



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 10, 2020 – 11:26 AM BST

PDB ID : 1YA8  
Title : Crystal Structure of Human Liver Carboxylesterase in complex with cleavage products of Mevastatin  
Authors : Fleming, C.D.; Bencharit, S.; Edwards, C.C.; Hyatt, J.L.; Morton, C.L.; Howard-Williams, E.L.; Potter, P.M.; Redinbo, M.R.  
Deposited on : 2004-12-17  
Resolution : 3.00 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.13.1  
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) : 2.13.1

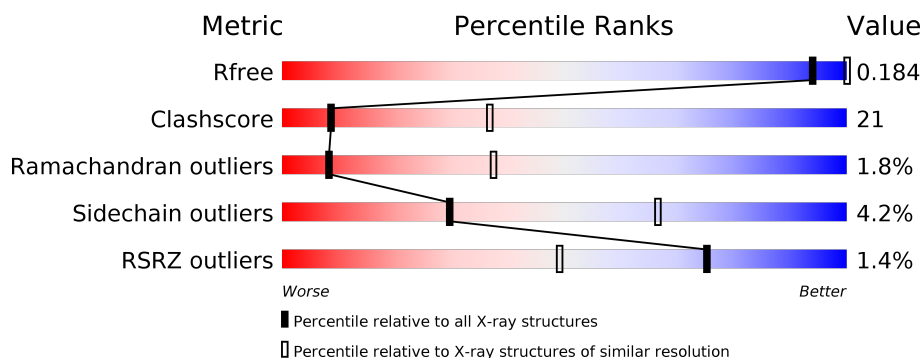
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	532	<div> <div>%</div> <div> <div></div> <div>63%</div> <div>34%</div> <div>••</div> </div> </div>
1	B	532	<div> <div>2%</div> <div> <div></div> <div>64%</div> <div>34%</div> <div>•</div> </div> </div>
1	C	532	<div> <div>%</div> <div> <div></div> <div>61%</div> <div>35%</div> <div>•</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	A	1179	-	-	-	X
2	NAG	C	1379	-	-	-	X

## 2 Entry composition [i](#)

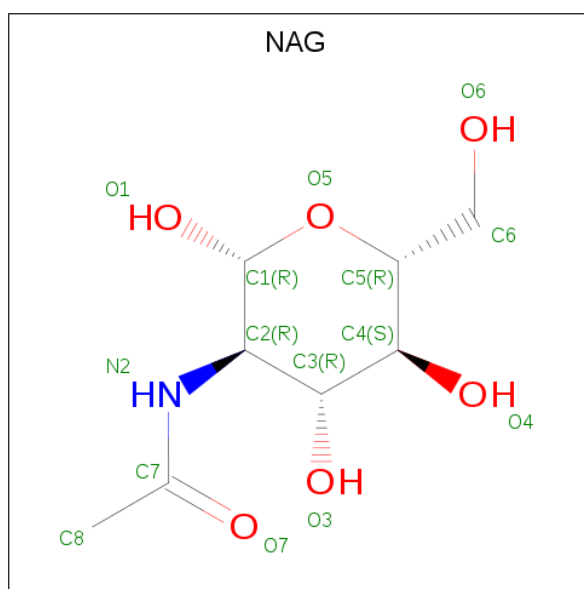
There are 7 unique types of molecules in this entry. The entry contains 12945 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called CES1 protein.

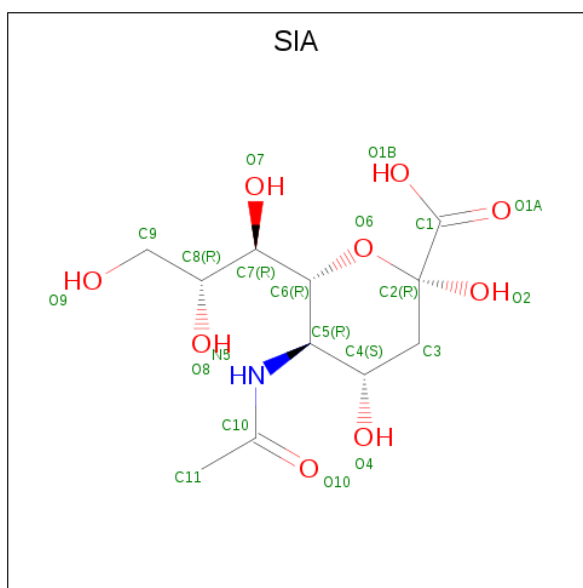
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	532	Total	C	N	O	S	0	0	0
			4130	2662	685	763	20			
1	B	532	Total	C	N	O	S	0	0	0
			4130	2662	685	763	20			
1	C	532	Total	C	N	O	S	0	0	0
			4131	2662	685	764	20			

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is N-acetyl-alpha-neuraminic acid (three-letter code: SIA) (formula:  $C_{11}H_{19}NO_9$ ).



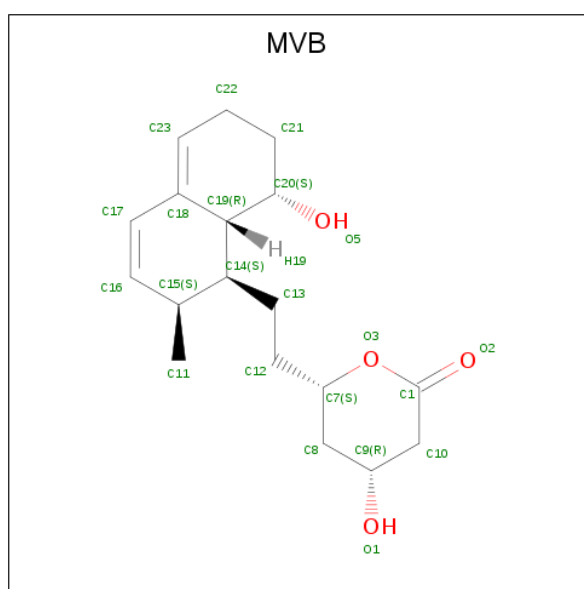
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			21	11	1	9		
3	B	1	Total	C	N	O	0	0
			21	11	1	9		
3	C	1	Total	C	N	O	0	0
			21	11	1	9		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula:  $O_4S$ ).



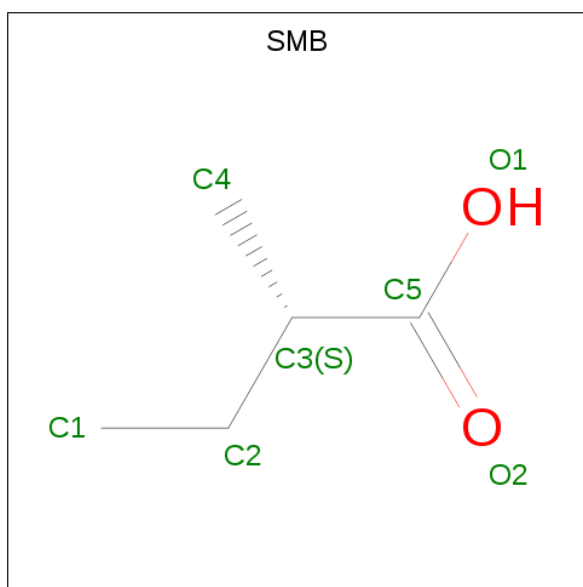
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O S 5 4 1	0	0
4	A	1	Total O S 5 4 1	0	0
4	B	1	Total O S 5 4 1	0	0
4	B	1	Total O S 5 4 1	0	0
4	C	1	Total O S 5 4 1	0	0
4	C	1	Total O S 5 4 1	0	0

- Molecule 5 is (1S,7S,8S,8AR)-1,2,3,7,8,8A-HEXAHYDRO-7-METHYL-8-[2-[(2R,4R)-TETRAHYDRO-4-HYDROXY-6-OXO-2H-PYRAN-2-YL]ETHYL]-1-NAPHTHALENOL (three-letter code: MVB) (formula: C<sub>18</sub>H<sub>26</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 22 18 4	0	0
5	C	1	Total C O 22 18 4	0	0

- Molecule 6 is 2-METHYLBUTANOIC ACID (three-letter code: SMB) (formula: C<sub>5</sub>H<sub>10</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			7	5	2		
6	B	1	Total	C	O	0	0
			7	5	2		
6	B	1	Total	C	O	0	0
			7	5	2		
6	C	1	Total	C	O	0	0
			7	5	2		

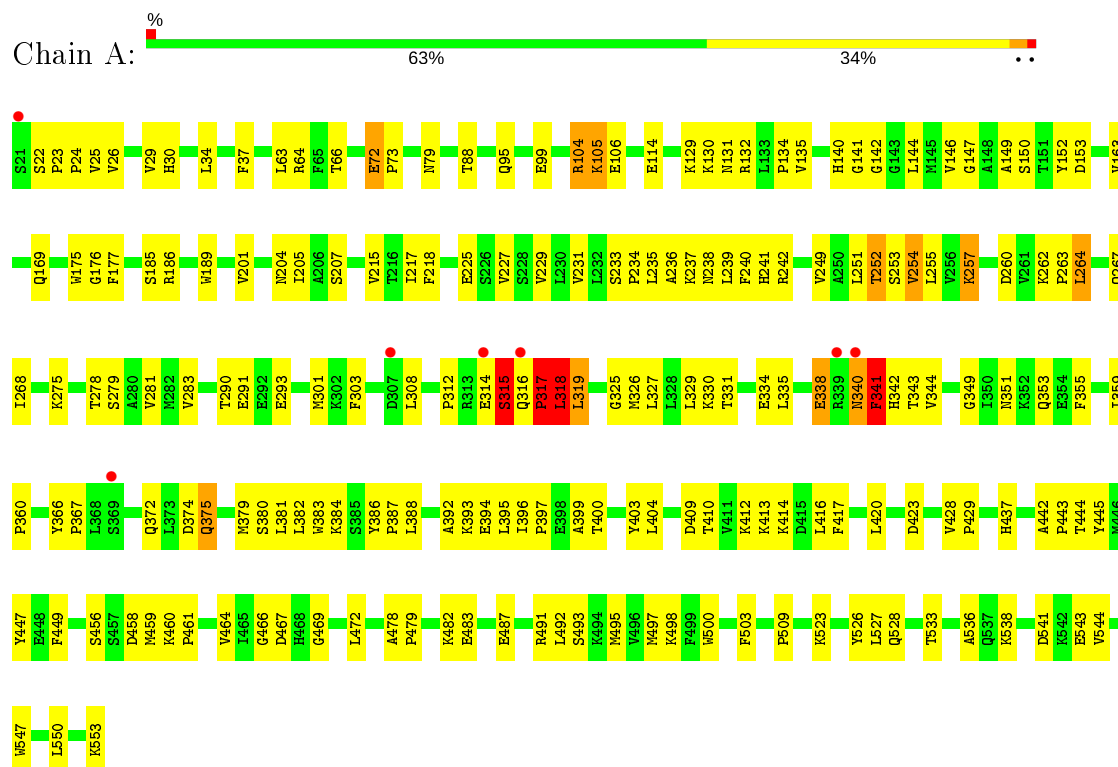
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	113	Total	O	0	0
			113	113		
7	B	116	Total	O	0	0
			116	116		
7	C	118	Total	O	0	0
			118	118		

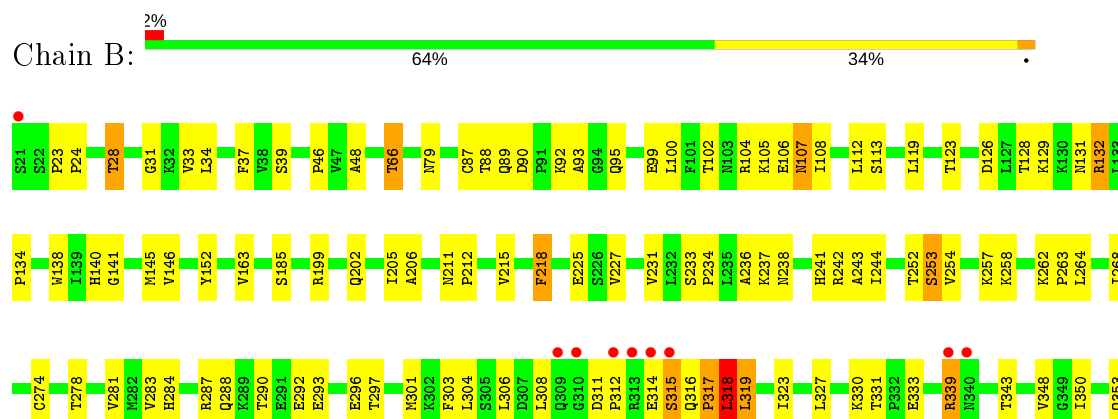
### 3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

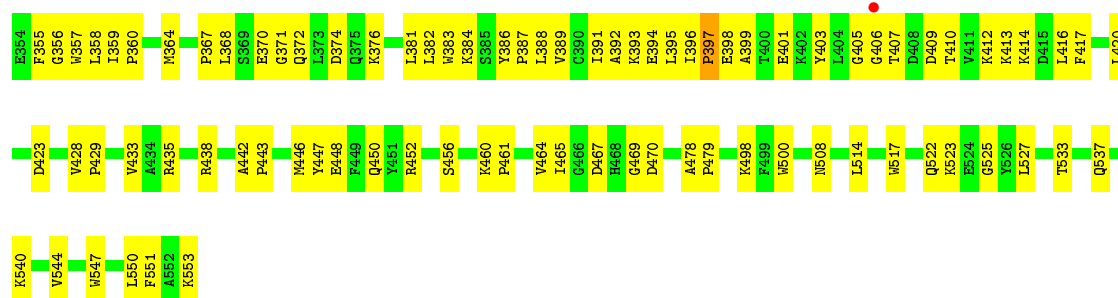
#### • Molecule 1: CES1 protein



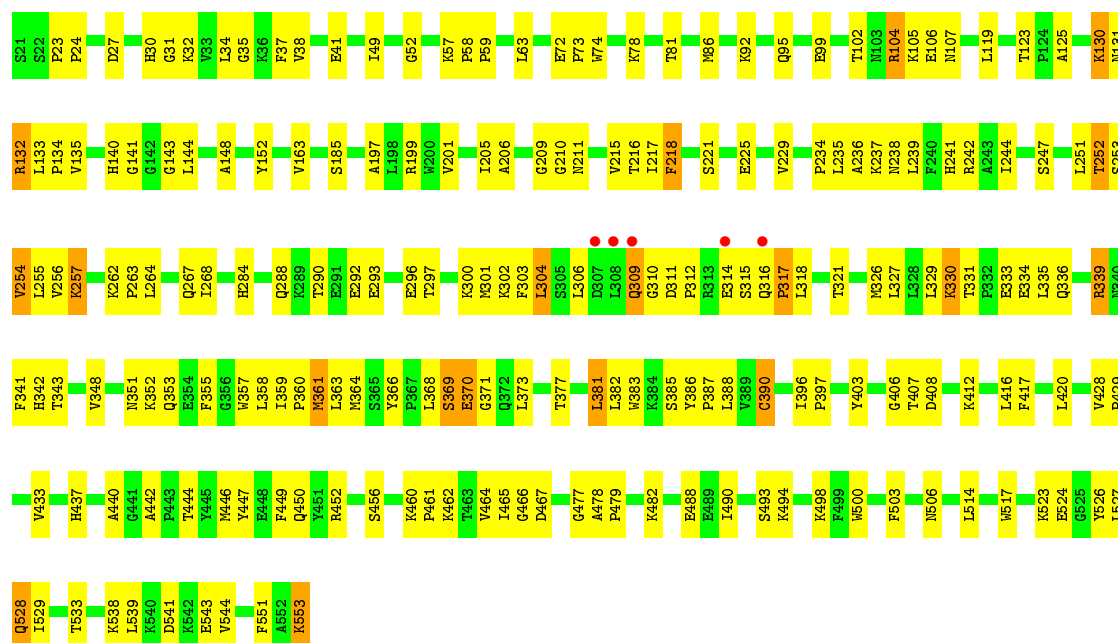
#### • Molecule 1: CES1 protein







• Molecule 1: CES1 protein



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	55.78Å 181.59Å 202.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	22.70 – 3.00 22.70 – 3.00	Depositor EDS
% Data completeness (in resolution range)	98.1 (22.70-3.00) 98.2 (22.70-3.00)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	0.13	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.79 (at 2.99Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.187 , 0.247 0.181 , 0.184	Depositor DCC
$R_{free}$ test set	2091 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	32.4	Xtriage
Anisotropy	0.342	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 61.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	12945	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.84% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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, MVB, SMB, NAG, SIA

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	0.39	0/4236	0.63	1/5754 (0.0%)
1	B	0.34	0/4236	0.59	0/5754
1	C	0.36	0/4237	0.61	0/5754
All	All	0.37	0/12709	0.61	1/17262 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	318	LEU	N-CA-C	-7.30	91.29	111.00

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	4130	0	4131	156	0
1	B	4130	0	4131	171	0
1	C	4131	0	4131	177	0
2	A	14	0	13	0	0
2	B	14	0	13	0	0
2	C	14	0	13	0	0
3	A	21	0	18	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	21	0	18	7	0
3	C	21	0	18	7	0
4	A	10	0	0	0	0
4	B	10	0	0	0	0
4	C	10	0	0	1	0
5	A	22	0	26	1	0
5	C	22	0	26	5	0
6	A	7	0	10	0	0
6	B	14	0	20	0	0
6	C	7	0	10	0	0
7	A	113	0	0	14	0
7	B	116	0	0	23	0
7	C	118	0	0	16	0
All	All	12945	0	12578	518	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 21.

All (518) 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:A:319:LEU:HD23	1:A:319:LEU:H	1.10	1.09
1:A:319:LEU:H	1:A:319:LEU:CD2	1.71	1.03
1:B:308:LEU:HD21	1:B:367:PRO:HG2	1.39	1.01
1:B:105:LYS:HE2	1:B:106:GLU:HG2	1.42	0.98
5:C:2031:MVB:H14	5:C:2031:MVB:H82	1.50	0.93
1:A:134:PRO:HG2	1:A:163:VAL:HG12	1.55	0.89
1:C:215:VAL:H	1:C:241:HIS:HD2	1.21	0.88
1:B:252:THR:HG22	1:B:254:VAL:HG12	1.54	0.87
1:C:99:GLU:HA	1:C:107:ASN:ND2	1.91	0.86
1:B:105:LYS:HG3	1:B:106:GLU:H	1.39	0.86
1:C:236:ALA:HA	1:C:239:LEU:HD12	1.58	0.85
1:A:423:ASP:OD2	1:A:543:GLU:HG2	1.77	0.85
1:C:134:PRO:HG2	1:C:163:VAL:HG12	1.56	0.85
1:A:215:VAL:H	1:A:241:HIS:HD2	1.23	0.83
1:A:318:LEU:N	1:A:318:LEU:HD12	1.94	0.83
7:B:4091:HOH:O	1:C:288:GLN:HG3	1.79	0.81
1:A:290:THR:OG1	1:A:293:GLU:HG3	1.82	0.80
1:A:257:LYS:HD2	1:A:318:LEU:O	1.82	0.79
1:C:105:LYS:HE2	1:C:106:GLU:HG2	1.64	0.79
1:A:319:LEU:N	1:A:319:LEU:CD2	2.45	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:215:VAL:H	1:B:241:HIS:HD2	1.29	0.78
1:C:130:LYS:HD2	1:C:131:ASN:N	1.98	0.78
1:A:319:LEU:HD23	1:A:319:LEU:N	1.93	0.77
1:A:242:ARG:HH11	1:A:242:ARG:HG2	1.49	0.77
1:B:498:LYS:HB3	1:B:514:LEU:HD11	1.66	0.77
1:C:131:ASN:C	1:C:132:ARG:HD2	2.06	0.76
1:B:253:SER:HB3	7:B:4074:HOH:O	1.86	0.76
1:A:262:LYS:HB3	1:A:263:PRO:HD3	1.67	0.75
1:A:105:LYS:HD3	1:A:106:GLU:H	1.52	0.75
1:C:334:GLU:HG3	7:C:4061:HOH:O	1.88	0.74
1:A:24:PRO:HG3	1:A:37:PHE:CZ	2.23	0.74
1:B:292:GLU:O	1:B:296:GLU:HG3	1.86	0.74
1:A:359:ILE:HB	1:A:360:PRO:HD3	1.70	0.74
1:B:396:ILE:HB	1:B:397:PRO:HD3	1.69	0.74
1:A:396:ILE:HB	1:A:397:PRO:HD3	1.70	0.73
1:C:353:GLN:NE2	1:C:465:ILE:H	1.87	0.72
1:C:369:SER:HA	5:C:2031:MVB:H15	1.69	0.72
1:B:95:GLN:O	1:B:99:GLU:HG3	1.90	0.72
1:B:257:LYS:NZ	1:B:318:LEU:HD12	2.05	0.72
1:C:290:THR:OG1	1:C:293:GLU:HG3	1.89	0.72
1:A:278:THR:OG1	1:A:281:VAL:HG23	1.89	0.72
1:A:267:GLN:HG2	7:A:4037:HOH:O	1.89	0.71
3:C:1382:SIA:O8	3:C:1382:SIA:N5	2.23	0.71
5:C:2031:MVB:H14	5:C:2031:MVB:C8	2.20	0.71
1:B:297:THR:O	1:B:301:MET:HG2	1.90	0.71
1:A:399:ALA:HB2	1:A:550:LEU:HD21	1.73	0.71
1:A:131:ASN:O	1:A:132:ARG:HD2	1.89	0.71
1:B:398:GLU:HB3	7:B:4100:HOH:O	1.90	0.70
1:B:28:THR:HG23	1:B:31:GLY:O	1.91	0.70
1:C:396:ILE:HB	1:C:397:PRO:HD3	1.72	0.70
1:A:267:GLN:HB3	7:A:4075:HOH:O	1.91	0.70
1:B:409:ASP:HB3	1:B:412:LYS:HB2	1.74	0.69
1:C:407:THR:OG1	1:C:412:LYS:HD2	1.93	0.68
1:A:227:VAL:O	1:A:231:VAL:HG23	1.94	0.68
1:A:95:GLN:O	1:A:99:GLU:HG3	1.93	0.68
1:C:312:PRO:HG2	1:C:383:TRP:NE1	2.09	0.68
1:A:428:VAL:HG13	1:A:544:VAL:HA	1.75	0.67
1:B:393:LYS:HA	1:B:396:ILE:HG12	1.76	0.67
1:B:290:THR:OG1	1:B:293:GLU:HG3	1.94	0.67
1:C:290:THR:HG23	1:C:293:GLU:OE2	1.94	0.67
1:B:23:PRO:HB2	1:B:34:LEU:HD21	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:134:PRO:HG2	1:B:163:VAL:HG12	1.77	0.66
1:C:456:SER:HB3	1:C:460:LYS:HD3	1.78	0.66
1:A:487:GLU:OE2	1:A:491:ARG:NH1	2.28	0.66
1:B:202:GLN:HB3	7:B:4018:HOH:O	1.96	0.66
1:A:105:LYS:HE2	1:A:106:GLU:HB3	1.78	0.66
1:B:215:VAL:H	1:B:241:HIS:CD2	2.13	0.66
1:C:215:VAL:H	1:C:241:HIS:CD2	2.09	0.66
1:C:132:ARG:HB3	1:C:211:ASN:HB2	1.79	0.65
1:C:99:GLU:HA	1:C:107:ASN:HD22	1.62	0.65
1:A:251:LEU:O	1:A:253:SER:N	2.29	0.65
1:A:375:GLN:HG2	1:A:413:LYS:NZ	2.12	0.65
1:A:403:TYR:O	1:A:416:LEU:HD13	1.96	0.65
1:B:132:ARG:NH2	1:B:206:ALA:HB1	2.11	0.65
1:A:379:MET:HG2	1:A:396:ILE:HG22	1.79	0.64
1:C:343:THR:HB	1:C:442:ALA:HB2	1.77	0.64
1:B:257:LYS:HZ1	1:B:318:LEU:HD12	1.62	0.64
1:B:126:ASP:OD2	1:B:129:LYS:HE3	1.96	0.64
3:C:1382:SIA:H8	3:C:1382:SIA:H113	1.78	0.64
1:B:242:ARG:HH11	1:B:242:ARG:HG2	1.61	0.64
1:B:461:PRO:HG2	1:B:464:VAL:HG23	1.80	0.64
1:C:253:SER:O	1:C:255:LEU:N	2.31	0.64
1:C:131:ASN:O	1:C:132:ARG:HD2	1.97	0.63
7:A:4107:HOH:O	1:B:281:VAL:HG13	1.99	0.63
1:A:201:VAL:HG13	1:A:205:ILE:HB	1.81	0.63
1:C:330:LYS:HG3	1:C:335:LEU:HD21	1.81	0.63
1:C:461:PRO:HG2	1:C:464:VAL:HG23	1.81	0.63
1:C:348:VAL:O	1:C:446:MET:HA	2.00	0.62
1:A:105:LYS:CD	1:A:106:GLU:H	2.11	0.62
3:B:1282:SIA:H113	3:B:1282:SIA:H6	1.80	0.62
1:C:95:GLN:O	1:C:99:GLU:HG3	1.98	0.62
1:B:105:LYS:HG3	1:B:106:GLU:N	2.14	0.62
1:B:284:HIS:O	1:B:288:GLN:HG2	1.99	0.62
1:B:414:LYS:HD3	7:B:4038:HOH:O	2.00	0.62
1:C:312:PRO:HG2	1:C:383:TRP:CD1	2.34	0.62
1:C:256:VAL:HG22	1:C:321:THR:HB	1.81	0.61
1:C:104:ARG:O	1:C:482:LYS:HE2	2.01	0.61
1:C:130:LYS:HD2	1:C:130:LYS:C	2.21	0.61
1:C:461:PRO:HG2	1:C:464:VAL:CG2	2.30	0.61
1:B:274:CYS:HA	7:B:4067:HOH:O	2.01	0.61
1:B:24:PRO:HG3	1:B:37:PHE:CE1	2.36	0.61
1:C:38:VAL:HG21	1:C:49:ILE:HD12	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:262:LYS:HE3	1:A:279:SER:OG	2.00	0.61
1:C:267:GLN:HE22	1:C:316:GLN:HG3	1.64	0.61
1:B:456:SER:HB3	1:B:460:LYS:HD3	1.82	0.60
1:B:409:ASP:O	1:B:413:LYS:HG3	2.01	0.60
1:A:242:ARG:HH11	1:A:242:ARG:CG	2.12	0.60
1:C:215:VAL:N	1:C:241:HIS:HD2	1.97	0.60
1:C:297:THR:O	1:C:301:MET:HG2	2.01	0.60
1:A:372:GLN:HB2	1:A:410:THR:HB	1.82	0.60
1:B:323:ILE:HG21	1:B:330:LYS:HA	1.82	0.60
1:B:348:VAL:O	1:B:446:MET:HA	2.01	0.60
1:C:216:THR:HG23	1:C:242:ARG:HB2	1.84	0.60
1:A:308:LEU:HD21	1:A:367:PRO:HG2	1.82	0.60
1:C:242:ARG:HG2	1:C:242:ARG:HH11	1.66	0.60
1:C:498:LYS:HB3	1:C:514:LEU:HD11	1.84	0.60
1:B:359:ILE:HB	1:B:360:PRO:HD3	1.84	0.59
1:C:359:ILE:HB	1:C:360:PRO:HD3	1.84	0.59
1:C:221:SER:HA	1:C:247:SER:O	2.01	0.59
1:A:456:SER:HB3	1:A:460:LYS:HD3	1.83	0.59
1:A:23:PRO:HB2	1:A:34:LEU:HD21	1.84	0.59
1:A:498:LYS:HD3	7:A:4040:HOH:O	2.03	0.59
1:B:374:ASP:OD2	1:B:376:LYS:HB2	2.02	0.58
1:B:478:ALA:N	1:B:479:PRO:CD	2.66	0.58
3:B:1282:SIA:H7	7:B:4025:HOH:O	2.02	0.58
1:B:319:LEU:H	1:B:319:LEU:HD23	1.67	0.58
1:A:64:ARG:O	1:A:66:THR:HG23	2.03	0.58
1:A:417:PHE:O	1:A:420:LEU:HB3	2.04	0.58
1:B:258:LYS:HE2	1:B:333:GLU:OE1	2.03	0.58
1:C:218:PHE:CB	1:C:244:ILE:HB	2.33	0.58
1:B:386:TYR:N	1:B:387:PRO:HD2	2.19	0.58
1:B:467:ASP:N	1:B:470:ASP:OD2	2.36	0.58
1:C:27:ASP:OD1	1:C:32:LYS:HG2	2.04	0.58
1:B:145:MET:HE1	1:B:303:PHE:HD1	1.68	0.58
1:C:381:LEU:HD13	1:C:417:PHE:CE2	2.39	0.58
1:B:241:HIS:C	1:B:242:ARG:HG3	2.24	0.57
1:A:318:LEU:CD1	1:A:318:LEU:N	2.64	0.57
1:B:403:TYR:CG	1:B:420:LEU:HD23	2.39	0.57
1:C:24:PRO:HG3	1:C:37:PHE:CE1	2.39	0.57
1:A:26:VAL:CG1	1:A:207:SER:HB3	2.34	0.57
1:B:355:PHE:CE1	1:B:360:PRO:HG3	2.39	0.57
1:C:377:THR:O	1:C:381:LEU:HB2	2.04	0.57
1:B:140:HIS:HD2	1:B:141:GLY:O	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:370:GLU:HB3	1:B:372:GLN:HG2	1.87	0.57
1:C:218:PHE:HB3	1:C:244:ILE:HB	1.86	0.57
1:A:185:SER:HB2	1:A:283:VAL:HG21	1.87	0.57
1:A:330:LYS:HG3	1:A:335:LEU:HG	1.87	0.57
1:B:461:PRO:HG2	1:B:464:VAL:CG2	2.35	0.57
1:C:102:THR:OG1	1:C:104:ARG:HG2	2.05	0.57
1:C:342:HIS:HA	7:C:4112:HOH:O	2.04	0.57
1:A:374:ASP:HB2	7:A:4045:HOH:O	2.03	0.56
1:C:358:LEU:O	1:C:363:LEU:HG	2.05	0.56
1:C:304:LEU:O	1:C:364:MET:HG2	2.05	0.56
1:A:343:THR:HA	7:A:4012:HOH:O	2.04	0.56
1:C:370:GLU:CD	1:C:370:GLU:H	2.08	0.56
1:C:382:LEU:HD23	1:C:396:ILE:HG23	1.87	0.56
1:A:383:TRP:CZ3	1:A:393:LYS:HB2	2.41	0.56
3:C:1382:SIA:H7	7:C:4037:HOH:O	2.05	0.56
1:B:353:GLN:NE2	1:B:465:ILE:H	2.04	0.56
1:B:372:GLN:HB2	1:B:410:THR:HB	1.87	0.56
1:C:225:GLU:O	1:C:229:VAL:HG23	2.06	0.56
1:C:284:HIS:O	1:C:288:GLN:HG2	2.05	0.56
1:A:241:HIS:O	1:A:242:ARG:HG3	2.06	0.55
1:A:341:PHE:CD2	1:A:341:PHE:N	2.73	0.55
1:A:527:LEU:HD11	1:A:533:THR:HG22	1.86	0.55
1:B:237:LYS:HG2	1:B:238:ASN:ND2	2.21	0.55
1:A:341:PHE:HD2	1:A:341:PHE:N	2.04	0.55
1:A:375:GLN:HG2	1:A:413:LYS:HZ1	1.69	0.55
1:A:437:HIS:HD2	1:A:444:THR:OG1	1.88	0.55
1:B:105:LYS:HE2	1:B:106:GLU:CG	2.27	0.55
1:C:368:LEU:O	5:C:2031:MVB:H7	2.05	0.55
1:A:241:HIS:C	1:A:242:ARG:HG3	2.27	0.55
1:A:264:LEU:O	1:A:268:ILE:HG13	2.07	0.55
1:B:131:ASN:C	1:B:132:ARG:HD2	2.27	0.55
1:B:262:LYS:HB3	1:B:263:PRO:HD3	1.89	0.55
1:B:100:LEU:HD13	1:B:358:LEU:CD1	2.37	0.55
1:B:393:LYS:HA	1:B:396:ILE:CG1	2.37	0.55
1:C:251:LEU:HD12	1:C:433:VAL:HG23	1.88	0.55
1:C:262:LYS:HB3	1:C:263:PRO:HD3	1.89	0.55
1:A:140:HIS:HD2	1:A:141:GLY:O	1.90	0.55
1:B:308:LEU:HD21	1:B:367:PRO:CG	2.27	0.55
1:C:329:LEU:C	1:C:330:LYS:HG2	2.26	0.55
1:C:437:HIS:HD2	1:C:444:THR:OG1	1.90	0.55
1:A:275:LYS:NZ	1:C:292:GLU:OE2	2.29	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:342:HIS:HB2	7:A:4113:HOH:O	2.07	0.54
1:B:407:THR:OG1	1:B:412:LYS:HD2	2.07	0.54
1:C:135:VAL:HB	1:C:215:VAL:HG22	1.89	0.54
1:C:538:LYS:HB3	1:C:541:ASP:HB2	1.89	0.54
1:B:311:ASP:HB3	1:B:314:GLU:HB2	1.90	0.54
1:B:392:ALA:HB1	1:B:394:GLU:OE1	2.07	0.54
1:B:540:LYS:O	1:B:544:VAL:HG23	2.07	0.54
1:A:26:VAL:HG13	1:A:207:SER:HB3	1.88	0.54
1:B:99:GLU:O	1:B:102:THR:HG22	2.07	0.54
1:C:23:PRO:HB2	1:C:34:LEU:HD21	1.90	0.54
1:A:340:ASN:HA	7:A:4102:HOH:O	2.08	0.54
1:B:357:TRP:O	1:B:360:PRO:HD2	2.08	0.54
1:B:447:TYR:C	1:B:447:TYR:CD2	2.80	0.54
1:B:257:LYS:HE3	1:B:318:LEU:O	2.07	0.54
1:B:317:PRO:HD2	7:B:4044:HOH:O	2.07	0.54
1:A:242:ARG:HD3	1:A:503:PHE:O	2.07	0.54
1:C:252:THR:HA	7:C:4105:HOH:O	2.06	0.54
1:C:478:ALA:N	1:C:479:PRO:CD	2.71	0.54
1:B:447:TYR:HB3	1:B:517:TRP:CZ2	2.44	0.53
1:C:526:TYR:OH	1:C:528:GLN:NE2	2.41	0.53
1:B:90:ASP:HB3	1:B:93:ALA:HB3	1.90	0.53
1:C:251:LEU:O	1:C:253:SER:N	2.40	0.53
1:B:407:THR:HG21	1:B:412:LYS:NZ	2.24	0.53
1:B:544:VAL:HB	7:B:4031:HOH:O	2.07	0.53
1:B:252:THR:HG22	1:B:254:VAL:CG1	2.34	0.53
1:A:104:ARG:O	1:A:482:LYS:HE2	2.08	0.53
1:B:428:VAL:HB	1:B:429:PRO:HD3	1.91	0.53
1:C:551:PHE:C	1:C:553:LYS:H	2.10	0.53
1:A:314:GLU:O	1:A:315:SER:C	2.47	0.53
1:B:237:LYS:O	1:B:238:ASN:HB2	2.07	0.53
1:C:106:GLU:HG3	7:C:4035:HOH:O	2.09	0.53
1:A:392:ALA:HB1	1:A:394:GLU:OE1	2.09	0.53
1:C:352:LYS:HB2	1:C:450:GLN:HG2	1.91	0.53
3:C:1382:SIA:H8	3:C:1382:SIA:C11	2.38	0.52
1:C:385:SER:O	1:C:388:LEU:HB2	2.08	0.52
1:B:24:PRO:HG3	1:B:37:PHE:CZ	2.44	0.52
1:A:403:TYR:CD1	1:A:420:LEU:HD23	2.45	0.52
1:A:461:PRO:HG2	1:A:464:VAL:CG2	2.39	0.52
3:A:1182:SIA:O2	3:A:1182:SIA:H5	2.10	0.52
1:A:478:ALA:N	1:A:479:PRO:CD	2.73	0.52
1:A:483:GLU:HB2	7:A:4065:HOH:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:52:GLY:HA3	3:C:1382:SIA:O9	2.09	0.52
1:C:234:PRO:HA	1:C:341:PHE:CE1	2.44	0.52
1:C:316:GLN:HE21	1:C:316:GLN:HA	1.74	0.52
1:A:88:THR:HG21	1:A:175:TRP:CH2	2.45	0.52
1:C:237:LYS:O	1:C:238:ASN:HB2	2.09	0.52
1:A:543:GLU:OE2	1:A:543:GLU:N	2.36	0.52
1:C:24:PRO:HD2	1:C:35:GLY:O	2.10	0.52
1:C:331:THR:HB	1:C:333:GLU:OE1	2.10	0.52
1:A:79:ASN:HB2	3:A:1182:SIA:C1	2.39	0.52
1:A:72:GLU:OE1	1:A:73:PRO:O	2.28	0.52
1:B:105:LYS:HG3	1:B:106:GLU:HG2	1.91	0.52
3:B:1282:SIA:C3	7:B:4010:HOH:O	2.57	0.52
1:B:343:THR:HA	7:B:4007:HOH:O	2.09	0.52
1:C:86:MET:HB3	1:C:148:ALA:HB2	1.92	0.52
1:C:30:HIS:HE1	7:C:4033:HOH:O	1.92	0.52
1:A:242:ARG:NH1	1:A:242:ARG:CG	2.70	0.51
1:A:349:GLY:HA3	1:A:447:TYR:CE1	2.45	0.51
1:B:399:ALA:HB2	1:B:550:LEU:HD21	1.92	0.51
1:B:417:PHE:O	1:B:420:LEU:HB3	2.09	0.51
1:C:199:ARG:NH1	7:C:4012:HOH:O	2.42	0.51
1:B:145:MET:HB2	1:B:304:LEU:HD21	1.93	0.51
1:C:257:LYS:NZ	1:C:257:LYS:HB3	2.25	0.51
1:C:407:THR:HG21	1:C:412:LYS:NZ	2.26	0.51
1:B:353:GLN:O	1:B:467:ASP:HA	2.11	0.51
1:B:104:ARG:HD2	1:B:108:ILE:HG12	1.93	0.51
1:B:435:ARG:O	1:B:438:ARG:HB3	2.10	0.51
1:A:312:PRO:HG2	1:A:383:TRP:NE1	2.26	0.51
1:A:355:PHE:CE1	1:A:360:PRO:HG3	2.46	0.51
1:B:319:LEU:N	1:B:319:LEU:HD23	2.26	0.51
1:C:125:ALA:HB2	1:C:133:LEU:HD12	1.93	0.51
1:C:268:ILE:HG12	1:C:301:MET:CE	2.41	0.51
1:C:237:LYS:HE2	1:C:342:HIS:HB2	1.92	0.51
1:A:492:LEU:HD12	1:A:495:MET:CE	2.41	0.50
1:B:152:TYR:N	1:B:152:TYR:CD1	2.79	0.50
1:C:72:GLU:HG3	7:C:4104:HOH:O	2.12	0.50
1:A:386:TYR:N	1:A:387:PRO:HD2	2.26	0.50
1:A:131:ASN:C	1:A:132:ARG:HD2	2.32	0.50
1:B:87:CYS:HB3	7:B:4061:HOH:O	2.11	0.50
1:C:538:LYS:O	1:C:541:ASP:HB2	2.11	0.50
1:C:403:TYR:O	1:C:416:LEU:HD13	2.11	0.50
1:A:225:GLU:O	1:A:229:VAL:HG23	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:283:VAL:HG12	1:B:287:ARG:NH1	2.27	0.50
3:B:1282:SIA:H32	7:B:4010:HOH:O	2.12	0.50
1:B:314:GLU:O	1:B:315:SER:C	2.50	0.50
1:C:527:LEU:HD11	1:C:533:THR:HG22	1.93	0.50
1:A:400:THR:HG23	1:A:404:LEU:HD12	1.94	0.49
1:C:355:PHE:CE1	1:C:360:PRO:HG3	2.46	0.49
1:C:452:ARG:NE	1:C:462:LYS:HA	2.27	0.49
1:A:301:MET:HB2	1:A:303:PHE:CE1	2.47	0.49
1:A:538:LYS:HB3	1:A:541:ASP:HB2	1.93	0.49
1:B:89:GLN:HB2	1:B:146:VAL:HG12	1.94	0.49
1:A:260:ASP:OD2	1:A:263:PRO:HD3	2.12	0.49
1:B:316:GLN:HG3	1:B:316:GLN:O	2.13	0.49
1:A:105:LYS:HD3	1:A:105:LYS:N	2.27	0.49
1:B:403:TYR:CE2	1:B:420:LEU:HA	2.47	0.49
1:A:392:ALA:HB3	1:A:395:LEU:HG	1.95	0.49
1:B:215:VAL:N	1:B:241:HIS:HD2	2.03	0.48
1:B:306:LEU:HB2	1:B:364:MET:CE	2.42	0.48
1:C:217:ILE:O	1:C:217:ILE:HG13	2.11	0.48
1:C:152:TYR:N	1:C:152:TYR:CD1	2.80	0.48
1:C:234:PRO:HA	1:C:341:PHE:HE1	1.77	0.48
1:A:409:ASP:HB3	1:A:412:LYS:HB2	1.95	0.48
1:B:452:ARG:HG2	1:B:452:ARG:HH11	1.78	0.48
1:C:119:LEU:HD12	1:C:119:LEU:C	2.33	0.48
1:C:517:TRP:CE3	1:C:527:LEU:HD23	2.49	0.48
1:A:217:ILE:O	1:A:217:ILE:HG13	2.13	0.48
1:A:249:VAL:O	1:A:252:THR:HB	2.13	0.48
1:A:553:LYS:HB2	7:A:4088:HOH:O	2.13	0.48
1:B:428:VAL:HG13	1:B:544:VAL:HA	1.95	0.48
1:C:132:ARG:NH2	1:C:206:ALA:HB1	2.28	0.48
1:C:301:MET:O	1:C:302:LYS:HB2	2.13	0.48
1:C:235:LEU:HD12	1:C:327:LEU:HD12	1.95	0.48
1:C:428:VAL:HB	1:C:429:PRO:HD3	1.94	0.48
1:C:251:LEU:O	7:C:4072:HOH:O	2.20	0.48
1:B:420:LEU:HD22	1:B:547:TRP:HZ2	1.78	0.48
1:C:336:GLN:HB2	7:C:4030:HOH:O	2.14	0.48
1:B:102:THR:OG1	1:B:104:ARG:HG2	2.13	0.48
1:B:525:GLY:HA2	1:B:537:GLN:HG2	1.96	0.48
1:A:29:VAL:HG23	1:A:204:ASN:OD1	2.14	0.47
1:B:333:GLU:CD	1:B:333:GLU:H	2.17	0.47
1:A:351:ASN:ND2	1:A:449:PHE:HB3	2.28	0.47
1:B:319:LEU:CD2	1:B:319:LEU:N	2.77	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:353:GLN:HE22	1:B:465:ILE:H	1.61	0.47
1:C:329:LEU:O	1:C:330:LYS:HG2	2.14	0.47
1:C:528:GLN:O	1:C:533:THR:HG23	2.14	0.47
5:A:2011:MVB:H14	5:A:2011:MVB:H81	1.95	0.47
1:B:278:THR:OG1	1:B:281:VAL:HG23	2.14	0.47
1:C:206:ALA:HA	1:C:210:GLY:O	2.14	0.47
1:A:144:LEU:HB3	1:A:177:PHE:CE2	2.49	0.47
1:A:257:LYS:CD	1:A:318:LEU:O	2.59	0.47
1:B:112:LEU:O	1:B:113:SER:HB2	2.14	0.47
1:C:351:ASN:ND2	1:C:449:PHE:HB3	2.29	0.47
1:C:314:GLU:O	1:C:316:GLN:N	2.47	0.47
1:A:318:LEU:H	1:A:318:LEU:HD12	1.77	0.47
1:C:31:GLY:HA3	1:C:74:TRP:NE1	2.29	0.47
1:C:369:SER:C	1:C:371:GLY:H	2.17	0.47
1:B:317:PRO:O	1:B:318:LEU:HG	2.14	0.47
1:C:30:HIS:HB3	1:C:73:PRO:HA	1.96	0.47
1:B:126:ASP:OD2	1:B:128:THR:OG1	2.33	0.47
1:B:301:MET:HB3	1:B:303:PHE:CE2	2.50	0.47
1:B:99:GLU:HG2	1:B:107:ASN:OD1	2.15	0.47
1:C:119:LEU:HD12	1:C:119:LEU:O	2.15	0.47
1:B:227:VAL:CG1	1:B:243:ALA:HB1	2.44	0.47
1:B:383:TRP:O	1:B:386:TYR:HB2	2.15	0.47
1:C:526:TYR:CE2	1:C:539:LEU:HB2	2.50	0.47
1:A:428:VAL:HB	1:A:429:PRO:HD3	1.96	0.46
1:A:252:THR:O	1:A:252:THR:HG22	2.14	0.46
1:A:351:ASN:HB3	1:A:466:GLY:O	2.16	0.46
1:A:493:SER:O	1:A:497:MET:HG3	2.15	0.46
1:C:105:LYS:CE	1:C:106:GLU:HG2	2.40	0.46
1:C:74:TRP:CD2	1:C:78:LYS:HE2	2.50	0.46
1:A:152:TYR:N	1:A:152:TYR:CD1	2.83	0.46
1:C:284:HIS:HA	4:C:3385:SO4:O3	2.16	0.46
1:B:233:SER:HA	1:B:234:PRO:HD3	1.83	0.46
1:B:317:PRO:HG3	7:B:4088:HOH:O	2.14	0.46
1:B:382:LEU:CD1	1:B:389:VAL:HG21	2.46	0.46
1:C:390:CYS:HB3	7:C:4081:HOH:O	2.16	0.46
1:B:264:LEU:O	1:B:268:ILE:HG13	2.16	0.46
1:C:140:HIS:HD2	1:C:141:GLY:O	1.99	0.46
1:B:312:PRO:HG2	1:B:383:TRP:NE1	2.31	0.46
1:A:22:SER:O	1:A:37:PHE:HE1	1.98	0.46
3:B:1282:SIA:C7	7:B:4025:HOH:O	2.62	0.46
3:C:1382:SIA:O8	3:C:1382:SIA:C5	2.64	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:543:GLU:N	1:C:543:GLU:OE2	2.43	0.46
1:B:105:LYS:HG2	7:B:4026:HOH:O	2.15	0.46
1:B:48:ALA:HB3	1:B:123:THR:CG2	2.46	0.46
1:B:364:MET:CE	1:B:388:LEU:HD11	2.46	0.46
1:C:143:GLY:O	1:C:144:LEU:HB2	2.15	0.46
1:B:551:PHE:C	1:B:553:LYS:H	2.19	0.45
1:A:225:GLU:HG3	1:A:255:LEU:HD12	1.98	0.45
1:C:268:ILE:HG12	1:C:301:MET:HE2	1.97	0.45
1:A:240:PHE:HE2	1:A:344:VAL:HG21	1.82	0.45
1:C:447:TYR:CD2	1:C:447:TYR:C	2.90	0.45
1:C:57:LYS:HD3	1:C:63:LEU:HD11	1.97	0.45
1:A:105:LYS:CG	1:A:106:GLU:N	2.79	0.45
1:A:24:PRO:HG3	1:A:37:PHE:CE1	2.52	0.45
1:A:409:ASP:O	1:A:413:LYS:HG3	2.17	0.45
1:B:39:SER:OG	1:B:46:PRO:HB3	2.16	0.45
1:A:186:ARG:CD	1:A:326:MET:HG3	2.47	0.45
1:A:380:SER:O	1:A:384:LYS:HG3	2.17	0.45
1:A:420:LEU:HD22	1:A:547:TRP:HZ2	1.80	0.45
1:B:368:LEU:HA	7:B:4037:HOH:O	2.16	0.45
1:C:361:MET:SD	1:C:363:LEU:HD23	2.57	0.45
1:B:323:ILE:HD11	1:B:331:THR:HA	1.99	0.45
1:C:264:LEU:O	1:C:268:ILE:HG13	2.17	0.45
1:C:237:LYS:O	1:C:238:ASN:CB	2.64	0.45
1:C:23:PRO:HA	1:C:24:PRO:HD3	1.88	0.45
1:A:104:ARG:CZ	1:A:153:ASP:HB2	2.47	0.44
1:B:233:SER:OG	1:B:327:LEU:HD12	2.17	0.44
1:B:119:LEU:HD12	1:B:119:LEU:O	2.17	0.44
1:B:254:VAL:HB	7:B:4089:HOH:O	2.16	0.44
1:C:386:TYR:N	1:C:387:PRO:HD2	2.33	0.44
1:A:237:LYS:O	1:A:238:ASN:HB2	2.17	0.44
1:B:100:LEU:HD13	1:B:358:LEU:HD11	1.98	0.44
1:C:316:GLN:HE21	1:C:316:GLN:CA	2.29	0.44
1:C:408:ASP:HB3	7:C:4059:HOH:O	2.15	0.44
1:C:257:LYS:HB3	1:C:257:LYS:HZ2	1.82	0.44
1:A:114:GLU:OE2	1:A:291:GLU:HB2	2.17	0.44
1:A:235:LEU:HD12	1:A:327:LEU:HA	1.99	0.44
1:B:447:TYR:HB3	1:B:517:TRP:HZ2	1.82	0.44
1:C:24:PRO:HG3	1:C:37:PHE:CZ	2.52	0.44
1:C:353:GLN:O	1:C:467:ASP:HA	2.18	0.44
1:B:145:MET:CB	1:B:304:LEU:HD21	2.47	0.44
1:A:130:LYS:HD3	7:A:4038:HOH:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:233:SER:HA	1:A:234:PRO:HD3	1.84	0.44
1:B:522:GLN:HG2	7:B:4032:HOH:O	2.16	0.44
1:C:369:SER:O	5:C:2031:MVB:H113	2.17	0.44
1:A:340:ASN:N	1:A:340:ASN:OD1	2.49	0.44
1:B:264:LEU:HD23	7:B:4044:HOH:O	2.18	0.44
1:C:373:LEU:HD21	1:C:381:LEU:HD12	2.00	0.44
1:A:23:PRO:HA	1:A:24:PRO:HD3	1.86	0.43
1:A:25:VAL:HG22	1:A:34:LEU:HD23	2.00	0.43
1:A:353:GLN:O	1:A:467:ASP:HA	2.18	0.43
1:B:423:ASP:O	1:B:428:VAL:HG23	2.17	0.43
1:C:353:GLN:HE22	1:C:465:ILE:H	1.63	0.43
1:A:312:PRO:HG2	1:A:383:TRP:CD1	2.53	0.43
1:A:341:PHE:CZ	1:A:343:THR:HG22	2.54	0.43
1:B:202:GLN:HG2	7:B:4034:HOH:O	2.18	0.43
1:C:252:THR:HG22	1:C:254:VAL:HG12	2.00	0.43
1:A:257:LYS:HD2	1:A:319:LEU:HA	2.01	0.43
1:A:105:LYS:HE2	1:A:106:GLU:CB	2.48	0.43
1:B:382:LEU:HD11	1:B:391:ILE:HD12	2.00	0.43
1:C:330:LYS:HG3	1:C:335:LEU:CD2	2.47	0.43
1:A:176:GLY:HA2	1:A:189:TRP:HB2	2.00	0.43
3:B:1282:SIA:C11	3:B:1282:SIA:H6	2.49	0.43
1:B:257:LYS:NZ	1:B:317:PRO:CB	2.82	0.43
1:B:403:TYR:O	1:B:416:LEU:HD13	2.19	0.43
1:C:123:THR:O	1:C:123:THR:HG23	2.18	0.43
1:C:529:ILE:HA	1:C:533:THR:HG23	2.01	0.43
1:A:382:LEU:HG	1:A:396:ILE:HD12	2.00	0.43
1:B:429:PRO:O	1:B:433:VAL:HG23	2.19	0.43
1:C:102:THR:OG1	1:C:104:ARG:CG	2.66	0.43
1:C:311:ASP:HB3	1:C:314:GLU:HB2	2.00	0.43
1:A:30:HIS:HD2	7:A:4043:HOH:O	2.02	0.42
1:B:371:GLY:HA2	1:B:414:LYS:HD2	2.00	0.42
1:B:403:TYR:CD1	1:B:420:LEU:HD23	2.54	0.42
1:C:403:TYR:CD1	1:C:420:LEU:HD23	2.54	0.42
1:C:490:ILE:O	1:C:494:LYS:HG3	2.18	0.42
1:C:551:PHE:C	1:C:553:LYS:N	2.73	0.42
1:A:142:GLY:HA3	1:A:146:VAL:O	2.19	0.42
1:B:236:ALA:O	1:B:237:LYS:C	2.57	0.42
1:B:317:PRO:C	1:B:318:LEU:HG	2.40	0.42
1:B:407:THR:HG21	1:B:412:LYS:HZ3	1.84	0.42
1:C:132:ARG:N	1:C:132:ARG:HD2	2.30	0.42
1:C:333:GLU:HB2	7:C:4061:HOH:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:492:LEU:HD12	1:A:495:MET:HE3	2.01	0.42
1:B:384:LYS:O	1:B:387:PRO:HD2	2.19	0.42
1:C:197:ALA:O	1:C:201:VAL:HG23	2.20	0.42
1:C:242:ARG:HD3	1:C:503:PHE:O	2.18	0.42
1:C:526:TYR:CD2	1:C:539:LEU:HB2	2.55	0.42
1:C:132:ARG:HH21	1:C:206:ALA:HB1	1.85	0.42
1:C:58:PRO:HA	1:C:59:PRO:HD2	1.95	0.42
1:B:386:TYR:N	1:B:387:PRO:CD	2.81	0.42
1:C:131:ASN:O	1:C:209:GLY:HA2	2.20	0.42
1:C:86:MET:HB3	1:C:148:ALA:CB	2.49	0.42
1:A:135:VAL:HB	1:A:215:VAL:HG22	2.01	0.42
1:A:469:GLY:O	1:A:472:LEU:HB2	2.20	0.42
1:A:63:LEU:HA	1:A:63:LEU:HD23	1.79	0.42
1:C:351:ASN:HB3	1:C:466:GLY:O	2.19	0.42
1:A:104:ARG:NH2	1:A:150:SER:O	2.45	0.42
1:B:199:ARG:HG2	1:B:199:ARG:HH11	1.83	0.42
1:B:330:LYS:HB3	1:B:330:LYS:HE2	1.84	0.42
1:B:350:ILE:O	1:B:448:GLU:HA	2.19	0.42
1:B:242:ARG:NH1	1:B:242:ARG:HG2	2.32	0.42
1:B:79:ASN:O	3:B:1282:SIA:O2	2.29	0.42
1:C:301:MET:HG3	1:C:303:PHE:CZ	2.54	0.42
1:A:241:HIS:O	1:A:242:ARG:CG	2.68	0.42
1:A:386:TYR:C	1:A:388:LEU:H	2.23	0.42
1:B:66:THR:HG22	1:B:287:ARG:HH21	1.84	0.42
1:B:469:GLY:N	7:B:4013:HOH:O	2.46	0.42
1:C:477:GLY:HA2	1:C:493:SER:OG	2.20	0.42
1:A:129:LYS:HB3	1:A:129:LYS:HE2	1.82	0.41
1:B:227:VAL:O	1:B:231:VAL:HG23	2.19	0.41
1:B:442:ALA:HA	1:B:443:PRO:HD3	1.91	0.41
1:C:130:LYS:CD	1:C:130:LYS:C	2.87	0.41
1:C:341:PHE:CG	1:C:342:HIS:N	2.87	0.41
1:B:316:GLN:HA	1:B:317:PRO:HD3	1.82	0.41
1:C:218:PHE:N	1:C:218:PHE:CD1	2.88	0.41
1:C:339:ARG:N	1:C:339:ARG:HD2	2.35	0.41
1:A:264:LEU:HB2	7:A:4060:HOH:O	2.20	0.41
1:A:442:ALA:O	1:A:443:PRO:C	2.57	0.41
1:A:543:GLU:O	1:A:544:VAL:C	2.58	0.41
1:B:132:ARG:N	1:B:132:ARG:HD2	2.35	0.41
1:C:130:LYS:HD3	1:C:132:ARG:HD3	2.03	0.41
1:C:386:TYR:C	1:C:388:LEU:H	2.24	0.41
1:C:38:VAL:CG2	1:C:49:ILE:HD12	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:149:ALA:HB2	1:A:169:GLN:HG3	2.03	0.41
1:A:413:LYS:O	1:A:414:LYS:C	2.59	0.41
1:A:458:ASP:C	1:A:460:LYS:H	2.24	0.41
1:B:467:ASP:HB3	1:B:470:ASP:OD2	2.19	0.41
1:C:428:VAL:HG13	1:C:544:VAL:HG22	2.01	0.41
1:A:312:PRO:O	1:A:315:SER:HB2	2.20	0.41
1:A:317:PRO:C	1:A:318:LEU:HD12	2.40	0.41
1:A:527:LEU:HD11	1:A:533:THR:CG2	2.50	0.41
1:B:107:ASN:HD22	1:B:108:ILE:H	1.68	0.41
1:B:138:TRP:HA	1:B:218:PHE:O	2.20	0.41
1:B:257:LYS:NZ	1:B:317:PRO:HB3	2.36	0.41
1:C:306:LEU:HB2	1:C:364:MET:CE	2.51	0.41
1:C:309:GLN:H	1:C:309:GLN:HG2	1.69	0.41
1:C:30:His:HD2	7:C:4092:HOH:O	2.03	0.41
1:C:310:GLY:HA3	7:C:4086:HOH:O	2.20	0.41
1:A:526:TYR:CZ	1:A:536:ALA:HB3	2.55	0.41
1:B:257:LYS:HZ1	1:B:317:PRO:HB2	1.85	0.41
1:C:205:ILE:HA	1:C:205:ILE:HD12	1.90	0.41
1:C:78:LYS:HG3	7:C:4038:HOH:O	2.19	0.41
1:A:445:TYR:CZ	1:A:509:PRO:HD2	2.56	0.41
1:A:491:ARG:HH11	1:A:491:ARG:HG3	1.85	0.41
1:B:218:PHE:CB	1:B:244:ILE:HB	2.50	0.41
1:B:257:LYS:HZ1	1:B:317:PRO:CB	2.33	0.41
1:B:527:LEU:HD11	1:B:533:THR:HG22	2.03	0.41
1:A:236:ALA:HA	1:A:239:LEU:HD12	2.03	0.41
1:B:92:LYS:HB2	1:B:92:LYS:HE3	1.97	0.41
1:A:140:HIS:CD2	1:A:147:GLY:HA3	2.56	0.41
1:A:301:MET:HG3	1:A:303:PHE:CZ	2.56	0.41
1:B:315:SER:O	1:B:316:GLN:C	2.59	0.41
1:C:460:LYS:HA	1:C:461:PRO:HD2	1.90	0.41
1:A:325:GLY:HA2	1:A:329:LEU:HD23	2.04	0.40
1:A:553:LYS:HE2	7:A:4111:HOH:O	2.20	0.40
1:B:237:LYS:HE2	1:B:238:ASN:HD21	1.86	0.40
1:C:339:ARG:CG	1:C:440:ALA:HA	2.52	0.40
1:A:88:THR:CG2	1:A:175:TRP:CH2	3.04	0.40
1:A:331:THR:OG1	1:A:334:GLU:HG3	2.22	0.40
1:B:395:LEU:HD22	1:B:550:LEU:HD12	2.02	0.40
1:B:401:GLU:OE2	1:B:405:GLY:HA3	2.21	0.40
1:C:52:GLY:O	3:C:1382:SIA:H91	2.22	0.40
1:A:366:TYR:HA	1:A:367:PRO:HD3	1.91	0.40
1:B:339:ARG:HD2	1:B:339:ARG:N	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:423:ASP:OD1	1:B:540:LYS:HD2	2.21	0.40
1:C:267:GLN:NE2	1:C:316:GLN:HG3	2.34	0.40
1:C:523:LYS:O	1:C:524:GLU:HB2	2.22	0.40
1:B:211:ASN:HA	1:B:212:PRO:HD2	1.96	0.40
1:B:508:ASN:HB3	7:B:4014:HOH:O	2.22	0.40
1:C:296:GLU:O	1:C:300:LYS:HG3	2.21	0.40

There are no symmetry-related clashes.

## 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	530/532 (100%)	479 (90%)	43 (8%)	8 (2%)	10	42
1	B	530/532 (100%)	471 (89%)	50 (9%)	9 (2%)	9	39
1	C	530/532 (100%)	471 (89%)	48 (9%)	11 (2%)	7	33
All	All	1590/1596 (100%)	1421 (89%)	141 (9%)	28 (2%)	8	37

All (28) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	252	THR
1	A	341	PHE
1	C	41	GLU
1	C	254	VAL
1	A	317	PRO
1	A	338	GLU
1	A	375	GLN
1	B	317	PRO
1	C	315	SER
1	C	317	PRO
1	C	406	GLY

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Mol	Chain	Res	Type
1	A	459	MET
1	B	315	SER
1	B	406	GLY
1	C	252	THR
1	C	390	CYS
1	A	315	SER
1	B	318	LEU
1	C	185	SER
1	B	185	SER
1	B	253	SER
1	C	304	LEU
1	C	318	LEU
1	C	357	TRP
1	A	254	VAL
1	B	356	GLY
1	B	205	ILE
1	B	397	PRO

### 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	448/448 (100%)	429 (96%)	19 (4%)	30	66
1	B	448/448 (100%)	433 (97%)	15 (3%)	38	73
1	C	448/448 (100%)	426 (95%)	22 (5%)	25	61
All	All	1344/1344 (100%)	1288 (96%)	56 (4%)	30	66

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	72	GLU
1	A	104	ARG
1	A	105	LYS
1	A	218	PHE
1	A	254	VAL

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Mol	Chain	Res	Type
1	A	257	LYS
1	A	264	LEU
1	A	315	SER
1	A	316	GLN
1	A	317	PRO
1	A	318	LEU
1	A	319	LEU
1	A	338	GLU
1	A	340	ASN
1	A	341	PHE
1	A	381	LEU
1	A	500	TRP
1	A	523	LYS
1	A	528	GLN
1	B	28	THR
1	B	33	VAL
1	B	66	THR
1	B	88	THR
1	B	107	ASN
1	B	132	ARG
1	B	218	PHE
1	B	225	GLU
1	B	318	LEU
1	B	319	LEU
1	B	339	ARG
1	B	381	LEU
1	B	450	GLN
1	B	500	TRP
1	B	523	LYS
1	C	81	THR
1	C	92	LYS
1	C	104	ARG
1	C	130	LYS
1	C	132	ARG
1	C	218	PHE
1	C	257	LYS
1	C	309	GLN
1	C	317	PRO
1	C	326	MET
1	C	330	LYS
1	C	339	ARG
1	C	361	MET

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Mol	Chain	Res	Type
1	C	366	TYR
1	C	369	SER
1	C	370	GLU
1	C	381	LEU
1	C	488	GLU
1	C	500	TRP
1	C	506	ASN
1	C	528	GLN
1	C	553	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (43) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	HIS
1	A	69	GLN
1	A	140	HIS
1	A	160	HIS
1	A	238	ASN
1	A	241	HIS
1	A	288	GLN
1	A	316	GLN
1	A	336	GLN
1	A	351	ASN
1	A	372	GLN
1	A	375	GLN
1	A	436	ASN
1	A	437	HIS
1	A	528	GLN
1	A	534	GLN
1	A	537	GLN
1	B	45	GLN
1	B	140	HIS
1	B	238	ASN
1	B	241	HIS
1	B	336	GLN
1	B	351	ASN
1	B	372	GLN
1	B	375	GLN
1	B	436	ASN
1	B	437	HIS
1	B	537	GLN
1	C	30	HIS

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Mol	Chain	Res	Type
1	C	69	GLN
1	C	107	ASN
1	C	140	HIS
1	C	241	HIS
1	C	316	GLN
1	C	351	ASN
1	C	353	GLN
1	C	372	GLN
1	C	375	GLN
1	C	436	ASN
1	C	437	HIS
1	C	528	GLN
1	C	537	GLN
1	C	549	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

18 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
3	SIA	B	1282	-	18,21,21	0.73	0	21,31,31	0.92	0
3	SIA	C	1382	-	18,21,21	0.88	1 (5%)	21,31,31	0.84	1 (4%)
5	MVB	A	2011	-	24,24,24	3.24	14 (58%)	32,34,34	1.97	8 (25%)
4	SO4	C	3385	-	4,4,4	0.26	0	6,6,6	0.06	0
6	SMB	B	4002	-	3,6,6	1.18	0	3,7,7	0.72	0
2	NAG	C	1379	1	14,14,15	0.53	0	17,19,21	0.75	1 (5%)
6	SMB	A	4001	-	3,6,6	1.12	0	3,7,7	0.74	0
2	NAG	A	1179	1	14,14,15	0.65	0	17,19,21	0.63	0
4	SO4	B	3284	-	4,4,4	0.25	0	6,6,6	0.05	0
4	SO4	A	3285	-	4,4,4	0.25	0	6,6,6	0.10	0
4	SO4	C	3184	-	4,4,4	0.27	0	6,6,6	0.10	0
2	NAG	B	1279	1	14,14,15	0.62	0	17,19,21	0.60	0
3	SIA	A	1182	-	18,21,21	0.96	1 (5%)	21,31,31	0.82	0
5	MVB	C	2031	-	24,24,24	3.05	13 (54%)	32,34,34	1.80	5 (15%)
6	SMB	C	4003	-	3,6,6	1.14	0	3,7,7	0.70	0
4	SO4	B	3384	-	4,4,4	0.28	0	6,6,6	0.12	0
4	SO4	A	3185	-	4,4,4	0.25	0	6,6,6	0.07	0
6	SMB	B	4004	-	3,6,6	1.13	0	3,7,7	0.70	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
3	SIA	B	1282	-	-	8/14/38/38	0/1/1/1
3	SIA	C	1382	-	-	7/14/38/38	0/1/1/1
5	MVB	A	2011	-	-	3/5/44/44	0/3/3/3
6	SMB	B	4002	-	-	2/2/6/6	-
2	NAG	C	1379	1	-	5/6/23/26	0/1/1/1
6	SMB	A	4001	-	-	2/2/6/6	-
2	NAG	A	1179	1	-	6/6/23/26	0/1/1/1
2	NAG	B	1279	1	-	2/6/23/26	0/1/1/1
3	SIA	A	1182	-	-	8/14/38/38	0/1/1/1
5	MVB	C	2031	-	-	2/5/44/44	0/3/3/3
6	SMB	C	4003	-	-	2/2/6/6	-
6	SMB	B	4004	-	-	2/2/6/6	-

All (29) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	2011	MVB	C19-C18	6.61	1.61	1.52
5	A	2011	MVB	C15-C14	6.56	1.61	1.54
5	C	2031	MVB	C19-C18	6.53	1.61	1.52
5	C	2031	MVB	O3-C1	5.78	1.43	1.34
5	A	2011	MVB	C19-C14	5.48	1.62	1.54
5	A	2011	MVB	O3-C1	5.38	1.42	1.34
5	C	2031	MVB	C19-C14	5.17	1.62	1.54
5	C	2031	MVB	C15-C14	5.00	1.59	1.54
5	A	2011	MVB	C19-C20	4.08	1.60	1.54
5	A	2011	MVB	C15-C16	4.02	1.56	1.50
5	A	2011	MVB	C21-C20	3.88	1.58	1.52
5	C	2031	MVB	C21-C20	3.86	1.58	1.52
5	C	2031	MVB	C15-C16	3.73	1.56	1.50
5	C	2031	MVB	C19-C20	3.56	1.59	1.54
5	C	2031	MVB	C10-C1	2.60	1.56	1.50
5	C	2031	MVB	C21-C22	2.59	1.58	1.52
5	A	2011	MVB	C13-C14	2.52	1.58	1.53
5	A	2011	MVB	C17-C16	2.50	1.38	1.33
3	A	1182	SIA	O6-C2	2.47	1.45	1.43
5	A	2011	MVB	C21-C22	2.44	1.58	1.52
5	A	2011	MVB	C10-C1	2.39	1.56	1.50
5	A	2011	MVB	C23-C18	2.34	1.38	1.33
5	A	2011	MVB	C10-C9	2.24	1.56	1.52
5	C	2031	MVB	C17-C16	2.24	1.37	1.33
5	C	2031	MVB	C13-C14	2.18	1.57	1.53
5	C	2031	MVB	C10-C9	2.17	1.55	1.52
5	A	2011	MVB	C22-C23	2.11	1.55	1.50
3	C	1382	SIA	C3-C2	2.06	1.54	1.51
5	C	2031	MVB	C23-C18	2.03	1.37	1.33

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	2011	MVB	O3-C1-O2	5.53	123.82	117.88
5	C	2031	MVB	O3-C1-O2	5.49	123.78	117.88
5	C	2031	MVB	C19-C14-C15	-5.38	107.84	110.70
5	A	2011	MVB	C19-C14-C15	-4.88	108.11	110.70
5	A	2011	MVB	C13-C12-C7	3.46	120.43	114.03
5	A	2011	MVB	C12-C13-C14	3.13	118.76	113.90
5	A	2011	MVB	C11-C15-C14	3.10	117.56	114.52
5	A	2011	MVB	C13-C14-C19	2.79	116.29	112.50
5	C	2031	MVB	C11-C15-C16	-2.71	106.57	110.85
3	C	1382	SIA	C9-C8-C7	-2.53	106.92	112.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	2031	MVB	C13-C14-C19	2.53	115.93	112.50
2	C	1379	NAG	C2-N2-C7	-2.43	119.44	122.90
5	A	2011	MVB	C11-C15-C16	-2.38	107.09	110.85
5	C	2031	MVB	C13-C12-C7	2.20	118.10	114.03
5	A	2011	MVB	O3-C1-C10	-2.07	114.87	118.86

There are no chirality outliers.

All (49) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	1282	SIA	C5-C6-C7-C8
3	B	1282	SIA	C5-C6-C7-O7
3	B	1282	SIA	O6-C6-C7-C8
3	B	1282	SIA	O6-C6-C7-O7
3	B	1282	SIA	C11-C10-N5-C5
3	B	1282	SIA	O10-C10-N5-C5
5	A	2011	MVB	C13-C12-C7-C8
3	C	1382	SIA	C5-C6-C7-C8
3	C	1382	SIA	O6-C6-C7-C8
3	C	1382	SIA	C11-C10-N5-C5
3	C	1382	SIA	O10-C10-N5-C5
6	A	4001	SMB	C1-C2-C3-C4
6	A	4001	SMB	C1-C2-C3-C5
2	A	1179	NAG	C8-C7-N2-C2
2	A	1179	NAG	O7-C7-N2-C2
2	C	1379	NAG	C8-C7-N2-C2
2	C	1379	NAG	O7-C7-N2-C2
6	C	4003	SMB	C1-C2-C3-C4
6	C	4003	SMB	C1-C2-C3-C5
3	A	1182	SIA	C5-C6-C7-C8
3	A	1182	SIA	C5-C6-C7-O7
3	A	1182	SIA	O6-C6-C7-O7
3	A	1182	SIA	C11-C10-N5-C5
3	A	1182	SIA	O10-C10-N5-C5
6	B	4004	SMB	C1-C2-C3-C4
6	B	4004	SMB	C1-C2-C3-C5
6	B	4002	SMB	C1-C2-C3-C4
6	B	4002	SMB	C1-C2-C3-C5
2	C	1379	NAG	O5-C5-C6-O6
2	B	1279	NAG	C8-C7-N2-C2
2	B	1279	NAG	O7-C7-N2-C2
2	A	1179	NAG	O5-C5-C6-O6

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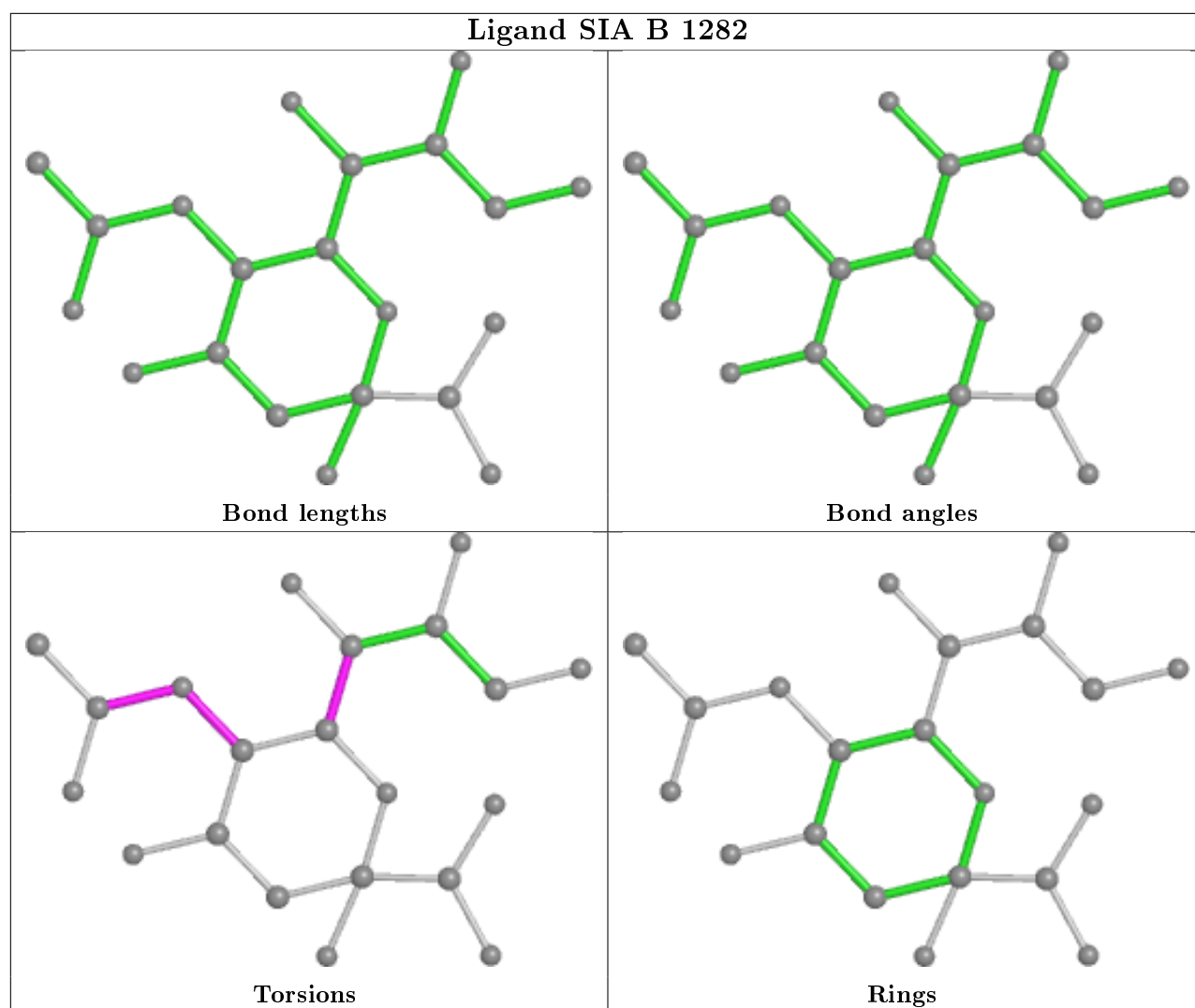
Mol	Chain	Res	Type	Atoms
2	A	1179	NAG	C4-C5-C6-O6
2	C	1379	NAG	C4-C5-C6-O6
2	A	1179	NAG	C1-C2-N2-C7
3	B	1282	SIA	C4-C5-N5-C10
3	A	1182	SIA	C6-C5-N5-C10
5	A	2011	MVB	C13-C12-C7-O3
5	A	2011	MVB	C12-C13-C14-C19
3	C	1382	SIA	C6-C5-N5-C10
3	A	1182	SIA	C4-C5-N5-C10
3	C	1382	SIA	C5-C6-C7-O7
3	A	1182	SIA	O6-C6-C7-C8
3	C	1382	SIA	C4-C5-N5-C10
5	C	2031	MVB	C12-C13-C14-C19
3	B	1282	SIA	C6-C5-N5-C10
2	C	1379	NAG	C1-C2-N2-C7
2	A	1179	NAG	C3-C2-N2-C7
5	C	2031	MVB	C12-C13-C14-C15

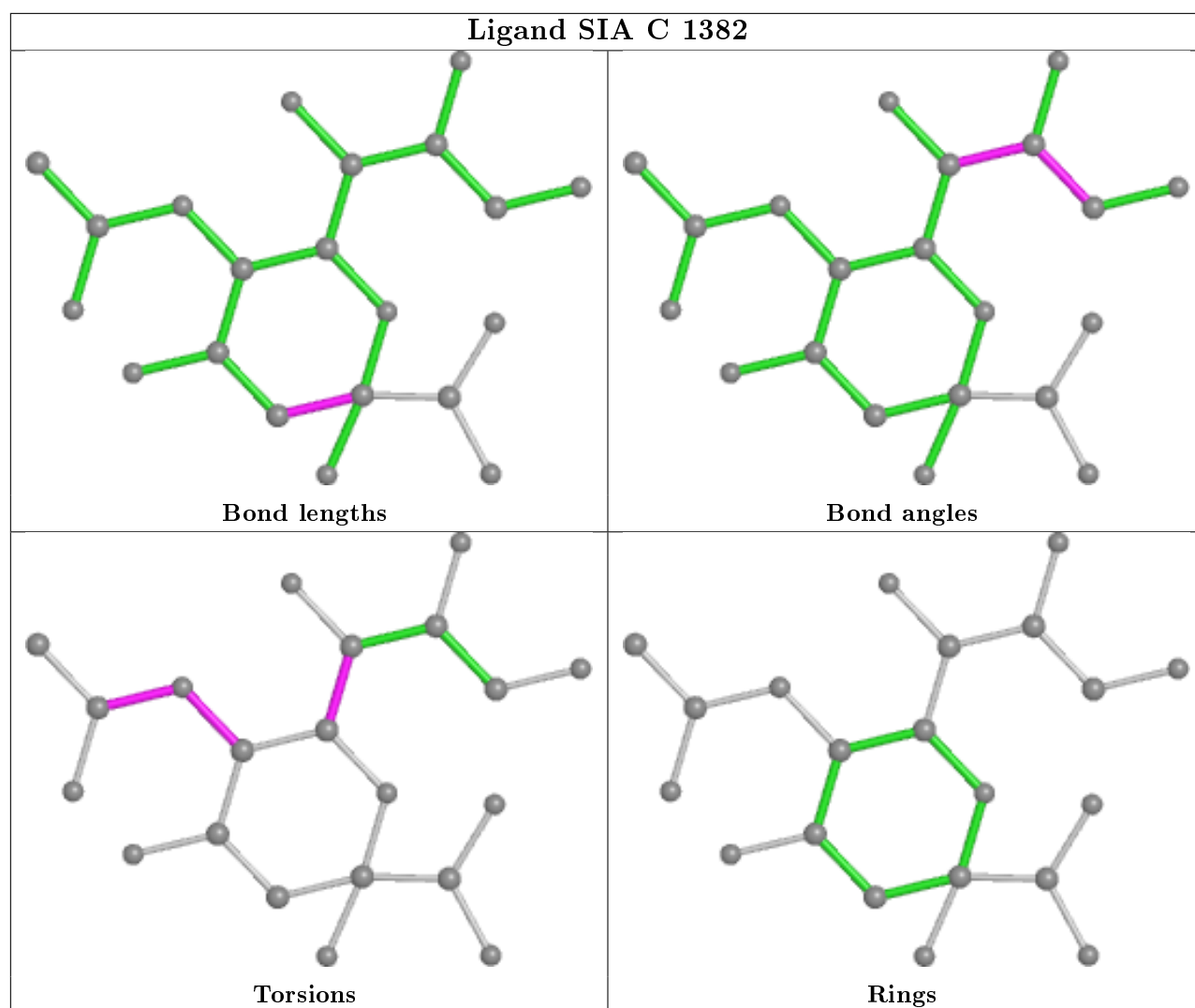
There are no ring outliers.

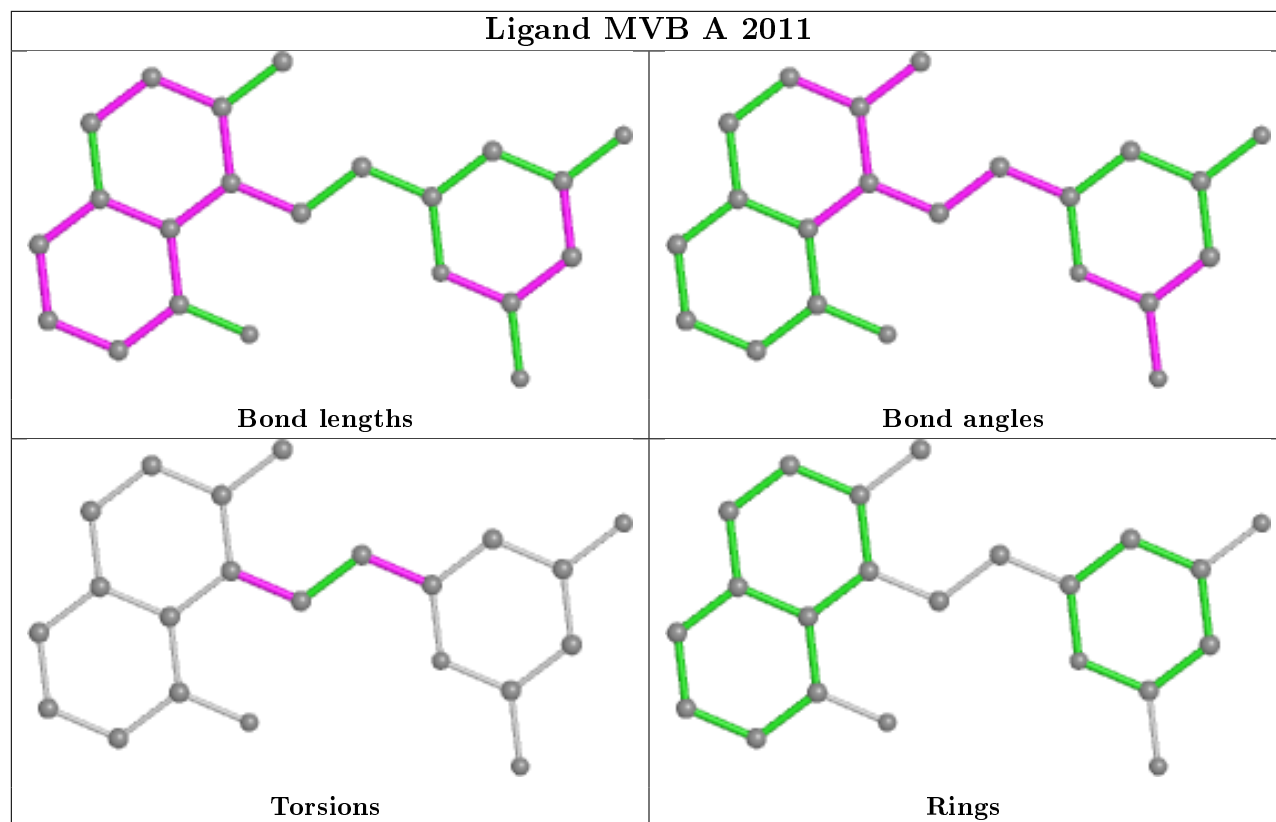
6 monomers are involved in 23 short contacts:

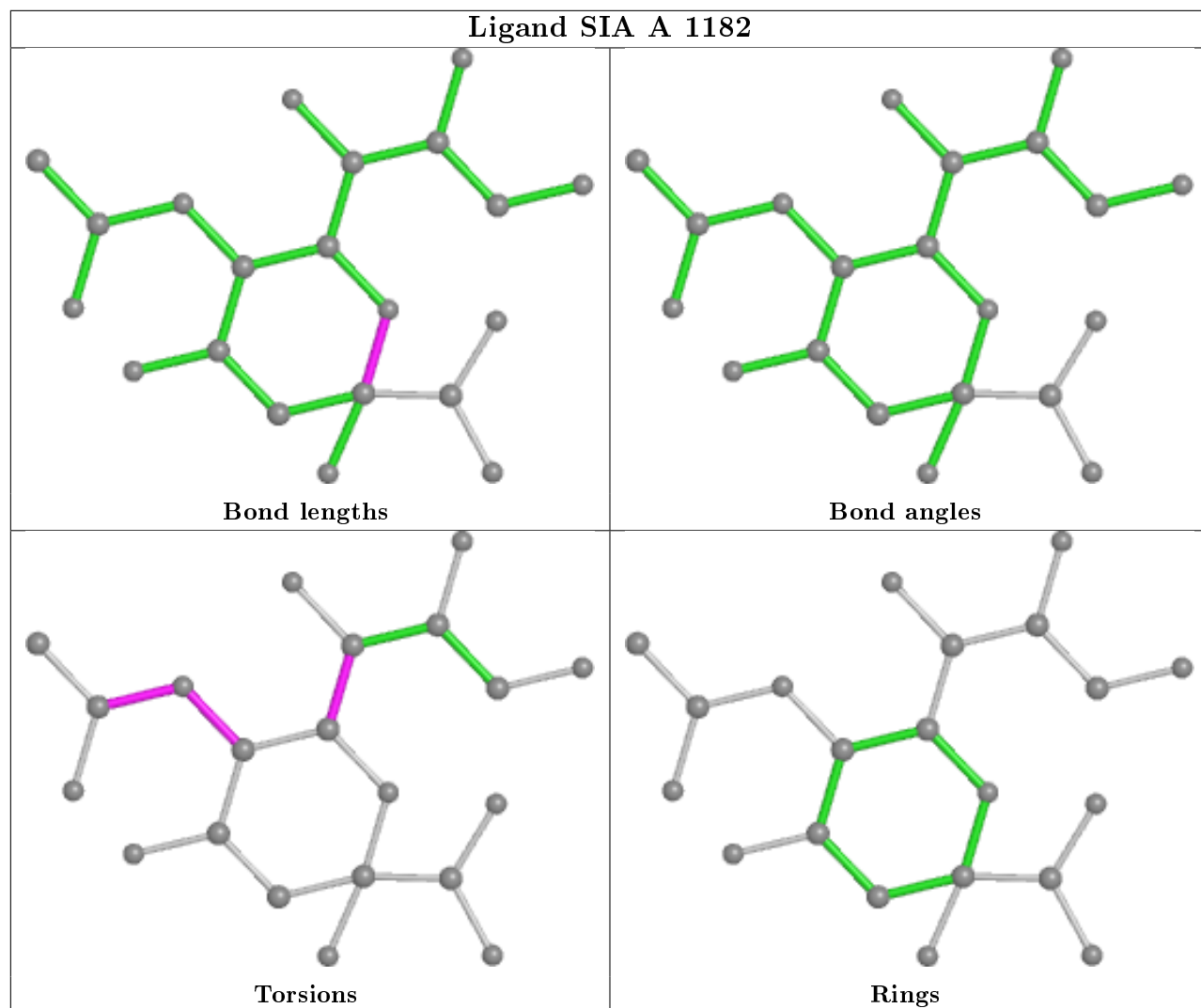
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1282	SIA	7	0
3	C	1382	SIA	7	0
5	A	2011	MVB	1	0
4	C	3385	SO4	1	0
3	A	1182	SIA	2	0
5	C	2031	MVB	5	0

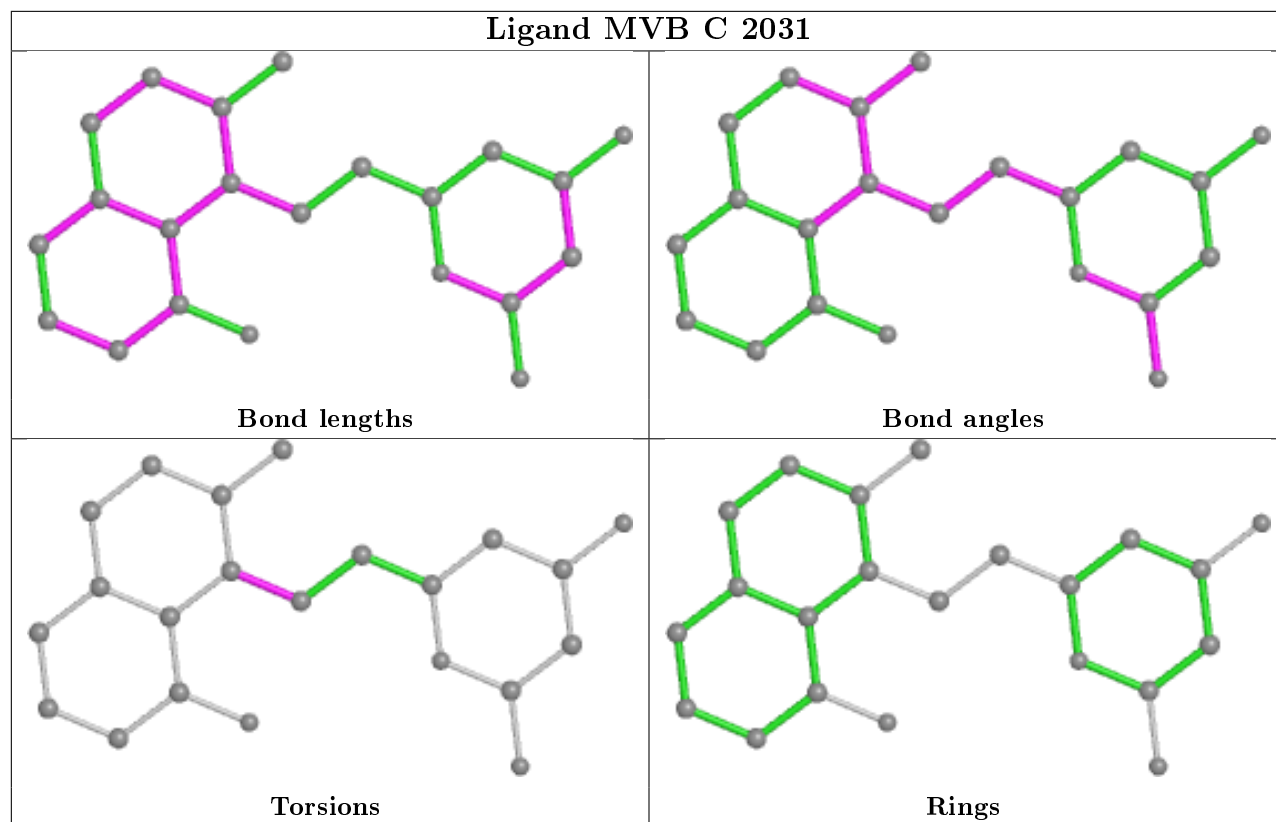
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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











## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	532/532 (100%)	-0.64	7 (1%) 77 51	3, 20, 74, 92	0
1	B	532/532 (100%)	-0.49	10 (1%) 66 37	6, 26, 84, 98	0
1	C	532/532 (100%)	-0.71	5 (0%) 84 63	3, 20, 56, 89	0
All	All	1596/1596 (100%)	-0.61	22 (1%) 75 49	3, 22, 79, 98	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	340	ASN	4.3
1	A	21	SER	3.8
1	A	340	ASN	3.4
1	A	314	GLU	3.2
1	B	21	SER	2.9
1	C	308	LEU	2.8
1	B	309	GLN	2.8
1	C	309	GLN	2.8
1	B	339	ARG	2.7
1	A	339	ARG	2.6
1	B	313	ARG	2.6
1	A	307	ASP	2.6
1	B	312	PRO	2.5
1	A	316	GLN	2.4
1	B	315	SER	2.4
1	C	316	GLN	2.3
1	B	314	GLU	2.2
1	C	314	GLU	2.2
1	B	310	GLY	2.1
1	B	406	GLY	2.1
1	C	307	ASP	2.1
1	A	369	SER	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 6.4 Ligands ⓘ

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, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

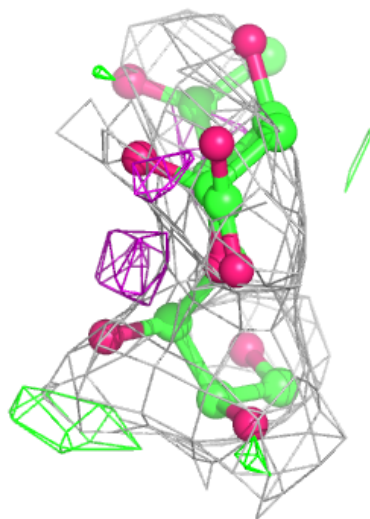
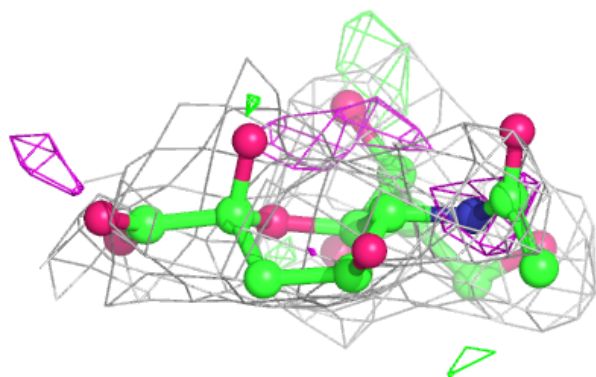
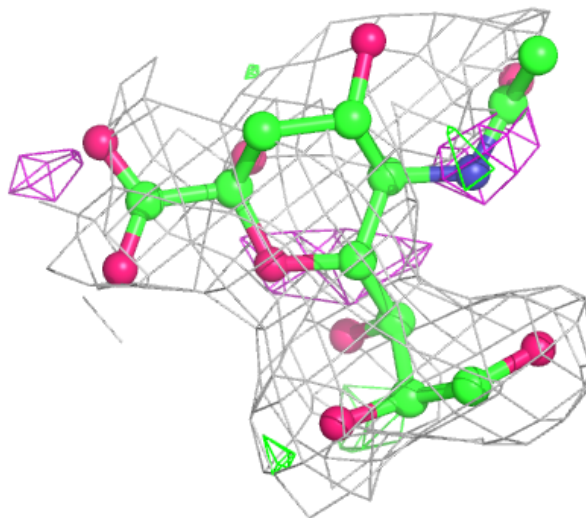
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	SIA	A	1182	21/21	0.71	0.37	46,73,75,76	0
5	MVB	A	2011	22/22	0.72	0.28	57,68,71,72	0
2	NAG	A	1179	14/15	0.74	0.48	54,59,60,62	0
5	MVB	C	2031	22/22	0.74	0.33	52,64,68,70	0
2	NAG	C	1379	14/15	0.79	0.43	52,57,58,60	0
3	SIA	B	1282	21/21	0.80	0.28	31,55,61,62	0
3	SIA	C	1382	21/21	0.82	0.27	48,58,62,64	0
2	NAG	B	1279	14/15	0.86	0.39	46,49,52,52	0
6	SMB	B	4004	7/7	0.88	0.32	61,63,64,65	0
4	SO4	C	3184	5/5	0.90	0.29	77,77,77,78	0
6	SMB	B	4002	7/7	0.90	0.21	58,59,60,60	0
4	SO4	B	3284	5/5	0.93	0.19	81,82,82,82	0
6	SMB	C	4003	7/7	0.94	0.18	63,65,65,65	0
4	SO4	A	3185	5/5	0.94	0.24	96,96,97,97	0
6	SMB	A	4001	7/7	0.95	0.17	66,67,68,68	0
4	SO4	B	3384	5/5	0.96	0.16	66,67,67,68	0
4	SO4	C	3385	5/5	0.96	0.20	85,85,86,86	0
4	SO4	A	3285	5/5	0.96	0.17	78,78,79,79	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.



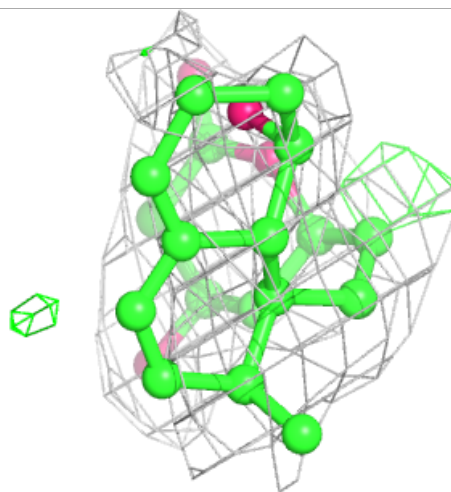
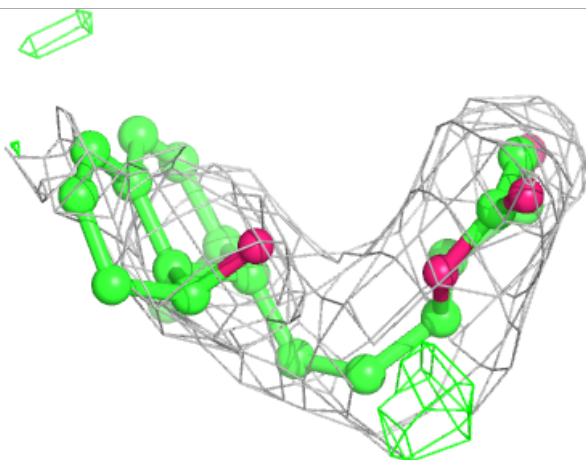
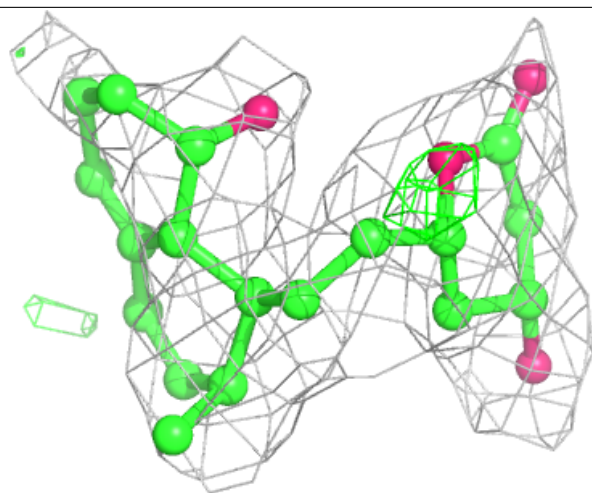
**Electron density around SIA A 1182:**

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



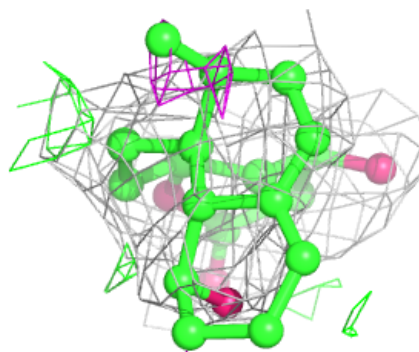
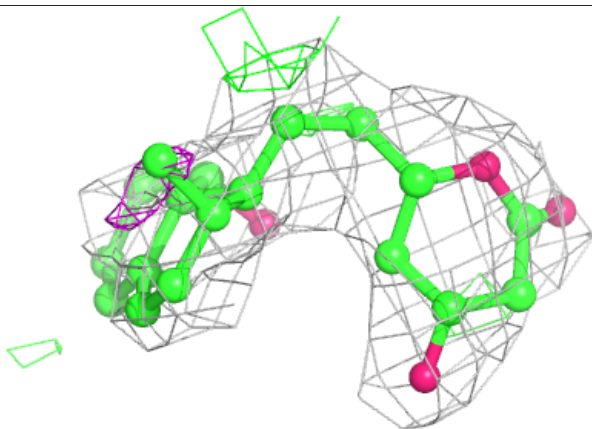
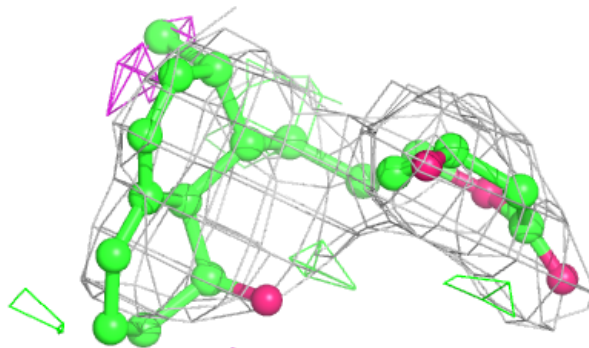
**Electron density around MVB A 2011:**

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



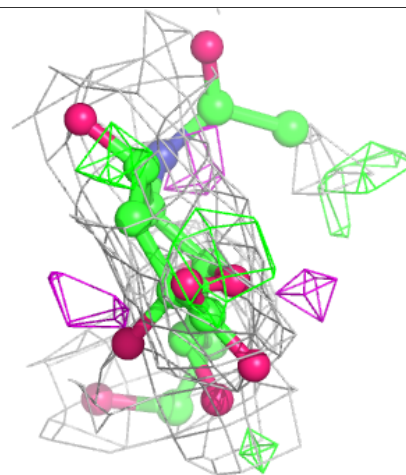
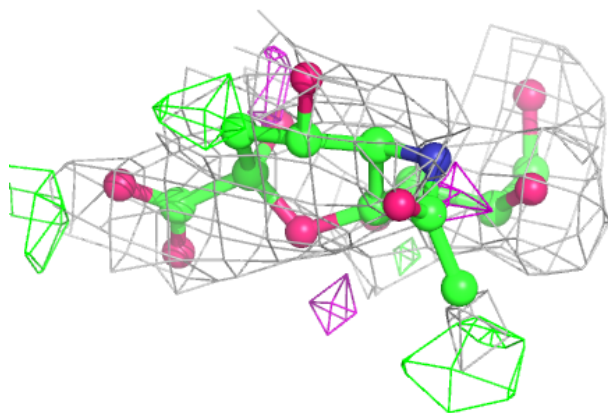
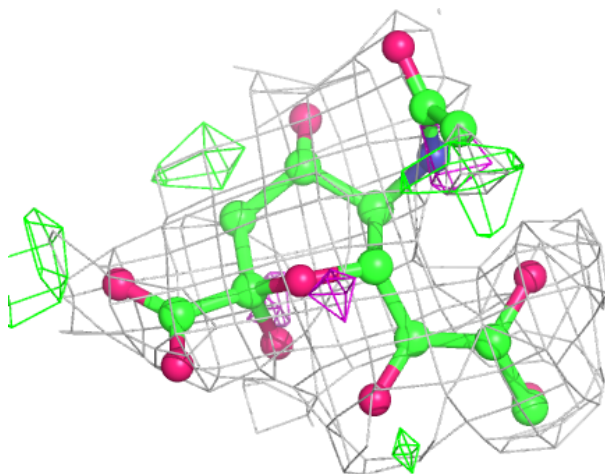
**Electron density around MVB C 2031:**

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



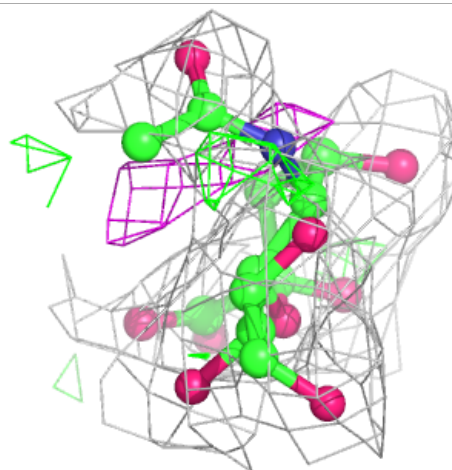
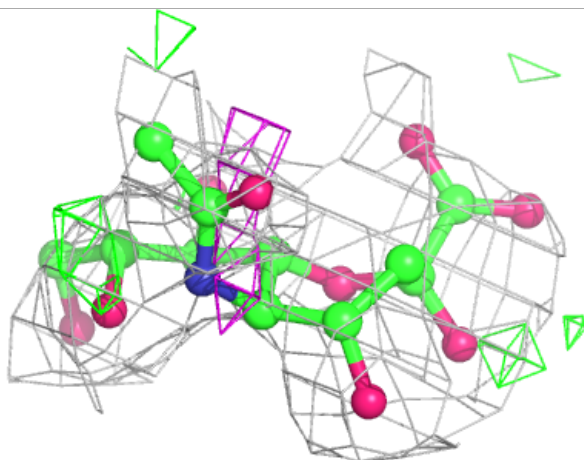
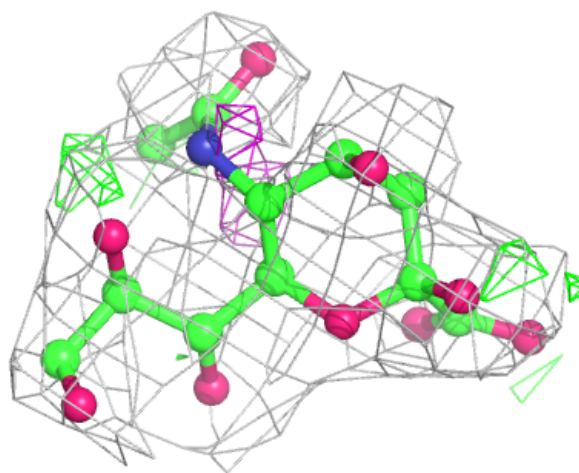
**Electron density around SIA B 1282:**

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



**Electron density around SIA C 1382:**

$2mF_o-DF_c$  (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.