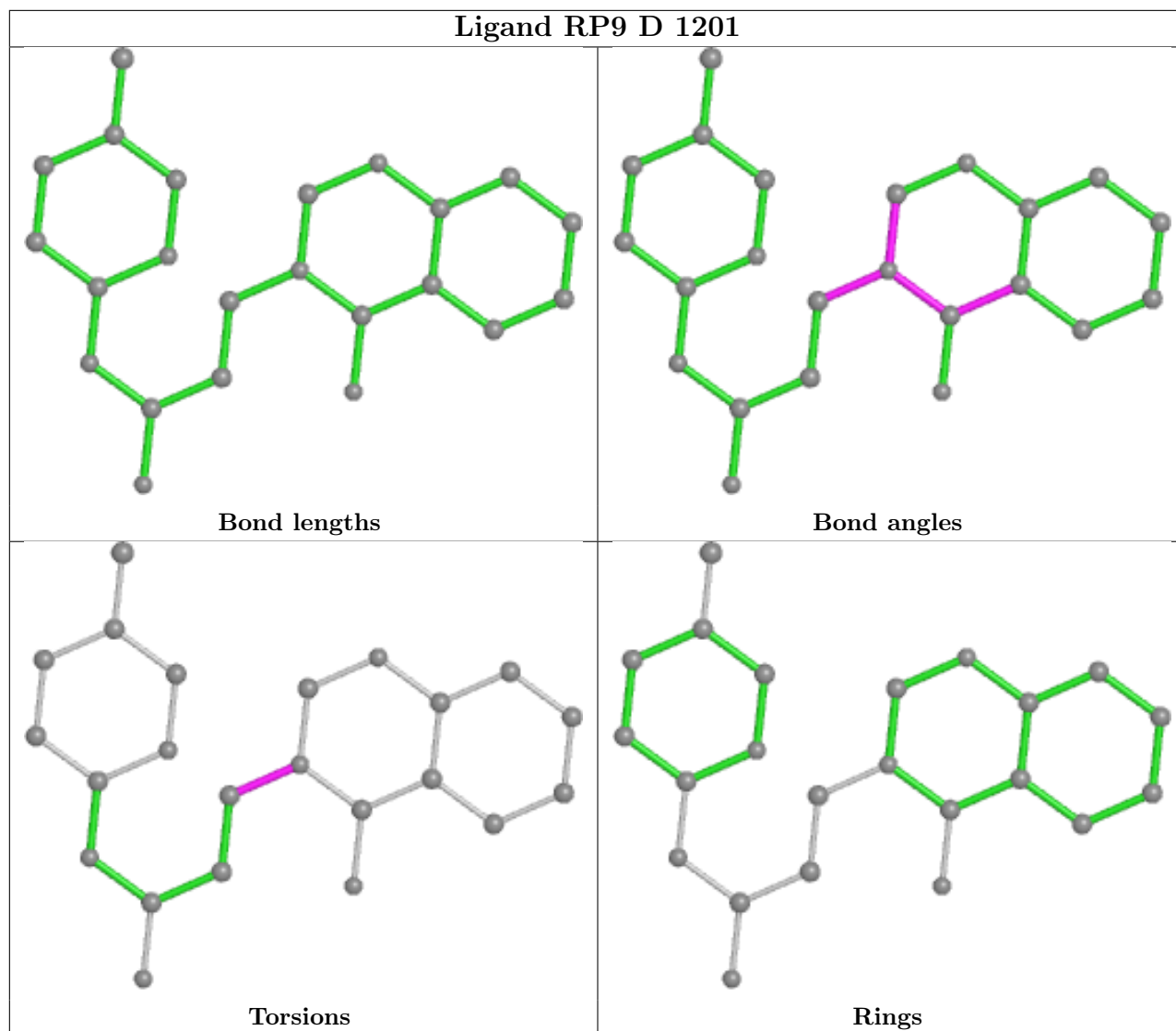
2 monomers are involved in 2 short contacts:

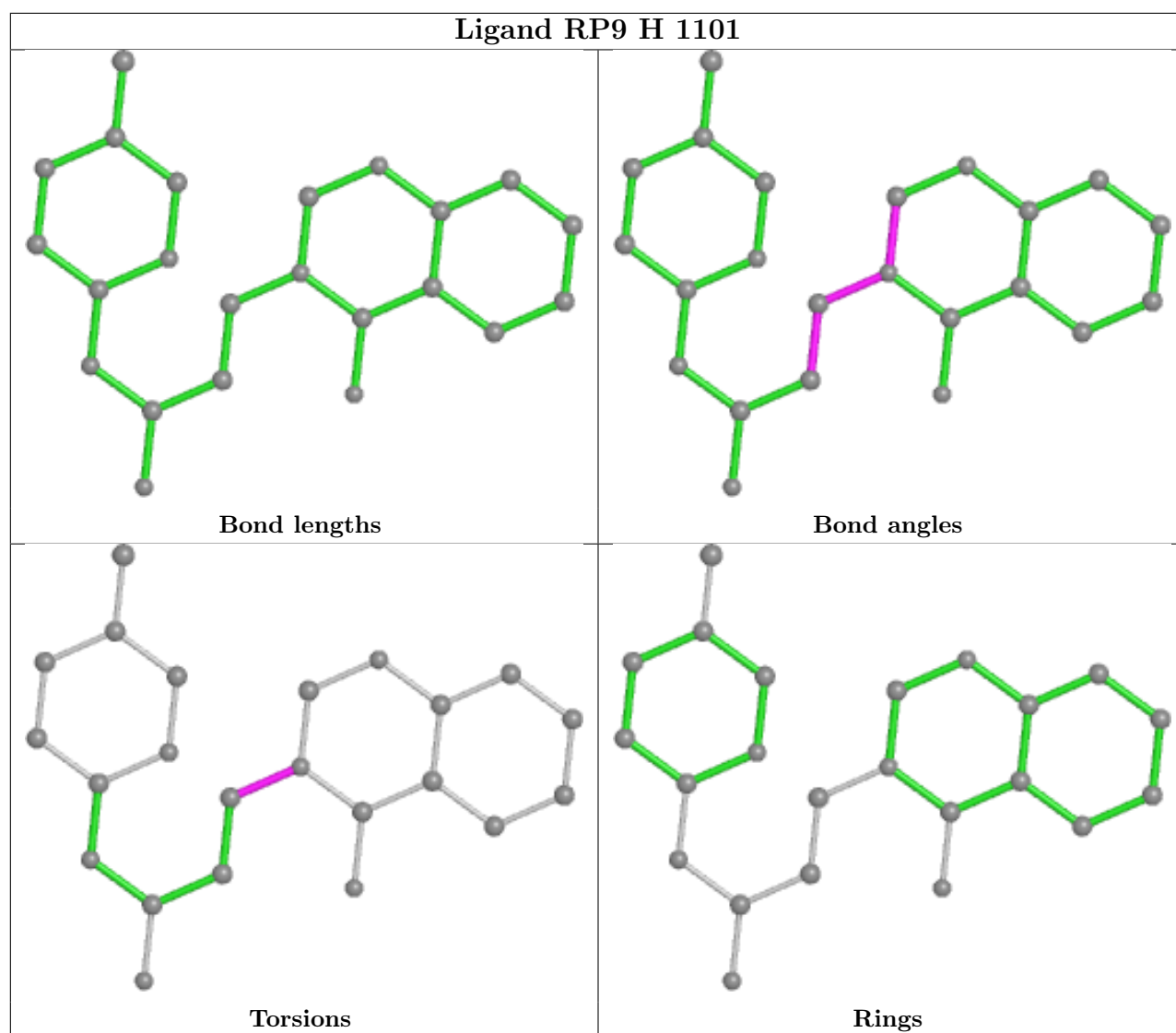
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	1101	RP9	1	0
4	D	1204	SO4	1	0

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 [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%)	0.64	77 (9%) 8 5	98, 138, 208, 307	0
1	D	827/840 (98%)	0.52	39 (4%) 31 19	89, 128, 199, 258	0
1	G	826/840 (98%)	0.59	71 (8%) 10 5	97, 138, 212, 307	0
2	B	328/344 (95%)	0.79	43 (13%) 3 2	109, 143, 210, 258	0
2	E	328/344 (95%)	0.77	32 (9%) 7 4	92, 134, 201, 286	0
2	H	328/344 (95%)	0.78	25 (7%) 13 7	84, 117, 196, 258	0
3	C	248/271 (91%)	0.55	15 (6%) 21 12	101, 130, 167, 234	0
3	F	248/271 (91%)	0.60	6 (2%) 59 44	87, 110, 152, 227	0
3	I	248/271 (91%)	0.51	7 (2%) 53 37	87, 114, 151, 247	0
All	All	4207/4365 (96%)	0.62	315 (7%) 14 8	84, 131, 203, 307	0

All (315) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	1043	TRP	14.2
1	A	1017	LEU	9.2
2	B	1043	TRP	8.1
2	B	1035	HIS	8.0
2	H	1039	CYS	7.3
2	H	1035	HIS	7.0
2	E	1040	HIS	6.6
2	H	1043	TRP	6.5
3	F	264	GLN	6.4
2	E	1035	HIS	6.2
3	C	267	HIS	5.6
2	E	882	ARG	5.0
2	B	884	TYR	4.8
2	E	1039	CYS	4.7
2	H	1033	LEU	4.6

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Mol	Chain	Res	Type	RSRZ
3	I	267	HIS	4.5
2	H	798	ASP	4.5
1	A	1097	PHE	4.4
3	F	263	GLN	4.3
1	D	2	SER	4.3
2	B	1033	LEU	4.2
2	B	883	LEU	4.2
1	G	318	ASP	4.2
1	A	297	LEU	4.1
1	A	1016	ASN	4.1
1	A	1018	GLY	4.1
2	B	828	LEU	4.0
1	G	291	MET	4.0
3	I	266	PRO	4.0
2	B	878	PHE	4.0
2	B	1039	CYS	3.9
1	G	131	ILE	3.9
2	E	896	VAL	3.9
1	A	131	ILE	3.9
2	B	886	SER	3.9
1	A	926	LEU	3.9
2	B	896	VAL	3.9
3	F	266	PRO	3.8
2	H	890	ARG	3.8
3	C	155	LEU	3.7
3	F	267	HIS	3.7
1	A	89	LEU	3.6
1	A	367	LEU	3.6
2	B	720	GLY	3.6
1	A	77	LEU	3.6
2	B	776	LYS	3.5
1	A	1114	TYR	3.5
2	H	828	LEU	3.5
1	A	1115	ASP	3.5
1	A	79	ILE	3.5
2	B	932	LYS	3.5
1	A	57	MET	3.5
1	A	39	LEU	3.4
1	G	133	LEU	3.4
1	G	253	ILE	3.4
1	G	306	GLY	3.4
1	A	195	VAL	3.4

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Mol	Chain	Res	Type	RSRZ
2	B	826	SER	3.4
2	B	802	PHE	3.3
2	H	839	PHE	3.3
1	G	303	GLU	3.3
1	D	1129	LEU	3.3
2	H	829	VAL	3.3
1	G	317	LEU	3.3
1	G	64	MET	3.3
1	A	87	CYS	3.3
1	A	60	LYS	3.2
1	A	135	LEU	3.2
1	G	323	PHE	3.2
2	B	800	LEU	3.2
1	G	1097	PHE	3.2
2	B	831	PHE	3.2
1	A	246	LEU	3.2
1	A	1029	LEU	3.2
1	G	1129	LEU	3.2
1	D	133	LEU	3.2
1	A	953	TRP	3.2
1	A	33	ILE	3.2
1	G	280	LEU	3.1
2	E	886	SER	3.1
2	H	1040	HIS	3.1
1	A	930	VAL	3.1
1	D	23	PHE	3.0
1	A	273	LEU	3.0
1	G	387	LEU	3.0
2	B	855	PHE	3.0
1	A	1035	GLY	3.0
2	E	1041	GLU	3.0
2	B	860	ILE	3.0
2	B	755	LEU	3.0
2	H	1041	GLU	3.0
2	B	829	VAL	2.9
2	B	875	LEU	2.9
1	G	327	ARG	2.9
1	A	145	LEU	2.9
2	E	829	VAL	2.9
1	A	32	LEU	2.9
1	A	64	MET	2.9
1	D	390	ILE	2.9

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Mol	Chain	Res	Type	RSRZ
2	E	828	LEU	2.9
1	G	1040	VAL	2.9
1	A	9	ALA	2.8
2	E	831	PHE	2.8
1	A	61	ILE	2.8
1	A	1019	GLU	2.8
1	D	328	LEU	2.8
1	A	23	PHE	2.8
1	G	100	ILE	2.8
2	H	772	ILE	2.8
2	E	890	ARG	2.8
2	H	1038	ASP	2.8
2	H	738	TYR	2.8
2	E	878	PHE	2.8
1	G	911	ALA	2.8
1	G	1076	PHE	2.8
2	B	890	ARG	2.8
1	A	933	LEU	2.8
1	G	314	LEU	2.8
1	D	195	VAL	2.7
2	B	839	PHE	2.7
1	A	356	LEU	2.7
1	A	327	ARG	2.7
1	G	9	ALA	2.7
1	G	232	ILE	2.7
2	E	867	LEU	2.7
1	G	1039	LEU	2.7
1	A	1079	GLU	2.7
1	A	304	LEU	2.7
1	G	5	TYR	2.6
2	E	1042	LEU	2.6
2	B	913	TYR	2.6
2	B	865	ILE	2.6
1	D	1	MET	2.6
1	D	91	TYR	2.6
1	D	317	LEU	2.6
1	G	1043	LEU	2.6
2	E	778	LEU	2.6
1	G	858	LEU	2.6
1	D	376	VAL	2.6
1	A	133	LEU	2.6
1	D	998	PHE	2.6

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Mol	Chain	Res	Type	RSRZ
1	D	31	LEU	2.6
1	G	66	LEU	2.6
1	D	9	ALA	2.6
1	A	63	VAL	2.6
1	G	1118	SER	2.6
1	G	77	LEU	2.6
1	G	230	ILE	2.6
3	F	181	LEU	2.5
1	A	143	ILE	2.5
1	D	121	ILE	2.5
1	A	152	LEU	2.5
2	E	826	SER	2.5
1	A	78	PHE	2.5
2	E	839	PHE	2.5
2	E	802	PHE	2.5
1	G	1004	VAL	2.5
1	G	966	LEU	2.5
2	B	811	LEU	2.5
2	B	864	ASN	2.5
2	B	867	LEU	2.5
3	F	254	ILE	2.5
1	A	914	LEU	2.5
2	E	906	LEU	2.5
1	D	237	ILE	2.5
1	D	5	TYR	2.5
2	H	775	ILE	2.5
2	E	875	LEU	2.5
2	B	935	ILE	2.5
2	H	1032	ASP	2.5
2	E	972	MET	2.4
1	G	1108	VAL	2.4
2	E	1033	LEU	2.4
2	B	775	ILE	2.4
2	E	945	LEU	2.4
1	A	59	GLY	2.4
1	D	55	VAL	2.4
1	A	140	PHE	2.4
1	G	237	ILE	2.4
1	A	359	ILE	2.4
3	C	76	ILE	2.4
1	A	1000	LEU	2.4
1	D	761	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	169	PHE	2.4
3	C	161	TYR	2.4
1	A	100	ILE	2.4
1	D	66	LEU	2.4
2	E	738	TYR	2.4
1	D	974	LEU	2.4
3	C	147	LEU	2.4
3	C	181	LEU	2.4
1	G	2	SER	2.4
2	E	881	ALA	2.4
1	D	360	VAL	2.3
1	D	1030	PHE	2.3
2	B	1041	GLU	2.3
1	A	1129	LEU	2.3
1	D	32	LEU	2.3
1	D	1004	VAL	2.3
1	G	36	ASN	2.3
1	A	31	LEU	2.3
1	A	285	LEU	2.3
2	B	803	LYS	2.3
1	G	390	ILE	2.3
3	C	132	PHE	2.3
1	A	792	LEU	2.3
2	B	781	LEU	2.3
1	A	19	VAL	2.3
1	G	302	VAL	2.3
2	H	767	PHE	2.3
1	G	49	LEU	2.3
1	G	272	LEU	2.3
1	G	336	LEU	2.3
1	A	1008	CYS	2.3
1	G	283	LEU	2.3
2	B	926	LEU	2.3
1	G	290	GLN	2.3
1	G	180	PHE	2.3
1	G	297	LEU	2.3
2	H	917	ILE	2.3
1	G	1088	PHE	2.3
1	G	143	ILE	2.3
2	B	986	PHE	2.3
1	G	1019	GLU	2.2
1	A	977	CYS	2.2

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Mol	Chain	Res	Type	RSRZ
3	C	164	LEU	2.2
2	E	935	ILE	2.2
1	D	1133	VAL	2.2
3	C	153	PHE	2.2
1	A	328	LEU	2.2
1	G	39	LEU	2.2
1	G	258	ILE	2.2
1	D	159	LEU	2.2
1	G	32	LEU	2.2
1	G	974	LEU	2.2
2	E	803	LYS	2.2
2	B	823	LEU	2.2
1	D	1132	VAL	2.2
1	D	297	LEU	2.2
3	C	197	LEU	2.2
1	A	1037	ILE	2.2
1	D	231	ILE	2.2
1	G	78	PHE	2.2
1	G	79	ILE	2.2
1	G	231	ILE	2.2
2	B	799	ALA	2.2
1	A	830	ILE	2.2
2	H	873	ILE	2.2
1	A	34	ALA	2.2
3	I	66	LEU	2.2
1	G	324	VAL	2.2
3	C	222	ILE	2.2
1	G	328	LEU	2.2
1	G	69	PRO	2.2
3	I	264	GLN	2.2
1	D	180	PHE	2.2
2	B	767	PHE	2.2
2	B	809	PHE	2.2
3	I	64	LEU	2.2
1	A	1116	ASP	2.2
2	B	798	ASP	2.2
1	A	858	LEU	2.2
2	H	801	ASP	2.2
2	H	955	PRO	2.2
1	A	6	VAL	2.2
1	G	1094	ILE	2.2
3	C	116	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	39	LEU	2.1
2	B	929	LEU	2.1
2	H	826	SER	2.1
2	H	964	ILE	2.1
1	G	88	ILE	2.1
1	G	792	LEU	2.1
1	D	377	THR	2.1
3	C	194	CYS	2.1
1	A	1139	ILE	2.1
1	A	849	VAL	2.1
1	D	253	ILE	2.1
1	G	321	VAL	2.1
3	C	156	GLN	2.1
1	D	232	ILE	2.1
1	A	317	LEU	2.1
1	A	91	TYR	2.1
2	E	913	TYR	2.1
1	A	752	LEU	2.1
1	D	356	LEU	2.1
3	C	146	ILE	2.1
1	A	912	LEU	2.1
1	D	1000	LEU	2.1
1	A	358	PRO	2.1
1	G	1037	ILE	2.1
2	E	860	ILE	2.1
1	A	49	LEU	2.1
1	G	997	LEU	2.1
2	B	951	LEU	2.1
1	D	140	PHE	2.1
1	A	381	ALA	2.1
1	D	33	ILE	2.1
3	I	26	TRP	2.1
1	G	117	GLU	2.1
1	A	88	ILE	2.1
1	G	1132	VAL	2.1
2	H	1031	PRO	2.1
1	A	816	LEU	2.1
1	G	132	GLY	2.1
1	A	1007	PHE	2.0
2	H	982	LEU	2.0
3	I	222	ILE	2.0
1	A	777	PRO	2.0

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Mol	Chain	Res	Type	RSRZ
1	G	310	ILE	2.0
1	G	921	ILE	2.0
1	G	139	LEU	2.0
1	G	836	VAL	2.0
2	E	907	LEU	2.0
2	E	908	LEU	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	TPO	E	893	11/12	0.83	0.21	190,199,241,241	6
2	TPO	H	893	11/12	0.84	0.24	134,144,195,195	5
2	TPO	B	893	11/12	0.86	0.14	187,202,243,245	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
4	SO4	I	303	5/5	0.65	0.22	149,153,156,206	0
4	SO4	C	302	5/5	0.71	0.14	158,162,173,226	0
4	SO4	D	1211	5/5	0.73	0.17	165,167,176,231	0
4	SO4	H	1102	5/5	0.74	0.26	159,164,164,212	0
4	SO4	F	302	5/5	0.76	0.26	158,163,169,230	0
4	SO4	D	1210	5/5	0.76	0.20	150,156,163,214	0
4	SO4	D	1204	5/5	0.76	0.37	139,146,162,232	0
4	SO4	A	1202	5/5	0.77	0.20	140,144,150,202	0
4	SO4	C	303	5/5	0.77	0.15	159,159,164,211	0

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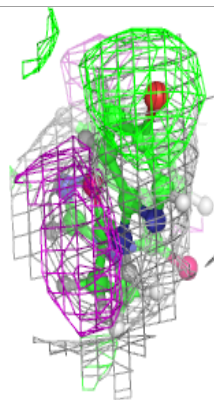
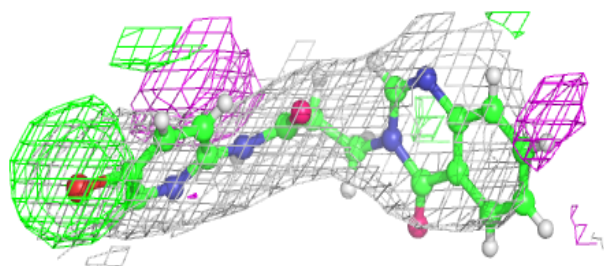
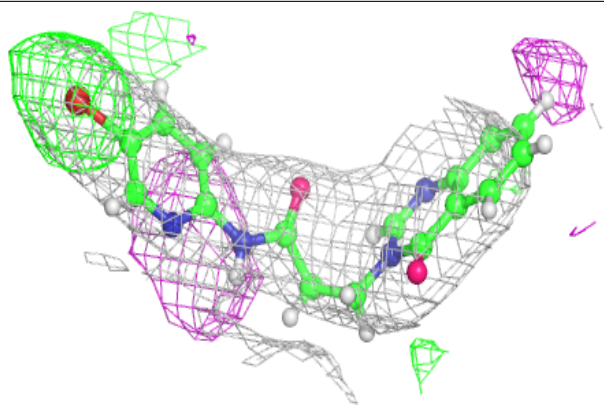
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	SO4	B	1102	5/5	0.78	0.12	173,176,179,246	0
4	SO4	G	1204	5/5	0.80	0.15	150,154,163,215	0
4	SO4	D	1203	5/5	0.80	0.17	134,140,147,188	0
4	SO4	G	1203	5/5	0.80	0.20	139,139,144,182	0
4	SO4	D	1209	5/5	0.81	0.17	177,182,188,246	0
4	SO4	H	1103	5/5	0.81	0.16	170,173,182,248	0
4	SO4	F	304	5/5	0.81	0.15	141,148,155,194	0
4	SO4	A	1203	5/5	0.82	0.17	171,172,177,224	0
4	SO4	G	1202	5/5	0.82	0.12	146,147,150,193	0
4	SO4	H	1105	5/5	0.82	0.29	146,148,162,212	0
4	SO4	G	1205	5/5	0.82	0.23	155,159,174,233	0
4	SO4	G	1207	5/5	0.83	0.41	165,167,176,238	0
4	SO4	D	1205	5/5	0.83	0.19	149,157,170,228	0
4	SO4	D	1206	5/5	0.83	0.13	152,157,161,214	0
4	SO4	D	1207	5/5	0.83	0.26	140,141,158,200	0
4	SO4	A	1205	5/5	0.83	0.22	146,149,172,213	0
5	RP9	H	1101	23/23	0.83	0.37	114,122,147,351	13
4	SO4	D	1208	5/5	0.84	0.16	156,166,168,239	0
4	SO4	F	301	5/5	0.85	0.27	136,147,154,219	0
4	SO4	A	1204	5/5	0.86	0.11	149,150,152,192	0
5	RP9	B	1101	23/23	0.86	0.32	120,125,156,350	13
5	RP9	D	1201	23/23	0.86	0.44	118,128,156,437	13
4	SO4	G	1206	5/5	0.86	0.11	165,170,180,220	0
4	SO4	G	1201	5/5	0.87	0.21	147,148,152,185	0
4	SO4	D	1202	5/5	0.87	0.17	136,140,147,184	0
4	SO4	E	1101	5/5	0.88	0.13	152,154,169,219	0
4	SO4	A	1201	5/5	0.88	0.14	146,146,149,179	0
4	SO4	H	1104	5/5	0.92	0.10	145,148,158,207	0
4	SO4	C	301	5/5	0.92	0.22	133,134,135,150	0
4	SO4	I	301	5/5	0.93	0.17	149,153,159,206	0
4	SO4	I	302	5/5	0.93	0.19	122,123,127,138	0
4	SO4	B	1103	5/5	0.94	0.08	161,161,172,232	0
4	SO4	F	303	5/5	0.95	0.20	115,115,119,130	0

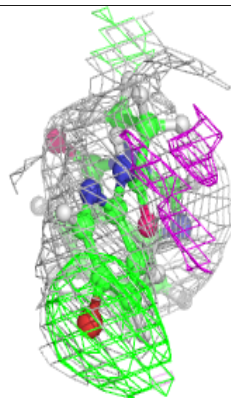
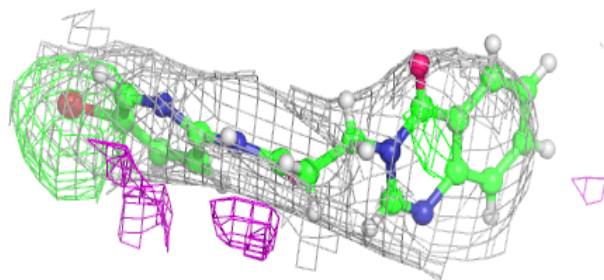
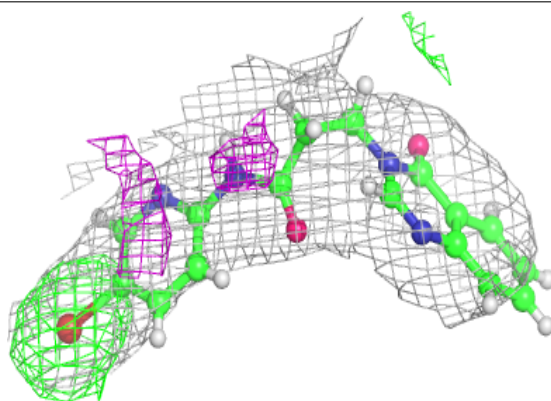
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

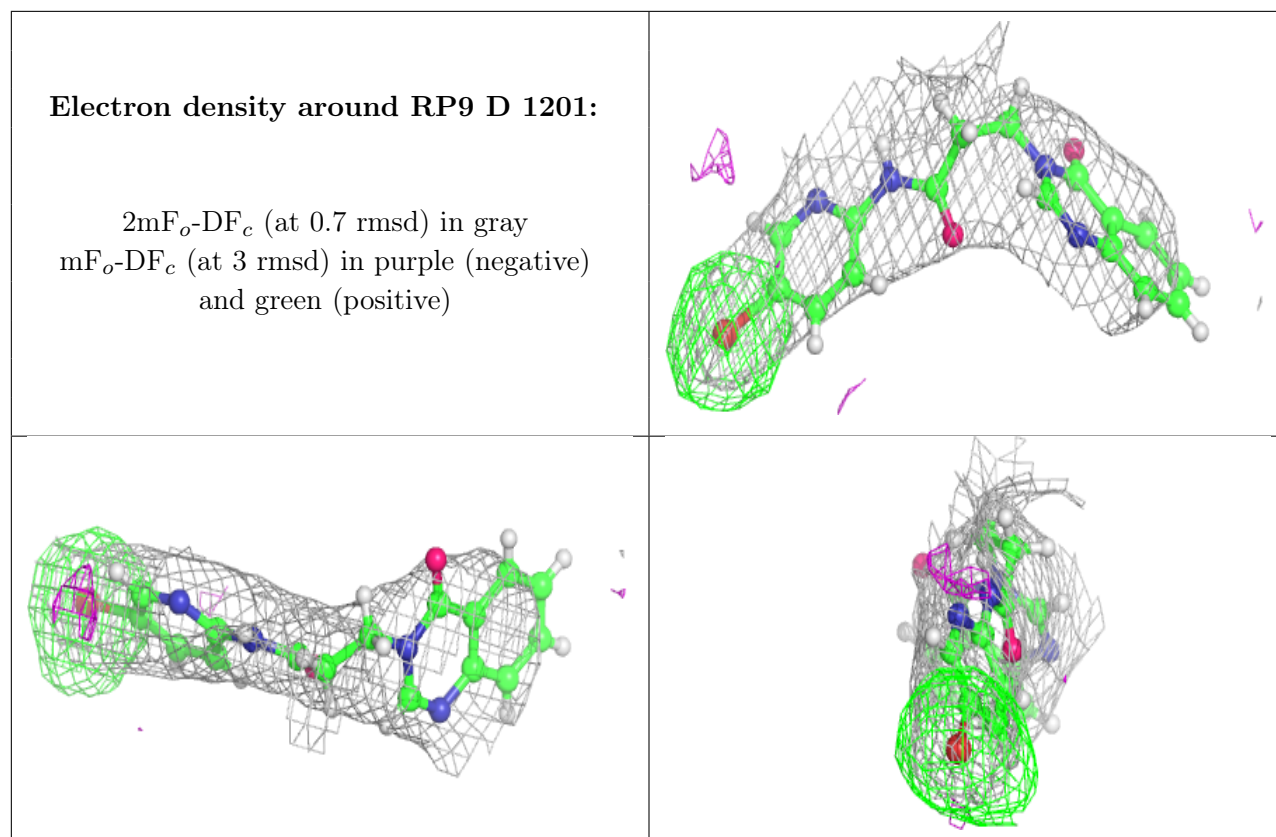
Electron density around RP9 H 1101:

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

**Electron density around RP9 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)





6.5 Other polymers [i](#)

There are no such residues in this entry.