



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 06:30 AM UTC

PDB ID : 8BUS / pdb_00008bus
Title : Structure of DDB1 bound to DS59-engaged CDK12-cyclin K
Authors : Kozicka, Z.; Kempf, G.; Focht, V.; Thoma, N.H.
Deposited on : 2022-11-30
Resolution : 3.26 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

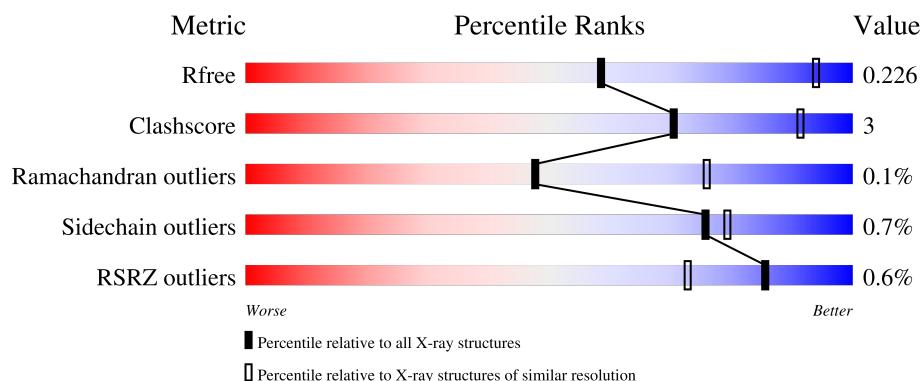
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.26 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1605 (3.30-3.22)
Clashscore	190562	1660 (3.30-3.22)
Ramachandran outliers	187476	1630 (3.30-3.22)
Sidechain outliers	187428	1629 (3.30-3.22)
RSRZ outliers	180081	1605 (3.30-3.22)

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	88% 10% .
1	D	840	% 88% 10% .
1	G	840	84% 14% .
2	B	344	% 84% 9% 6% .
2	E	344	3% 87% 8% .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	H	344	% 88% 8%
3	C	271	88%
3	F	271	87%
3	I	271	% 85% 7% 8%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 67538 atoms, of which 33668 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
1	D	826	Total	C	H	N	O	S	6451	0	0
			12938	4105	6451	1094	1252	36			
1	A	827	Total	C	H	N	O	S	6462	0	0
			12957	4111	6462	1095	1253	36			
1	G	826	Total	C	H	N	O	S	6453	0	0
			12939	4106	6453	1093	1251	36			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
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
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
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
2	E	329	Total	C	H	N	O	P	S	2698	0	0
			5385	1723	2698	454	492	1	17			
2	B	325	Total	C	H	N	O	P	S	2664	0	0
			5310	1695	2664	447	486	1	17			
2	H	330	Total	C	H	N	O	P	S	2703	0	0
			5396	1726	2703	455	494	1	17			

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
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
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
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
3	F	248	Total	C	H	N	O	S	2049	0	0
			4112	1341	2049	346	363	13			

Continued on next page...

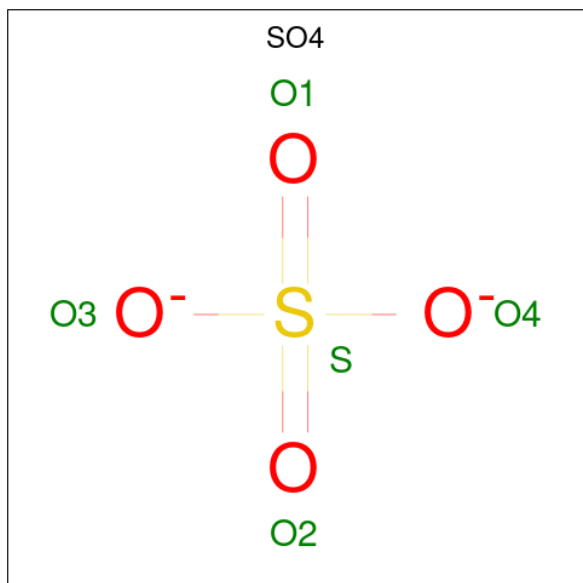
Continued from previous page...

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	C	248	Total	C	H	N	O	S	2049	0	0
			4112	1341	2049	346	363	13			
3	I	248	Total	C	H	N	O	S	2049	0	0
			4112	1341	2049	346	363	13			

There are 12 discrepancies between the modelled and reference sequences:

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

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



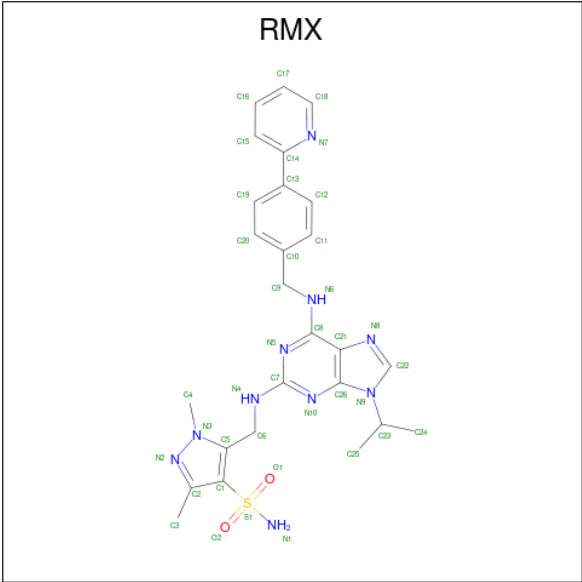
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	D	1	Total	O	S	0	0
			5	4	1		

Continued on next page...

Continued from previous page...

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

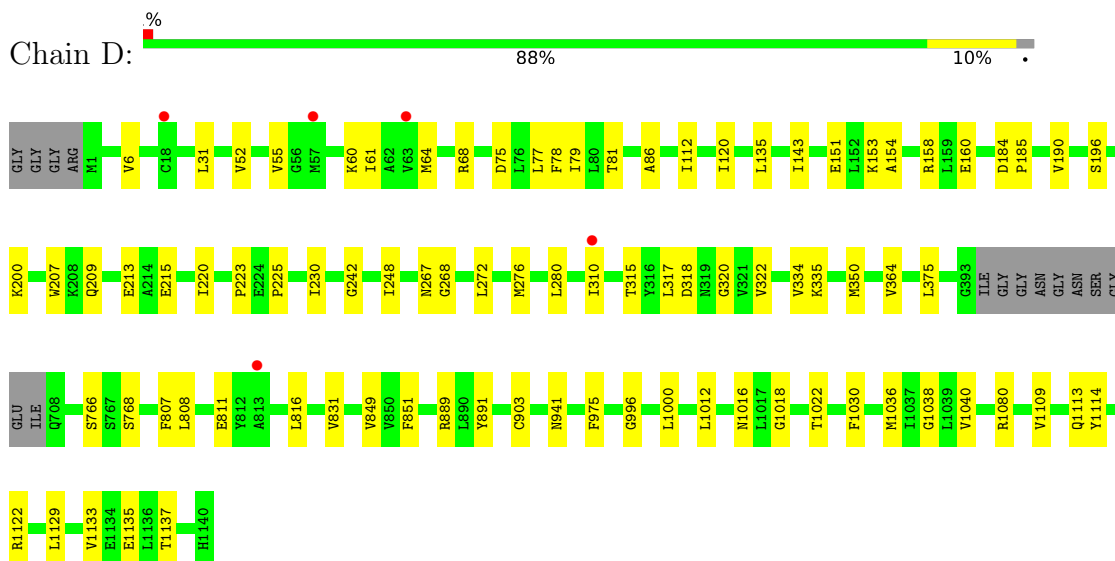
- Molecule 5 is 1,3-dimethyl-5-[[[9-propan-2-yl-6-[(4-pyridin-2-ylphenyl)methylamino]purin-2-yl]amino]methyl]pyrazole-4-sulfonamide (CCD ID: RMX) (formula: C₂₆H₃₀N₁₀O₂S) (labeled as "Ligand of Interest" by depositor).



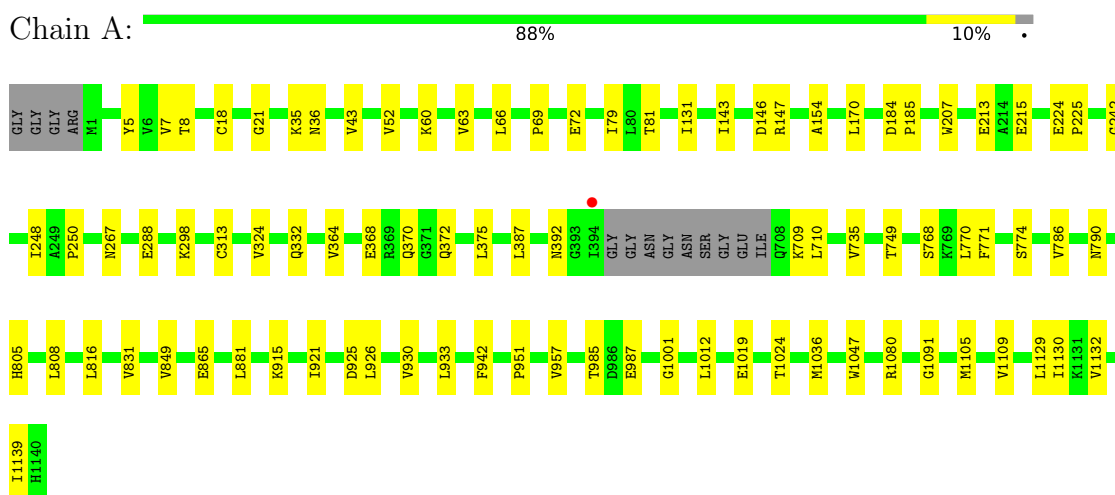
3 Residue-property plots [i](#)

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.

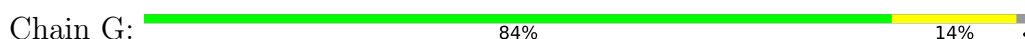
• Molecule 1: DNA damage-binding protein 1

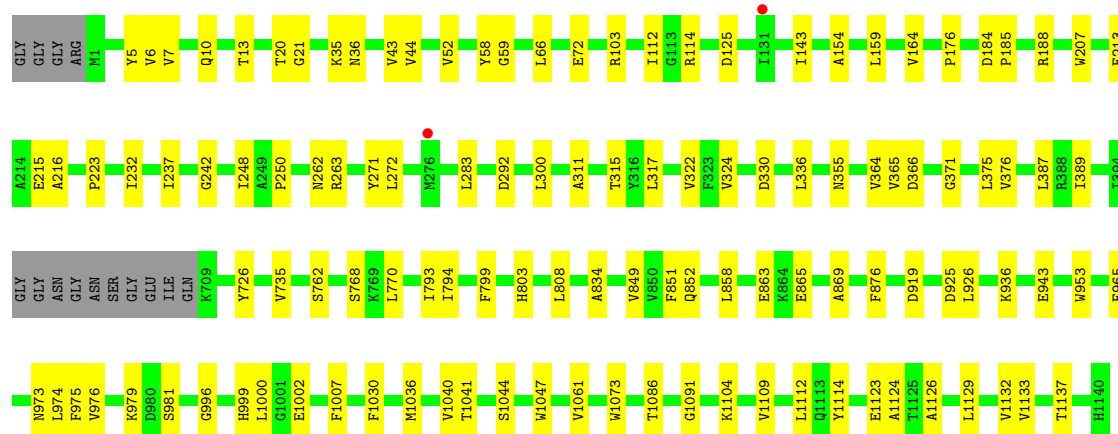


• Molecule 1: DNA damage-binding protein 1

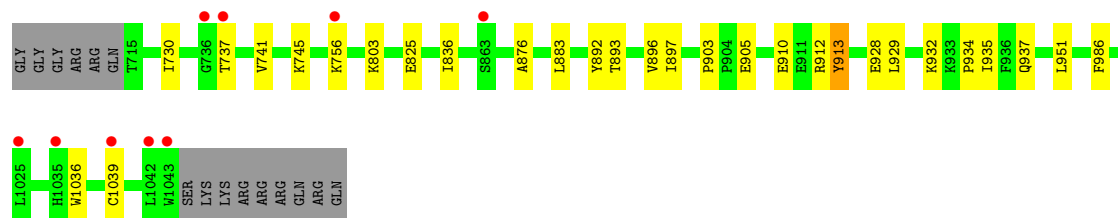
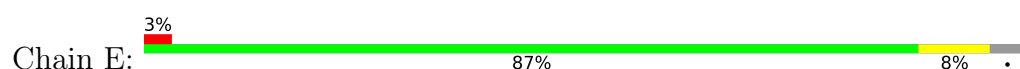


• Molecule 1: DNA damage-binding protein 1

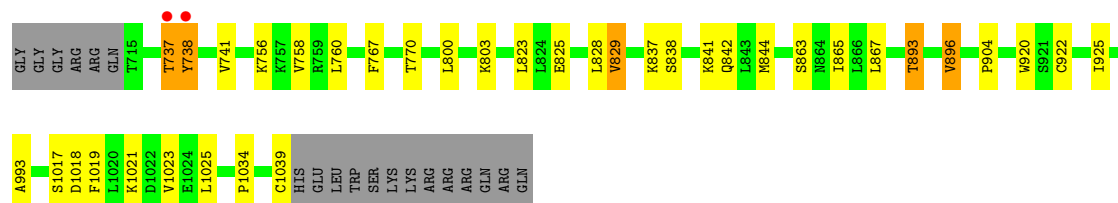
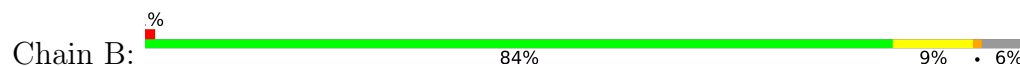




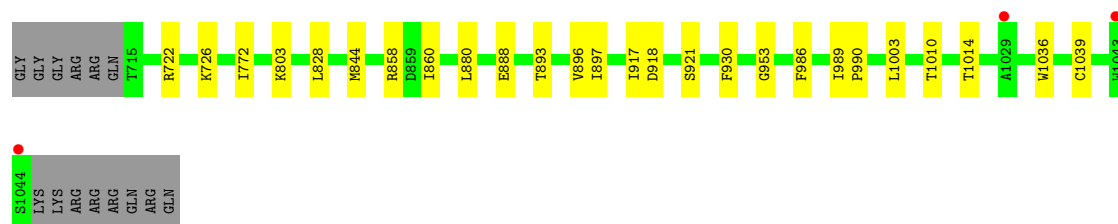
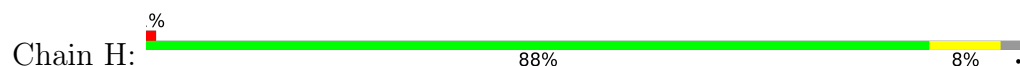
- Molecule 2: Cyclin-dependent kinase 12



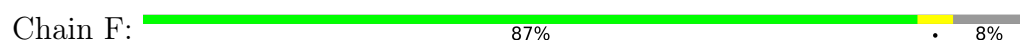
- Molecule 2: Cyclin-dependent kinase 12

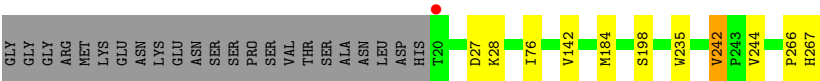


- Molecule 2: Cyclin-dependent kinase 12

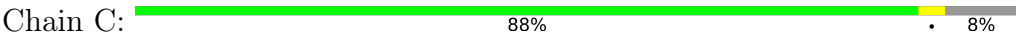


- Molecule 3: Cyclin-K

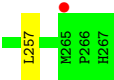
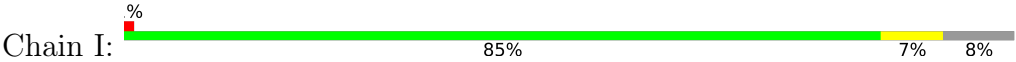




● Molecule 3: Cyclin-K



● 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	249.52Å 249.52Å 218.55Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	60.40 – 3.26 60.40 – 3.26	Depositor EDS
% Data completeness (in resolution range)	83.2 (60.40-3.26) 83.3 (60.40-3.26)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.45 (at 3.26Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.208 , 0.228 0.207 , 0.226	Depositor DCC
R_{free} test set	5017 reflections (4.10%)	wwPDB-VP
Wilson B-factor (Å ²)	119.1	Xtriage
Anisotropy	0.003	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 89.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.034 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	67538	wwPDB-VP
Average B, all atoms (Å ²)	142.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.62% 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: RMX, SO4, 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	0.16	0/6612	0.39	0/8942
1	D	0.17	0/6604	0.42	0/8931
1	G	0.16	0/6603	0.40	0/8930
2	B	0.22	0/2693	0.46	0/3630
2	E	0.21	0/2737	0.50	1/3691 (0.0%)
2	H	0.17	0/2743	0.38	0/3699
3	C	0.15	0/2120	0.34	0/2868
3	F	0.13	0/2120	0.33	0/2868
3	I	0.16	0/2120	0.38	0/2868
All	All	0.17	0/34352	0.41	1/46427 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	876	ALA	N-CA-C	5.73	123.00	110.80

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	6495	6462	6464	48	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	6487	6451	6451	44	1
1	G	6486	6453	6454	67	1
2	B	2646	2664	2663	25	1
2	E	2687	2698	2697	14	0
2	H	2693	2703	2702	15	0
3	C	2063	2049	2048	5	0
3	F	2063	2049	2048	10	0
3	I	2063	2049	2048	14	1
4	A	5	0	0	0	0
4	C	10	0	0	0	0
4	D	15	0	0	0	0
4	F	10	0	0	0	0
4	G	10	0	0	0	0
4	H	5	0	0	0	0
4	I	15	0	0	0	0
5	B	39	30	0	0	0
5	E	39	30	0	0	0
5	H	39	30	0	0	0
All	All	33870	33668	33575	230	2

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (230) 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:953:TRP:CH2	2:H:828:LEU:HD11	2.25	0.71
2:E:741:VAL:HG22	2:E:756:LYS:HG2	1.70	0.71
1:D:225:PRO:HG2	1:D:267:ASN:HB2	1.76	0.67
1:G:322:VAL:HG21	1:G:336:LEU:HD11	1.77	0.66
2:H:844:MET:HA	2:H:844:MET:HE2	1.78	0.64
1:G:7:VAL:HG22	1:G:1091:GLY:HA3	1.80	0.64
1:A:816:LEU:HD13	1:A:831:VAL:HG22	1.83	0.60
1:D:272:LEU:HD22	1:D:280:LEU:HD11	1.84	0.60
1:A:771:PHE:O	1:A:774:SER:HB2	2.03	0.59
3:C:231:TYR:OH	3:C:236:GLU:OE1	2.22	0.58
1:G:159:LEU:HD21	1:G:164:VAL:HG21	1.86	0.58
3:I:117:ILE:HG21	3:I:136:PRO:CB	2.33	0.58
1:A:7:VAL:HG22	1:A:1091:GLY:HA3	1.85	0.58
2:H:1010:THR:O	2:H:1014:THR:HG23	2.03	0.57
1:A:375:LEU:HB2	1:A:1012:LEU:HD21	1.87	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:770:LEU:HD13	1:A:865:GLU:HB2	1.87	0.57
1:G:834:ALA:HB2	1:G:869:ALA:HA	1.88	0.56
2:B:844:MET:HE1	2:B:922:CYS:SG	2.45	0.56
2:B:893:TPO:O	2:B:896:VAL:HG13	2.06	0.56
1:A:372:GLN:NE2	1:A:392:ASN:O	2.39	0.55
1:G:858:LEU:HD12	1:G:858:LEU:O	2.06	0.55
1:D:1022:THR:HG22	1:D:1135:GLU:OE2	2.06	0.55
1:D:6:VAL:HG22	1:D:1040:VAL:HG22	1.89	0.55
3:F:235:TRP:CZ2	3:F:244:VAL:HG22	2.41	0.55
1:G:271:TYR:HB2	1:G:283:LEU:HB3	1.87	0.55
2:H:722:ARG:HE	2:H:726:LYS:HG3	1.71	0.55
3:C:243:PRO:HG2	3:C:246:VAL:HG23	1.89	0.55
1:G:1002:GLU:HG3	1:G:1036:MET:HE3	1.88	0.54
2:E:803:LYS:HG3	3:F:142:VAL:HG21	1.90	0.54
2:E:951:LEU:HD21	2:E:986:PHE:HE2	1.73	0.54
2:B:993:ALA:HB2	2:B:1019:PHE:CE1	2.43	0.54
2:H:989:ILE:HG23	2:H:990:PRO:HD2	1.90	0.53
1:G:112:ILE:HD13	2:H:986:PHE:CE2	2.44	0.53
2:H:803:LYS:HA	3:I:142:VAL:HG11	1.91	0.53
1:A:21:GLY:HA3	1:A:66:LEU:HD13	1.90	0.52
1:G:262:ASN:O	1:G:272:LEU:N	2.31	0.52
2:B:738:TYR:HD2	2:B:770:THR:HG1	1.58	0.52
3:I:117:ILE:HG21	3:I:136:PRO:HB2	1.92	0.51
1:D:816:LEU:HD13	1:D:831:VAL:HG22	1.92	0.51
3:I:195:THR:CG2	3:I:257:LEU:HD11	2.40	0.51
1:A:207:TRP:HB3	1:A:242:GLY:HA2	1.92	0.51
1:A:1105:MET:SD	1:A:1130:ILE:HD11	2.50	0.51
1:D:889:ARG:HD2	1:D:891:TYR:CZ	2.45	0.51
1:D:1080:ARG:HD3	2:E:825:GLU:HA	1.92	0.51
3:F:184:MET:HE2	3:F:267:HIS:HA	1.92	0.51
3:I:91:PRO:HB3	3:I:131:GLN:HB3	1.92	0.51
1:A:213:GLU:HG2	1:A:215:GLU:H	1.75	0.51
1:G:5:TYR:HB3	1:G:1041:THR:HG23	1.93	0.51
1:A:925:ASP:OD1	1:A:926:LEU:N	2.44	0.51
1:G:925:ASP:OD1	1:G:926:LEU:N	2.44	0.50
1:A:18:CYS:SG	1:A:313:CYS:SG	3.08	0.50
2:B:1017:SER:O	2:B:1021:LYS:N	2.41	0.50
1:D:335:LYS:HB2	1:D:350:MET:SD	2.51	0.50
3:F:76:ILE:HD12	3:F:198:SER:HB3	1.93	0.50
1:A:288:GLU:HB2	1:A:298:LYS:HB2	1.93	0.50
1:D:768:SER:HB3	1:D:808:LEU:HD11	1.93	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:143:ILE:HG12	1:G:154:ALA:HB2	1.93	0.50
2:B:737:THR:OG1	2:B:738:TYR:N	2.45	0.50
2:H:772:ILE:HG23	3:I:155:LEU:HD13	1.94	0.50
1:A:370:GLN:C	1:A:372:GLN:H	2.20	0.49
1:D:364:VAL:HG22	1:D:375:LEU:HD13	1.93	0.49
1:G:1061:VAL:HG11	1:G:1104:LYS:HB3	1.93	0.49
1:D:1016:ASN:C	1:D:1018:GLY:H	2.19	0.49
1:A:768:SER:HB3	1:A:808:LEU:HD11	1.94	0.49
1:G:20:THR:HG23	1:G:315:THR:OG1	2.13	0.49
1:D:112:ILE:HD13	2:E:986:PHE:CE2	2.48	0.49
3:F:76:ILE:CD1	3:F:198:SER:HB3	2.43	0.49
1:D:207:TRP:HB3	1:D:242:GLY:HA2	1.94	0.49
1:A:368:GLU:OE1	1:A:368:GLU:N	2.45	0.49
3:I:117:ILE:HG21	3:I:136:PRO:HB3	1.95	0.49
2:E:730:ILE:HD11	2:E:745:LYS:CG	2.42	0.49
1:D:223:PRO:HD2	1:D:268:GLY:HA3	1.95	0.49
1:G:72:GLU:OE2	1:G:103:ARG:NH2	2.47	0.48
1:G:365:VAL:HG21	1:G:726:TYR:CE2	2.48	0.48
3:F:27:ASP:OD1	3:F:28:LYS:N	2.47	0.48
1:D:375:LEU:HB2	1:D:1012:LEU:HD21	1.95	0.48
3:F:235:TRP:HZ2	3:F:244:VAL:HG22	1.78	0.48
1:A:709:LYS:HG2	1:A:710:LEU:N	2.29	0.48
1:G:974:LEU:HD11	1:G:1000:LEU:HD22	1.94	0.48
1:A:1047:TRP:HZ3	1:A:1132:VAL:HG13	1.78	0.48
1:G:1047:TRP:HZ3	1:G:1132:VAL:HG13	1.78	0.48
1:A:1080:ARG:HD3	2:B:825:GLU:HA	1.95	0.47
3:I:195:THR:HG21	3:I:257:LEU:HD11	1.95	0.47
2:B:844:MET:HE2	2:B:844:MET:HA	1.96	0.47
2:B:865:ILE:HD12	2:B:925:ILE:HD13	1.97	0.47
2:B:841:LYS:HE2	2:B:1025:LEU:HD21	1.96	0.47
1:G:6:VAL:HG22	1:G:1040:VAL:HG22	1.96	0.47
3:F:242:VAL:O	3:F:242:VAL:HG12	2.14	0.47
1:A:224:GLU:N	1:A:225:PRO:HD2	2.30	0.47
1:A:324:VAL:HB	1:A:332:GLN:HB2	1.97	0.47
1:G:125:ASP:OD2	1:G:176:PRO:HB3	2.15	0.47
1:D:276:MET:HA	1:D:310:ILE:HG23	1.97	0.47
2:E:730:ILE:HD11	2:E:745:LYS:HG3	1.97	0.47
1:G:366:ASP:OD2	1:G:371:GLY:N	2.41	0.47
3:I:243:PRO:HG2	3:I:246:VAL:HG23	1.96	0.47
1:G:1109:VAL:HG11	1:G:1126:ALA:HA	1.95	0.47
1:G:979:LYS:O	1:G:981:SER:N	2.44	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:935:ILE:HD12	2:E:986:PHE:HZ	1.80	0.46
2:B:803:LYS:HG3	3:C:142:VAL:HG21	1.97	0.46
1:G:21:GLY:HA3	1:G:66:LEU:HD13	1.97	0.46
1:G:852:GLN:O	1:G:858:LEU:HA	2.15	0.46
1:A:35:LYS:O	1:A:36:ASN:C	2.58	0.46
2:B:893:TPO:O1P	2:B:893:TPO:HG22	2.15	0.46
1:D:143:ILE:HG12	1:D:154:ALA:HB2	1.97	0.46
1:A:915:LYS:HE3	1:A:957:VAL:O	2.16	0.46
1:G:232:ILE:HD13	1:G:237:ILE:HG23	1.97	0.46
1:G:936:LYS:HE3	1:G:943:GLU:OE1	2.16	0.45
3:I:117:ILE:HD11	3:I:140:VAL:HG21	1.97	0.45
1:D:1133:VAL:O	1:D:1137:THR:HG23	2.16	0.45
1:A:36:ASN:ND2	1:A:1001:GLY:O	2.46	0.45
2:H:858:ARG:NE	2:H:880:LEU:O	2.48	0.45
1:A:1109:VAL:HG12	1:A:1129:LEU:HD12	1.97	0.45
3:C:265:MET:HB2	3:C:267:HIS:ND1	2.31	0.45
1:G:248:ILE:HD12	1:G:300:LEU:O	2.16	0.45
1:G:58:TYR:HB3	1:G:1073:TRP:CB	2.46	0.45
1:G:213:GLU:HG2	1:G:215:GLU:H	1.81	0.45
1:G:114:ARG:HD3	2:H:930:PHE:O	2.17	0.45
1:G:975:PHE:HA	1:G:996:GLY:O	2.17	0.45
3:I:231:TYR:CE1	3:I:233:ARG:HB2	2.52	0.45
1:A:60:LYS:O	1:A:81:THR:HA	2.17	0.45
1:G:364:VAL:HG22	1:G:375:LEU:HD13	1.99	0.45
1:A:951:PRO:HG2	2:B:825:GLU:CB	2.47	0.44
1:G:10:GLN:O	1:G:1036:MET:HG2	2.17	0.44
1:D:1000:LEU:HD11	1:D:1036:MET:HE1	1.99	0.44
1:A:63:VAL:O	1:A:79:ILE:HA	2.17	0.44
2:E:892:TYR:HB3	2:E:913:TYR:CZ	2.53	0.44
1:G:13:THR:HB	1:G:355:ASN:HA	1.99	0.44
1:A:146:ASP:OD1	1:A:147:ARG:N	2.51	0.44
1:A:248:ILE:HG12	1:A:250:PRO:HD3	1.99	0.44
1:D:196:SER:O	1:D:200:LYS:N	2.49	0.44
1:G:762:SER:O	1:G:803:HIS:HA	2.18	0.44
1:G:223:PRO:HG3	1:G:263:ARG:HH11	1.82	0.44
1:G:1112:LEU:O	1:G:1123:GLU:HA	2.17	0.44
1:D:64:MET:HG3	1:D:77:LEU:HD11	2.00	0.44
1:D:220:ILE:HB	1:D:230:ILE:HB	2.00	0.44
1:G:770:LEU:HD13	1:G:865:GLU:HB2	2.00	0.44
1:D:213:GLU:HG2	1:D:215:GLU:H	1.82	0.44
1:A:131:ILE:HB	1:A:143:ILE:HB	1.99	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:207:TRP:HB3	1:G:242:GLY:HA2	1.98	0.43
1:G:1133:VAL:O	1:G:1137:THR:HG23	2.18	0.43
2:H:917:ILE:HG13	2:H:918:ASP:N	2.33	0.43
1:A:5:TYR:CE1	1:A:1091:GLY:HA2	2.54	0.43
2:B:828:LEU:O	2:B:1034:PRO:HD3	2.18	0.43
1:D:31:LEU:HD22	1:D:317:LEU:HD21	2.00	0.43
1:G:1007:PHE:CD1	1:G:1030:PHE:HB3	2.54	0.43
2:H:953:GLY:O	2:H:1003:LEU:HD11	2.19	0.43
1:G:849:VAL:HG11	1:G:851:PHE:CZ	2.54	0.43
1:D:849:VAL:HG11	1:D:851:PHE:CZ	2.53	0.43
2:E:928:GLU:O	2:E:932:LYS:HA	2.19	0.43
1:A:184:ASP:HB2	1:A:185:PRO:CD	2.49	0.43
1:G:1109:VAL:HG12	1:G:1129:LEU:HD12	2.00	0.43
1:D:184:ASP:HB2	1:D:185:PRO:CD	2.48	0.43
1:D:903:CYS:CB	1:D:941:ASN:HA	2.48	0.43
1:A:881:LEU:HD21	1:A:921:ILE:HG21	2.01	0.43
1:G:768:SER:HB3	1:G:808:LEU:HD11	2.01	0.43
1:G:973:ASN:OD1	1:G:999:HIS:ND1	2.52	0.43
2:E:836:ILE:HG23	2:E:929:LEU:HD13	2.01	0.42
1:A:43:VAL:HG23	1:A:52:VAL:HG11	2.01	0.42
1:G:311:ALA:HB2	1:G:324:VAL:HG13	2.00	0.42
1:D:975:PHE:HA	1:D:996:GLY:O	2.19	0.42
2:B:738:TYR:HD2	2:B:770:THR:OG1	2.03	0.42
2:B:738:TYR:CD1	2:B:758:VAL:HG22	2.55	0.42
2:B:738:TYR:CE1	2:B:758:VAL:HG22	2.54	0.42
1:D:68:ARG:HB2	1:D:75:ASP:OD1	2.19	0.42
1:A:368:GLU:N	1:A:368:GLU:CD	2.78	0.42
1:A:387:LEU:HD11	1:A:735:VAL:HG21	2.01	0.42
2:B:865:ILE:CD1	2:B:925:ILE:HD13	2.50	0.42
3:C:76:ILE:HD12	3:C:159:HIS:CE1	2.54	0.42
2:B:760:LEU:HD21	2:B:767:PHE:HD1	1.85	0.42
1:D:807:PHE:HB3	1:D:811:GLU:OE1	2.20	0.42
1:G:376:VAL:HG13	1:G:389:ILE:CD1	2.48	0.42
3:F:266:PRO:O	3:F:267:HIS:C	2.62	0.42
1:G:996:GLY:HA2	1:G:1086:THR:O	2.20	0.42
1:D:60:LYS:O	1:D:81:THR:HA	2.19	0.42
1:D:120:ILE:HG23	1:D:135:LEU:HD23	2.01	0.42
1:G:248:ILE:HG12	1:G:250:PRO:HD3	2.02	0.42
2:H:888:GLU:OE1	2:H:888:GLU:HA	2.19	0.42
1:A:790:ASN:HA	1:A:805:HIS:O	2.20	0.41
1:G:794:ILE:HG22	1:G:799:PHE:HA	2.01	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:35:LYS:O	1:G:36:ASN:C	2.63	0.41
1:G:188:ARG:NH1	1:G:216:ALA:O	2.53	0.41
2:E:934:PRO:HD2	2:E:937:GLN:OE1	2.21	0.41
2:B:741:VAL:HG22	2:B:756:LYS:HG3	2.02	0.41
1:G:184:ASP:HB2	1:G:185:PRO:CD	2.49	0.41
1:D:1109:VAL:HG12	1:D:1129:LEU:HD12	2.01	0.41
1:A:225:PRO:HG2	1:A:267:ASN:O	2.21	0.41
1:A:985:THR:HG22	1:A:987:GLU:H	1.85	0.41
1:G:44:VAL:HG21	1:G:317:LEU:HD22	2.01	0.41
1:G:387:LEU:HD11	1:G:735:VAL:HG21	2.02	0.41
1:D:1114:TYR:HB2	1:D:1122:ARG:HB3	2.03	0.41
1:A:8:THR:HG23	1:A:1036:MET:HE2	2.02	0.41
1:A:170:LEU:HD23	1:A:170:LEU:HA	1.93	0.41
1:A:933:LEU:HD22	1:A:942:PHE:HB3	2.03	0.41
2:B:838:SER:O	2:B:842:GLN:HG3	2.20	0.41
1:D:151:GLU:OE1	1:D:153:LYS:HE2	2.21	0.41
1:D:320:GLY:O	1:D:335:LYS:HA	2.20	0.41
1:D:322:VAL:N	1:D:334:VAL:O	2.53	0.41
1:D:1030:PHE:CZ	1:D:1038:GLY:HA3	2.56	0.41
2:B:800:LEU:O	2:B:800:LEU:HG	2.20	0.41
2:B:837:LYS:HB3	2:B:1023:VAL:HG21	2.02	0.41
2:B:904:PRO:HD3	2:B:920:TRP:CE2	2.55	0.41
1:G:876:PHE:CZ	1:G:919:ASP:HA	2.56	0.41
1:G:43:VAL:HG23	1:G:52:VAL:HG21	2.03	0.41
3:I:26:TRP:CD2	3:I:83:MET:HE2	2.56	0.41
1:D:1113:GLN:HA	1:D:1122:ARG:O	2.20	0.41
2:E:910:GLU:C	2:E:912:ARG:H	2.28	0.41
1:A:69:PRO:HG2	1:A:72:GLU:HG3	2.03	0.41
1:G:793:ILE:HG13	1:G:858:LEU:HD23	2.03	0.41
1:G:1114:TYR:CD1	1:G:1124:ALA:HB2	2.56	0.41
2:H:860:ILE:HB	2:H:921:SER:CB	2.51	0.41
1:A:364:VAL:HG22	1:A:375:LEU:HD13	2.03	0.41
1:A:749:THR:HG21	1:A:786:VAL:HG11	2.03	0.41
1:G:59:GLY:HA2	1:G:1073:TRP:CE3	2.56	0.41
1:D:320:GLY:HA3	1:D:335:LYS:HG3	2.03	0.40
1:G:768:SER:OG	1:G:863:GLU:OE2	2.26	0.40
2:H:803:LYS:HA	3:I:142:VAL:CG1	2.51	0.40
1:D:61:ILE:HG23	1:D:79:ILE:HG23	2.02	0.40
3:F:184:MET:CE	3:F:267:HIS:HA	2.51	0.40
1:G:965:PHE:O	1:G:976:VAL:HA	2.21	0.40
1:A:143:ILE:HG12	1:A:154:ALA:HB2	2.03	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1024:THR:HG21	1:A:1139:ILE:HG21	2.03	0.40
2:B:823:LEU:HB3	2:B:829:VAL:CG1	2.52	0.40
1:G:5:TYR:CE1	1:G:1091:GLY:HA2	2.56	0.40
3:I:159:HIS:O	3:I:162:GLN:HG2	2.22	0.40
1:D:78:PHE:HE1	1:D:86:ALA:HB1	1.87	0.40
1:D:158:ARG:HH12	1:D:160:GLU:HG2	1.87	0.40
1:D:190:VAL:O	1:D:209:GLN:HA	2.22	0.40
2:E:903:PRO:HB2	2:E:905:GLU:HG2	2.03	0.40
1:G:43:VAL:HG23	1:G:52:VAL:CG2	2.52	0.40
1:G:330:ASP:HA	1:G:355:ASN:HB3	2.02	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:1122:ARG:HE	1:G:292:ASP:OD1[2_565]	1.49	0.11
2:B:1018:ASP:OD2	3:I:232:ARG:H[5_554]	1.58	0.02

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	823/840 (98%)	801 (97%)	22 (3%)	0	100	100
1	D	822/840 (98%)	797 (97%)	24 (3%)	1 (0%)	48	76
1	G	822/840 (98%)	800 (97%)	22 (3%)	0	100	100
2	B	322/344 (94%)	313 (97%)	8 (2%)	1 (0%)	36	66
2	E	326/344 (95%)	315 (97%)	10 (3%)	1 (0%)	36	66
2	H	327/344 (95%)	317 (97%)	10 (3%)	0	100	100
3	C	246/271 (91%)	245 (100%)	1 (0%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	F	246/271 (91%)	245 (100%)	1 (0%)	0	100	100
3	I	246/271 (91%)	244 (99%)	2 (1%)	0	100	100
All	All	4180/4365 (96%)	4077 (98%)	100 (2%)	3 (0%)	48	76

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	737	THR
2	E	737	THR
1	D	318	ASP

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	722/728 (99%)	719 (100%)	3 (0%)	84	84
1	D	721/728 (99%)	716 (99%)	5 (1%)	76	79
1	G	721/728 (99%)	720 (100%)	1 (0%)	88	89
2	B	292/308 (95%)	286 (98%)	6 (2%)	47	66
2	E	296/308 (96%)	290 (98%)	6 (2%)	48	66
2	H	297/308 (96%)	293 (99%)	4 (1%)	61	73
3	C	223/242 (92%)	223 (100%)	0	100	100
3	F	223/242 (92%)	222 (100%)	1 (0%)	84	84
3	I	223/242 (92%)	222 (100%)	1 (0%)	84	84
All	All	3718/3834 (97%)	3691 (99%)	27 (1%)	76	79

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

Mol	Chain	Res	Type
1	D	52	VAL
1	D	55	VAL
1	D	248	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	315	THR
1	D	766	SER
2	E	883	LEU
2	E	896	VAL
2	E	897	ILE
2	E	913	TYR
2	E	1036	TRP
2	E	1039	CYS
3	F	242	VAL
1	A	849	VAL
1	A	930	VAL
1	A	1019	GLU
2	B	738	TYR
2	B	829	VAL
2	B	863	SER
2	B	867	LEU
2	B	896	VAL
2	B	1039	CYS
1	G	1044	SER
2	H	896	VAL
2	H	897	ILE
2	H	1036	TRP
2	H	1039	CYS
3	I	76	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
1	D	370	GLN
1	D	374	GLN
1	D	711	HIS
1	D	778	HIS
1	D	908	ASN
1	D	978	GLN
1	D	1140	HIS
2	E	780	GLN
2	E	797	GLN
2	E	1040	HIS
3	F	37	GLN
3	F	149	GLN
3	F	156	GLN
1	A	163	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	261	HIS
1	A	711	HIS
1	A	877	ASN
1	A	1015	GLN
1	A	1034	ASN
2	B	740	GLN
2	B	780	GLN
2	B	869	ASN
2	B	872	GLN
2	B	894	ASN
2	B	977	GLN
1	G	796	GLN
1	G	797	HIS
1	G	978	GLN
3	I	33	HIS
3	I	156	GLN
3	I	183	GLN
3	I	267	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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	H	893	2	8,10,11	1.65	1 (12%)	10,14,16	1.39	2 (20%)
2	TPO	E	893	2	8,10,11	1.71	1 (12%)	10,14,16	1.45	1 (10%)
2	TPO	B	893	2	8,10,11	1.78	1 (12%)	10,14,16	1.10	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	H	893	2	-	2/9/11/13	-
2	TPO	E	893	2	-	0/9/11/13	-
2	TPO	B	893	2	-	6/9/11/13	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	893	TPO	P-O1P	3.67	1.61	1.50
2	H	893	TPO	P-O1P	3.67	1.61	1.50
2	B	893	TPO	P-O1P	3.63	1.61	1.50

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	893	TPO	P-OG1-CB	-3.39	114.12	123.33
2	H	893	TPO	P-OG1-CB	-3.09	114.92	123.33
2	H	893	TPO	CG2-CB-CA	-2.25	108.87	113.26
2	B	893	TPO	P-OG1-CB	-2.18	117.39	123.33

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	893	TPO	N-CA-CB-CG2
2	B	893	TPO	N-CA-CB-OG1
2	B	893	TPO	C-CA-CB-CG2
2	B	893	TPO	O-C-CA-CB
2	B	893	TPO	CG2-CB-OG1-P
2	H	893	TPO	CB-OG1-P-O2P
2	B	893	TPO	CA-CB-OG1-P
2	H	893	TPO	CG2-CB-OG1-P

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	893	TPO	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

17 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	C	301	-	4,4,4	0.23	0	6,6,6	0.14	0
4	SO4	G	1201	-	4,4,4	0.25	0	6,6,6	0.05	0
5	RMX	H	1101	-	41,43,43	0.46	0	52,63,63	0.54	0
4	SO4	F	301	-	4,4,4	0.24	0	6,6,6	0.06	0
4	SO4	C	302	-	4,4,4	0.24	0	6,6,6	0.08	0
4	SO4	G	1202	-	4,4,4	0.25	0	6,6,6	0.10	0
4	SO4	H	1102	-	4,4,4	0.24	0	6,6,6	0.07	0
4	SO4	I	303	-	4,4,4	0.25	0	6,6,6	0.09	0
4	SO4	D	1203	-	4,4,4	0.23	0	6,6,6	0.10	0
4	SO4	F	302	-	4,4,4	0.24	0	6,6,6	0.08	0
4	SO4	D	1201	-	4,4,4	0.24	0	6,6,6	0.10	0
4	SO4	A	1201	-	4,4,4	0.25	0	6,6,6	0.08	0
4	SO4	D	1202	-	4,4,4	0.24	0	6,6,6	0.12	0
4	SO4	I	302	-	4,4,4	0.23	0	6,6,6	0.12	0
5	RMX	E	1101	-	41,43,43	0.43	0	52,63,63	0.58	0
4	SO4	I	301	-	4,4,4	0.25	0	6,6,6	0.14	0
5	RMX	B	1101	-	41,43,43	0.44	0	52,63,63	0.55	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	RMX	E	1101	-	-	2/22/24/24	0/5/5/5
5	RMX	H	1101	-	-	2/22/24/24	0/5/5/5

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	RMX	B	1101	-	-	2/22/24/24	0/5/5/5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

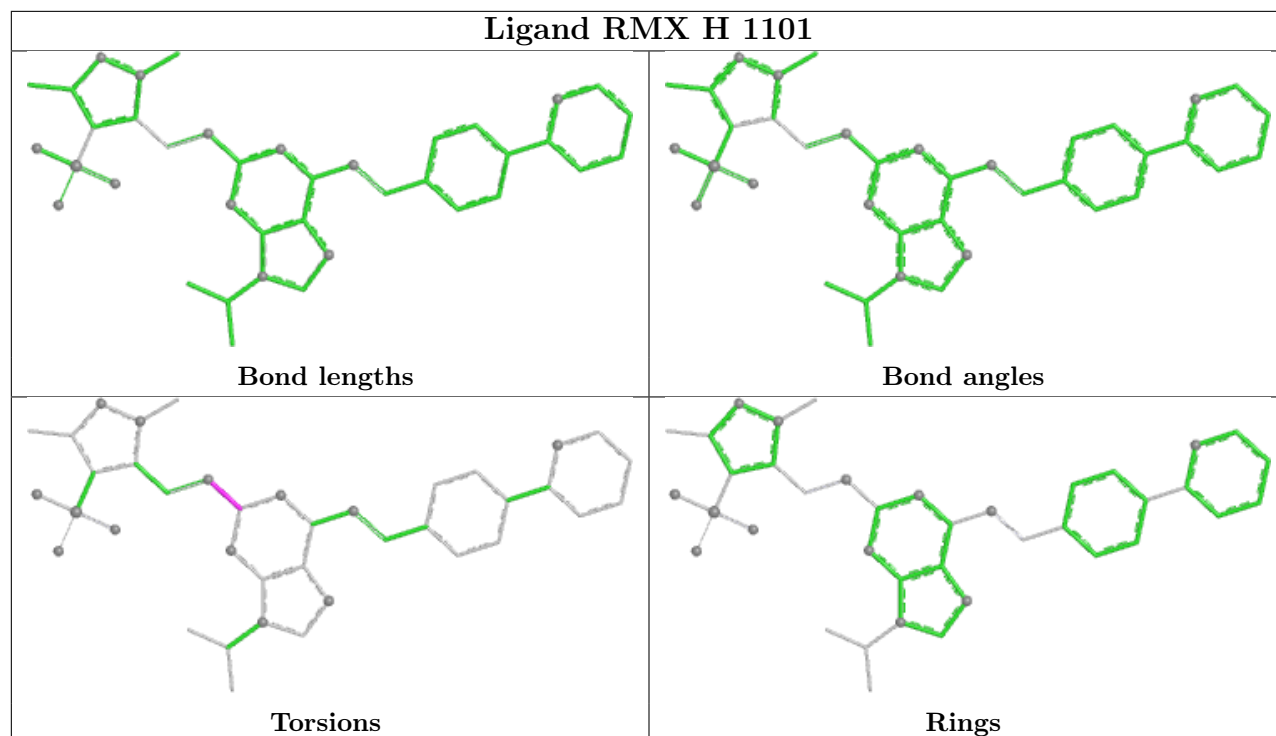
Mol	Chain	Res	Type	Atoms
5	E	1101	RMX	N10-C7-N4-C6
5	E	1101	RMX	N5-C7-N4-C6
5	B	1101	RMX	N10-C7-N4-C6
5	B	1101	RMX	N5-C7-N4-C6
5	H	1101	RMX	N10-C7-N4-C6
5	H	1101	RMX	N5-C7-N4-C6

There are no ring outliers.

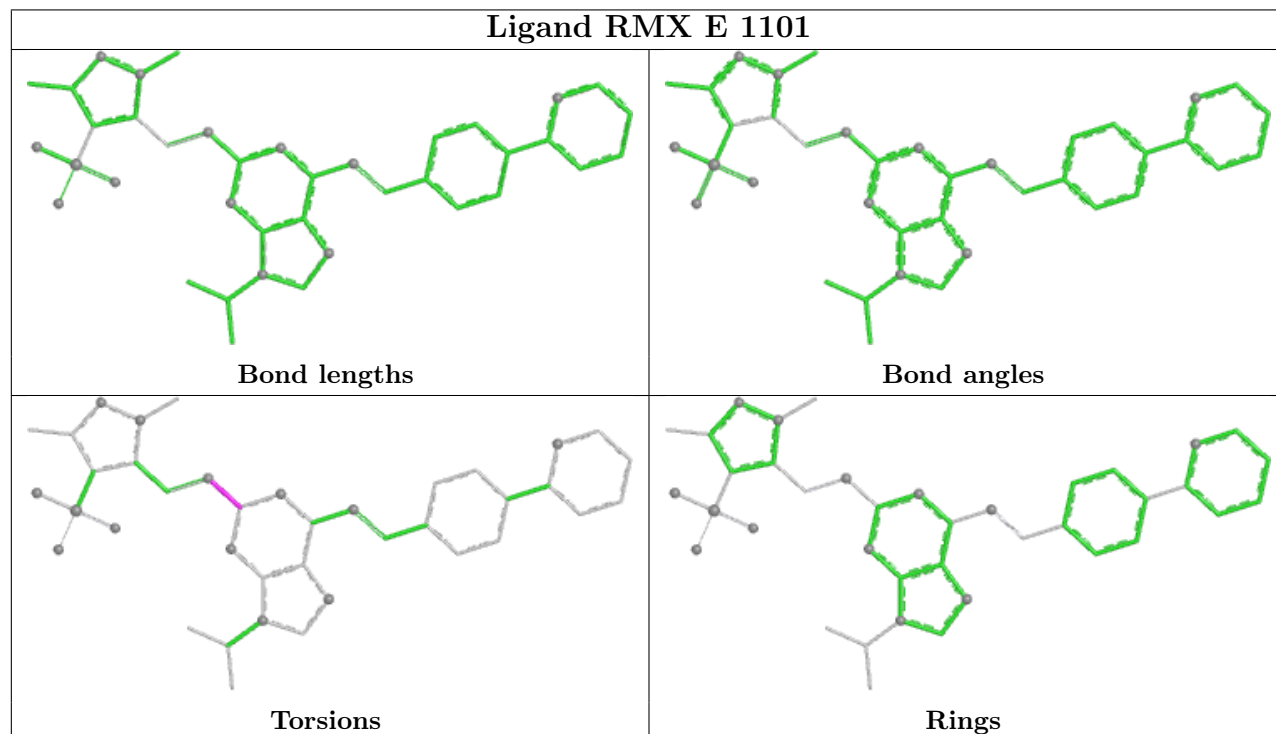
No monomer is involved in short contacts.

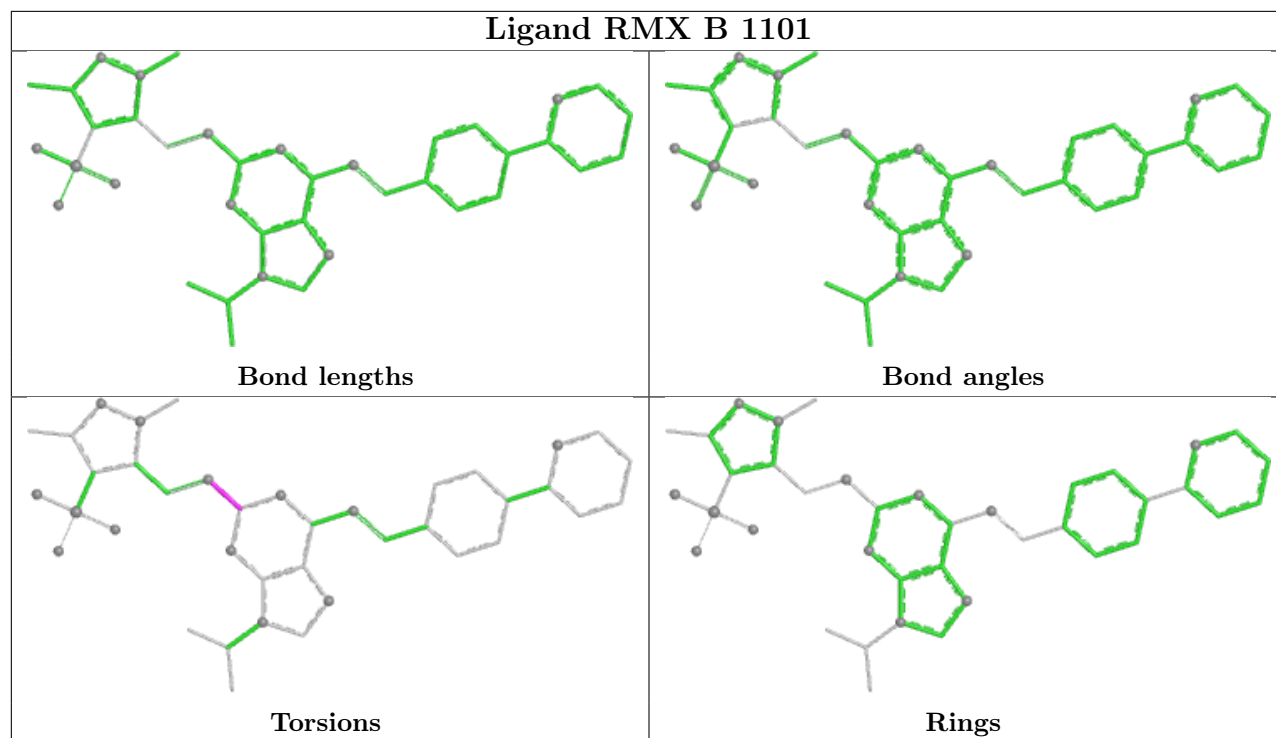
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

Ligand RMX H 1101



Ligand RMX E 1101





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	827/840 (98%)	-0.41	1 (0%) 92 90	37, 62, 106, 169	0
1	D	826/840 (98%)	-0.20	5 (0%) 85 73	38, 64, 113, 189	0
1	G	826/840 (98%)	-0.30	2 (0%) 91 85	41, 65, 112, 192	0
2	B	324/344 (94%)	-0.17	2 (0%) 85 73	40, 64, 108, 149	0
2	E	328/344 (95%)	-0.05	9 (2%) 56 38	44, 69, 113, 157	0
2	H	329/344 (95%)	-0.10	3 (0%) 81 65	36, 57, 103, 149	0
3	C	248/271 (91%)	-0.53	0 100 100	34, 51, 86, 114	0
3	F	248/271 (91%)	-0.47	1 (0%) 88 78	41, 61, 95, 116	0
3	I	248/271 (91%)	-0.38	2 (0%) 82 68	36, 53, 91, 119	0
All	All	4204/4365 (96%)	-0.28	25 (0%) 85 73	34, 62, 108, 192	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	737	THR	3.6
1	D	18	CYS	3.4
2	E	736	GLY	3.2
3	I	128	GLN	3.1
1	D	63	VAL	3.0
2	E	1043	TRP	2.9
2	E	1025	LEU	2.9
2	E	1042	LEU	2.6
2	B	738	TYR	2.4
2	H	1043	TRP	2.4
1	D	813	ALA	2.3
1	A	394	ILE	2.3
2	H	1044	SER	2.3
2	E	1035	HIS	2.2
3	F	20	THR	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
3	I	265	MET	2.2
1	D	310	ILE	2.2
2	E	863	SER	2.1
1	G	131	ILE	2.1
2	E	756	LYS	2.1
1	D	57	MET	2.1
2	H	1029	ALA	2.1
2	B	737	THR	2.0
2	E	1039	CYS	2.0
1	G	276	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	H	893	11/12	0.70	0.20	154,155,189,189	6
2	TPO	B	893	11/12	0.72	0.09	198,214,257,257	6
2	TPO	E	893	11/12	0.83	0.10	185,207,251,251	6

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	SO4	F	302	5/5	0.56	0.11	161,177,187,187	0
4	SO4	C	302	5/5	0.63	0.17	138,149,156,171	0
4	SO4	G	1201	5/5	0.65	0.17	132,138,139,145	0
4	SO4	H	1102	5/5	0.69	0.09	153,161,167,177	0
4	SO4	I	303	5/5	0.70	0.19	136,146,152,164	0

Continued on next page...

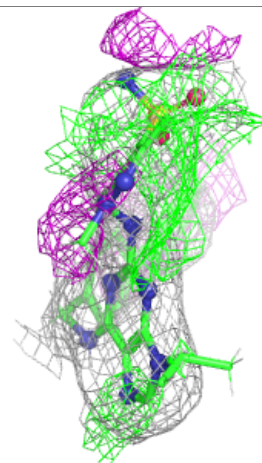
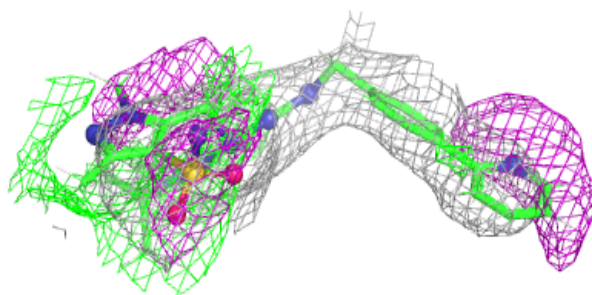
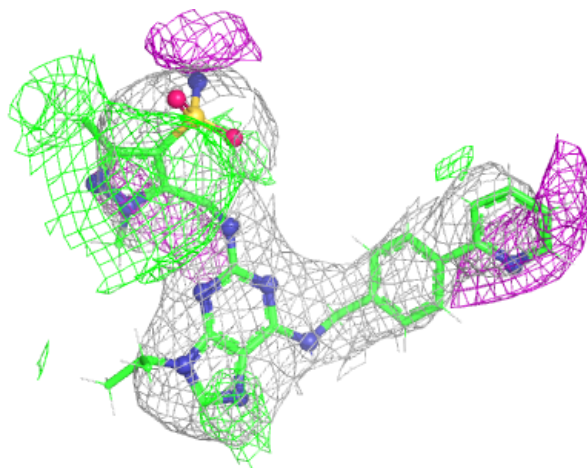
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	SO4	I	302	5/5	0.72	0.08	157,167,171,176	0
4	SO4	F	301	5/5	0.74	0.11	142,144,145,145	0
4	SO4	A	1201	5/5	0.76	0.13	133,138,140,143	0
4	SO4	I	301	5/5	0.79	0.18	108,110,114,115	0
4	SO4	D	1203	5/5	0.82	0.07	165,172,176,184	0
4	SO4	D	1201	5/5	0.82	0.13	136,137,141,141	0
4	SO4	C	301	5/5	0.84	0.14	109,114,116,117	0
5	RMX	H	1101	39/39	0.85	0.20	100,126,173,181	30
5	RMX	E	1101	39/39	0.87	0.15	112,137,187,190	30
5	RMX	B	1101	39/39	0.90	0.16	101,124,178,185	30
4	SO4	G	1202	5/5	0.90	0.12	132,134,137,138	0
4	SO4	D	1202	5/5	0.91	0.11	119,128,137,143	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.

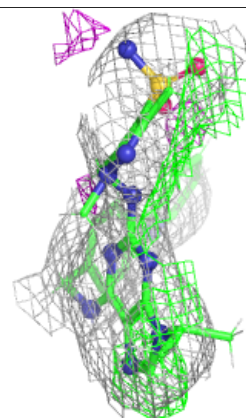
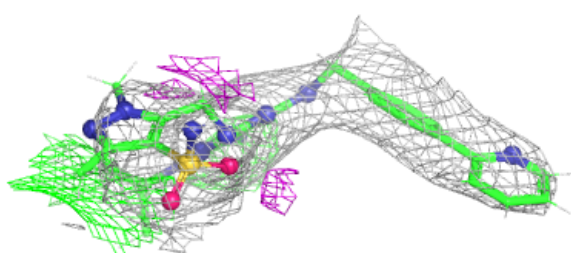
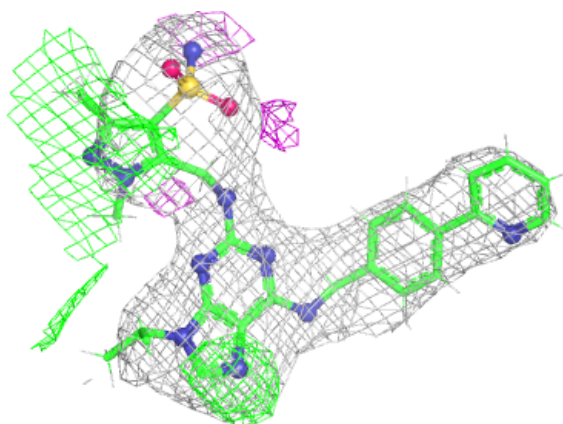
Electron density around RMX H 1101:

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

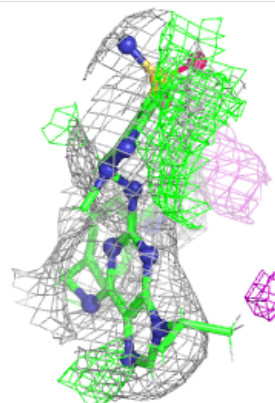
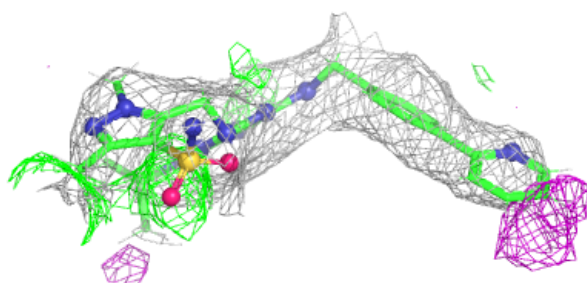
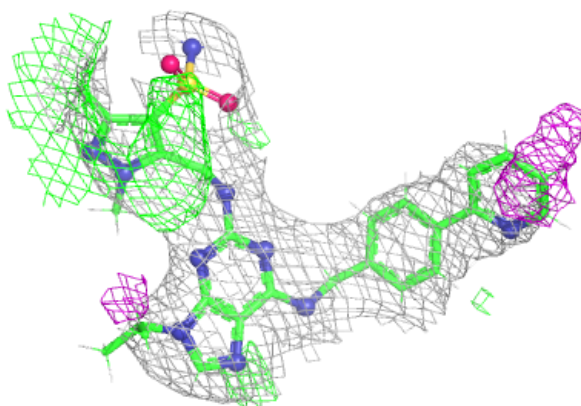


Electron density around RMX E 1101:

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

**Electron density around RMX 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.