



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 6, 2020 – 11:25 PM BST

PDB ID : 4CAJ
Title : Crystallographic structure of the mouse SIGN-R1 CRD domain in complex with sialic acid
Authors : Silva-Martin, N.; Bartual, S.G.; Hermoso, J.A.
Deposited on : 2013-10-08
Resolution : 2.19 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 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

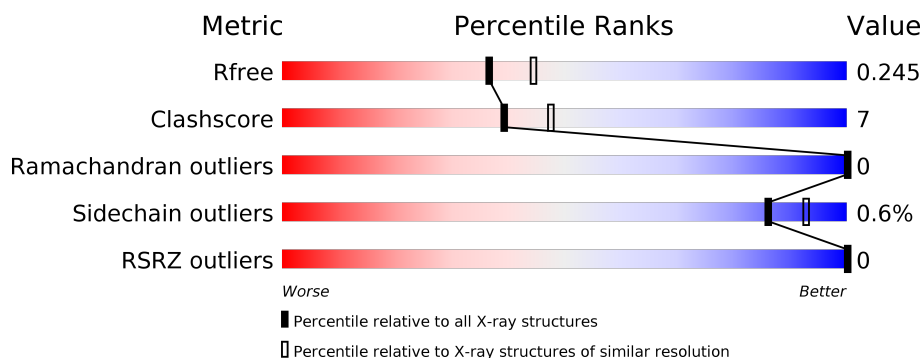
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.19 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on 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	158	<div> <div style="width: 65%;"></div> <div style="width: 18%;"></div> <div style="width: 17%;"></div> </div> <div>65% 18% 17%</div>
1	B	158	<div> <div style="width: 70%;"></div> <div style="width: 15%;"></div> <div style="width: 16%;"></div> </div> <div>70% 15% 16%</div>
1	C	158	<div> <div style="width: 68%;"></div> <div style="width: 15%;"></div> <div style="width: 16%;"></div> </div> <div>68% 15% 16%</div>
1	D	158	<div> <div style="width: 73%;"></div> <div style="width: 11%;"></div> <div style="width: 16%;"></div> </div> <div>73% 11% 16%</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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SO4	C	1327	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4976 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 CD209 ANTIGEN-LIKE PROTEIN B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	131	Total	C	N	O	S	0	0	0
			1065	678	179	199	9			
1	B	133	Total	C	N	O	S	0	0	0
			1080	688	181	202	9			
1	C	132	Total	C	N	O	S	0	0	0
			1073	684	180	200	9			
1	D	132	Total	C	N	O	S	0	0	0
			1073	684	180	200	9			

There are 92 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	168	MET	-	expression tag	UNP Q8CJ91
A	169	SER	-	expression tag	UNP Q8CJ91
A	170	ALA	-	expression tag	UNP Q8CJ91
A	171	LEU	-	expression tag	UNP Q8CJ91
A	172	LEU	-	expression tag	UNP Q8CJ91
A	173	ILE	-	expression tag	UNP Q8CJ91
A	174	LEU	-	expression tag	UNP Q8CJ91
A	175	ALA	-	expression tag	UNP Q8CJ91
A	176	LEU	-	expression tag	UNP Q8CJ91
A	177	VAL	-	expression tag	UNP Q8CJ91
A	178	GLY	-	expression tag	UNP Q8CJ91
A	179	ALA	-	expression tag	UNP Q8CJ91
A	180	ALA	-	expression tag	UNP Q8CJ91
A	181	VAL	-	expression tag	UNP Q8CJ91
A	182	ALA	-	expression tag	UNP Q8CJ91
A	183	ASP	-	expression tag	UNP Q8CJ91
A	184	TYR	-	expression tag	UNP Q8CJ91
A	185	LYS	-	expression tag	UNP Q8CJ91
A	186	ASP	-	expression tag	UNP Q8CJ91
A	187	ASP	-	expression tag	UNP Q8CJ91
A	188	ASP	-	expression tag	UNP Q8CJ91

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Chain	Residue	Modelled	Actual	Comment	Reference
A	189	ASP	-	expression tag	UNP Q8CJ91
A	190	LYS	-	expression tag	UNP Q8CJ91
B	168	MET	-	expression tag	UNP Q8CJ91
B	169	SER	-	expression tag	UNP Q8CJ91
B	170	ALA	-	expression tag	UNP Q8CJ91
B	171	LEU	-	expression tag	UNP Q8CJ91
B	172	LEU	-	expression tag	UNP Q8CJ91
B	173	ILE	-	expression tag	UNP Q8CJ91
B	174	LEU	-	expression tag	UNP Q8CJ91
B	175	ALA	-	expression tag	UNP Q8CJ91
B	176	LEU	-	expression tag	UNP Q8CJ91
B	177	VAL	-	expression tag	UNP Q8CJ91
B	178	GLY	-	expression tag	UNP Q8CJ91
B	179	ALA	-	expression tag	UNP Q8CJ91
B	180	ALA	-	expression tag	UNP Q8CJ91
B	181	VAL	-	expression tag	UNP Q8CJ91
B	182	ALA	-	expression tag	UNP Q8CJ91
B	183	ASP	-	expression tag	UNP Q8CJ91
B	184	TYR	-	expression tag	UNP Q8CJ91
B	185	LYS	-	expression tag	UNP Q8CJ91
B	186	ASP	-	expression tag	UNP Q8CJ91
B	187	ASP	-	expression tag	UNP Q8CJ91
B	188	ASP	-	expression tag	UNP Q8CJ91
B	189	ASP	-	expression tag	UNP Q8CJ91
B	190	LYS	-	expression tag	UNP Q8CJ91
C	168	MET	-	expression tag	UNP Q8CJ91
C	169	SER	-	expression tag	UNP Q8CJ91
C	170	ALA	-	expression tag	UNP Q8CJ91
C	171	LEU	-	expression tag	UNP Q8CJ91
C	172	LEU	-	expression tag	UNP Q8CJ91
C	173	ILE	-	expression tag	UNP Q8CJ91
C	174	LEU	-	expression tag	UNP Q8CJ91
C	175	ALA	-	expression tag	UNP Q8CJ91
C	176	LEU	-	expression tag	UNP Q8CJ91
C	177	VAL	-	expression tag	UNP Q8CJ91
C	178	GLY	-	expression tag	UNP Q8CJ91
C	179	ALA	-	expression tag	UNP Q8CJ91
C	180	ALA	-	expression tag	UNP Q8CJ91
C	181	VAL	-	expression tag	UNP Q8CJ91
C	182	ALA	-	expression tag	UNP Q8CJ91
C	183	ASP	-	expression tag	UNP Q8CJ91
C	184	TYR	-	expression tag	UNP Q8CJ91

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Chain	Residue	Modelled	Actual	Comment	Reference
C	185	LYS	-	expression tag	UNP Q8CJ91
C	186	ASP	-	expression tag	UNP Q8CJ91
C	187	ASP	-	expression tag	UNP Q8CJ91
C	188	ASP	-	expression tag	UNP Q8CJ91
C	189	ASP	-	expression tag	UNP Q8CJ91
C	190	LYS	-	expression tag	UNP Q8CJ91
D	168	MET	-	expression tag	UNP Q8CJ91
D	169	SER	-	expression tag	UNP Q8CJ91
D	170	ALA	-	expression tag	UNP Q8CJ91
D	171	LEU	-	expression tag	UNP Q8CJ91
D	172	LEU	-	expression tag	UNP Q8CJ91
D	173	ILE	-	expression tag	UNP Q8CJ91
D	174	LEU	-	expression tag	UNP Q8CJ91
D	175	ALA	-	expression tag	UNP Q8CJ91
D	176	LEU	-	expression tag	UNP Q8CJ91
D	177	VAL	-	expression tag	UNP Q8CJ91
D	178	GLY	-	expression tag	UNP Q8CJ91
D	179	ALA	-	expression tag	UNP Q8CJ91
D	180	ALA	-	expression tag	UNP Q8CJ91
D	181	VAL	-	expression tag	UNP Q8CJ91
D	182	ALA	-	expression tag	UNP Q8CJ91
D	183	ASP	-	expression tag	UNP Q8CJ91
D	184	TYR	-	expression tag	UNP Q8CJ91
D	185	LYS	-	expression tag	UNP Q8CJ91
D	186	ASP	-	expression tag	UNP Q8CJ91
D	187	ASP	-	expression tag	UNP Q8CJ91
D	188	ASP	-	expression tag	UNP Q8CJ91
D	189	ASP	-	expression tag	UNP Q8CJ91
D	190	LYS	-	expression tag	UNP Q8CJ91

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Ca 1 1	0	0
2	A	1	Total Ca 1 1	0	0
2	D	1	Total Ca 1 1	0	0
2	C	1	Total Ca 1 1	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



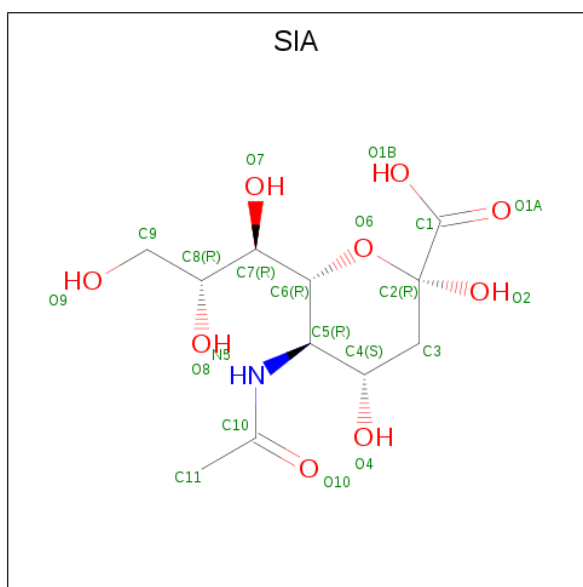
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total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

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

- Molecule 4 is N-acetyl-alpha-neuraminic acid (three-letter code: SIA) (formula: C₁₁H₁₉NO₉).



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

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Cl	0	0
			1	1		
5	C	1	Total	Cl	0	0
			1	1		

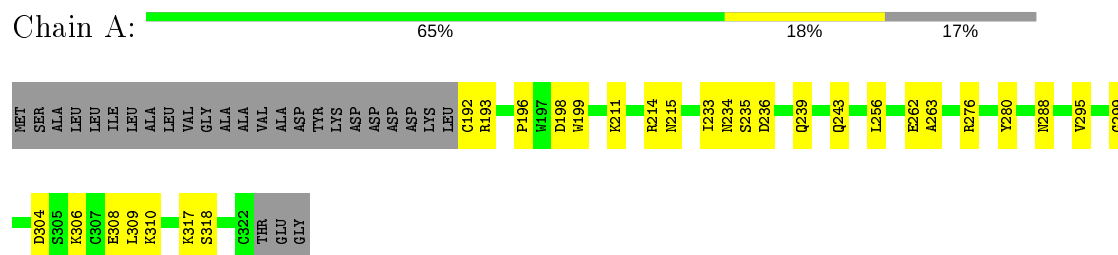
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	102	Total	O	0	0
			102	102		
6	B	121	Total	O	0	0
			121	121		
6	C	113	Total	O	0	0
			113	113		
6	D	130	Total	O	0	0
			130	130		

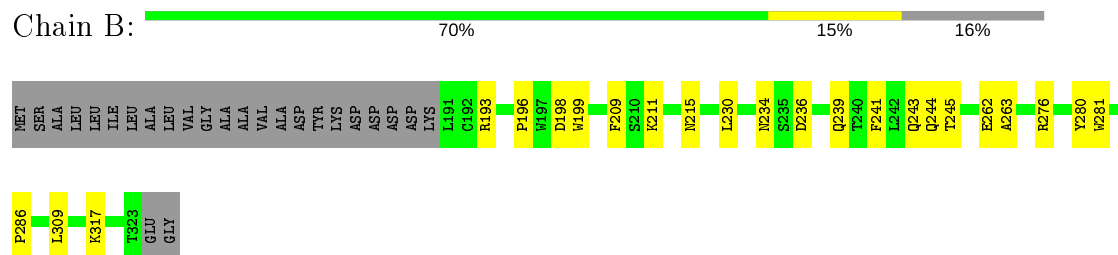
3 Residue-property plots

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.

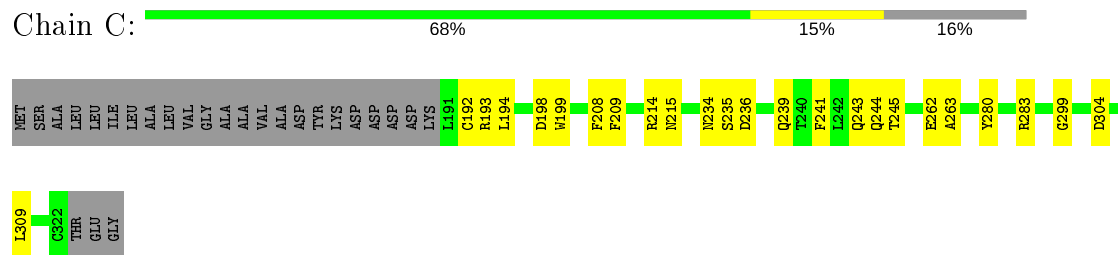
• Molecule 1: CD209 ANTIGEN-LIKE PROTEIN B



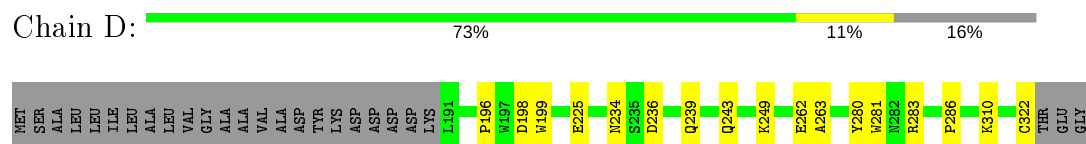
• Molecule 1: CD209 ANTIGEN-LIKE PROTEIN B



• Molecule 1: CD209 ANTIGEN-LIKE PROTEIN B



• Molecule 1: CD209 ANTIGEN-LIKE PROTEIN B



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	146.20Å 94.47Å 76.14Å 90.00° 121.42° 90.00°	Depositor
Resolution (Å)	14.95 – 2.19 42.98 – 2.19	Depositor EDS
% Data completeness (in resolution range)	98.1 (14.95-2.19) 98.0 (42.98-2.19)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.31 (at 2.20Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.205 , 0.281 0.219 , 0.245	Depositor DCC
R_{free} test set	2280 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å ²)	30.8	Xtriage
Anisotropy	0.396	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 88.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.398 for -h-2*k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4976	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 40.97 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.5287e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, CL, SO4, 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	0.72	0/1095	0.74	2/1482 (0.1%)
1	B	0.71	0/1110	0.72	0/1503
1	C	0.74	0/1103	0.74	1/1493 (0.1%)
1	D	0.68	0/1103	0.69	0/1493
All	All	0.71	0/4411	0.72	3/5971 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	304	ASP	CB-CG-OD2	-6.12	112.79	118.30
1	A	304	ASP	CB-CG-OD1	5.56	123.31	118.30
1	C	304	ASP	CB-CG-OD1	5.46	123.21	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	230	LEU	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1065	0	1006	24	0
1	B	1080	0	1024	14	0
1	C	1073	0	1017	19	0
1	D	1073	0	1017	14	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	40	0	0	3	0
3	B	40	0	0	0	0
3	C	40	0	0	3	0
3	D	30	0	0	1	0
4	A	21	0	17	1	0
4	B	21	0	17	0	0
4	C	21	0	17	0	0
5	A	1	0	0	0	0
5	C	1	0	0	0	0
6	A	102	0	0	3	0
6	B	121	0	0	1	0
6	C	113	0	0	2	0
6	D	130	0	0	4	0
All	All	4976	0	4115	64	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 7.

The worst 5 of 64 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:C:236:ASP:OD1	1:C:280:TYR:OH	1.95	0.83
1:D:225:GLU:OE1	6:D:2023:HOH:O	2.03	0.76
1:B:236:ASP:OD2	1:B:280:TYR:OH	2.10	0.69
1:A:288:ASN:N	4:A:1327:SIA:O2	2.25	0.68
1:B:276:ARG:NH2	6:B:2036:HOH:O	2.23	0.67

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	129/158 (82%)	121 (94%)	8 (6%)	0	100	100
1	B	131/158 (83%)	124 (95%)	7 (5%)	0	100	100
1	C	130/158 (82%)	122 (94%)	8 (6%)	0	100	100
1	D	130/158 (82%)	125 (96%)	5 (4%)	0	100	100
All	All	520/632 (82%)	492 (95%)	28 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	116/136 (85%)	115 (99%)	1 (1%)	78	88
1	B	118/136 (87%)	117 (99%)	1 (1%)	81	90
1	C	117/136 (86%)	116 (99%)	1 (1%)	78	88
1	D	117/136 (86%)	117 (100%)	0	100	100
All	All	468/544 (86%)	465 (99%)	3 (1%)	86	93

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	235	SER
1	B	211	LYS
1	C	235	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	244	GLN

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](#)

Of 39 ligands modelled in this entry, 6 are monoatomic - leaving 33 for Mogul analysis.

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	SO4	A	1329	-	4,4,4	0.14	0	6,6,6	0.22	0
3	SO4	A	1331	-	4,4,4	0.11	0	6,6,6	0.23	0
3	SO4	A	1325	-	4,4,4	0.15	0	6,6,6	0.19	0
3	SO4	C	1325	-	4,4,4	0.16	0	6,6,6	0.14	0
3	SO4	B	1332	-	4,4,4	0.14	0	6,6,6	0.14	0
3	SO4	B	1334	-	4,4,4	0.22	0	6,6,6	0.19	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	C	1333	-	4,4,4	0.22	0	6,6,6	0.20	0
3	SO4	A	1332	-	4,4,4	0.09	0	6,6,6	0.36	0
3	SO4	D	1329	-	4,4,4	0.15	0	6,6,6	0.75	0
3	SO4	D	1326	-	4,4,4	0.16	0	6,6,6	0.08	0
3	SO4	A	1333	-	4,4,4	0.10	0	6,6,6	0.26	0
3	SO4	A	1330	-	4,4,4	0.16	0	6,6,6	0.17	0
3	SO4	A	1324	-	4,4,4	0.18	0	6,6,6	0.19	0
4	SIA	A	1327	-	18,21,21	3.72	9 (50%)	21,31,31	1.10	1 (4%)
4	SIA	C	1328	2	18,21,21	3.38	7 (38%)	21,31,31	1.21	1 (4%)
3	SO4	D	1328	-	4,4,4	0.18	0	6,6,6	0.15	0
3	SO4	B	1331	-	4,4,4	0.14	0	6,6,6	0.16	0
3	SO4	D	1327	-	4,4,4	0.13	0	6,6,6	0.18	0
3	SO4	A	1326	-	4,4,4	0.09	0	6,6,6	0.24	0
3	SO4	C	1330	-	4,4,4	0.14	0	6,6,6	0.17	0
3	SO4	C	1331	-	4,4,4	0.17	0	6,6,6	0.21	0
3	SO4	B	1328	-	4,4,4	0.14	0	6,6,6	0.17	0
3	SO4	D	1325	-	4,4,4	0.17	0	6,6,6	0.39	0
3	SO4	B	1326	-	4,4,4	0.34	0	6,6,6	0.38	0
3	SO4	C	1332	-	4,4,4	0.19	0	6,6,6	0.14	0
3	SO4	C	1326	-	4,4,4	0.15	0	6,6,6	0.38	0
3	SO4	B	1327	-	4,4,4	0.15	0	6,6,6	0.14	0
4	SIA	B	1329	2	18,21,21	3.66	9 (50%)	21,31,31	1.48	3 (14%)
3	SO4	B	1324	-	4,4,4	0.21	0	6,6,6	0.49	0
3	SO4	B	1330	-	4,4,4	0.17	0	6,6,6	0.16	0
3	SO4	D	1324	-	4,4,4	0.15	0	6,6,6	0.39	0
3	SO4	C	1327	-	4,4,4	0.15	0	6,6,6	0.18	0
3	SO4	C	1324	-	4,4,4	0.15	0	6,6,6	0.29	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
4	SIA	C	1328	2	-	6/14/38/38	0/1/1/1
4	SIA	A	1327	-	-	1/14/38/38	0/1/1/1
4	SIA	B	1329	2	-	2/14/38/38	0/1/1/1

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1327	SIA	O6-C2	11.97	1.55	1.43
4	B	1329	SIA	O6-C2	11.64	1.54	1.43
4	C	1328	SIA	O6-C2	10.63	1.53	1.43
4	B	1329	SIA	C4-C5	-5.84	1.48	1.53
4	C	1328	SIA	C4-C5	-5.69	1.48	1.53

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1329	SIA	O6-C6-C5	3.94	113.62	109.78
4	B	1329	SIA	C11-C10-N5	3.52	122.06	116.10
4	C	1328	SIA	C11-C10-N5	3.06	121.28	116.10
4	A	1327	SIA	O10-C10-C11	-2.57	117.28	122.06
4	B	1329	SIA	O10-C10-C11	-2.27	117.83	122.06

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	1328	SIA	C5-C6-C7-C8
4	C	1328	SIA	C5-C6-C7-O7
4	C	1328	SIA	O6-C6-C7-C8
4	C	1328	SIA	O6-C6-C7-O7
4	A	1327	SIA	C4-C5-N5-C10

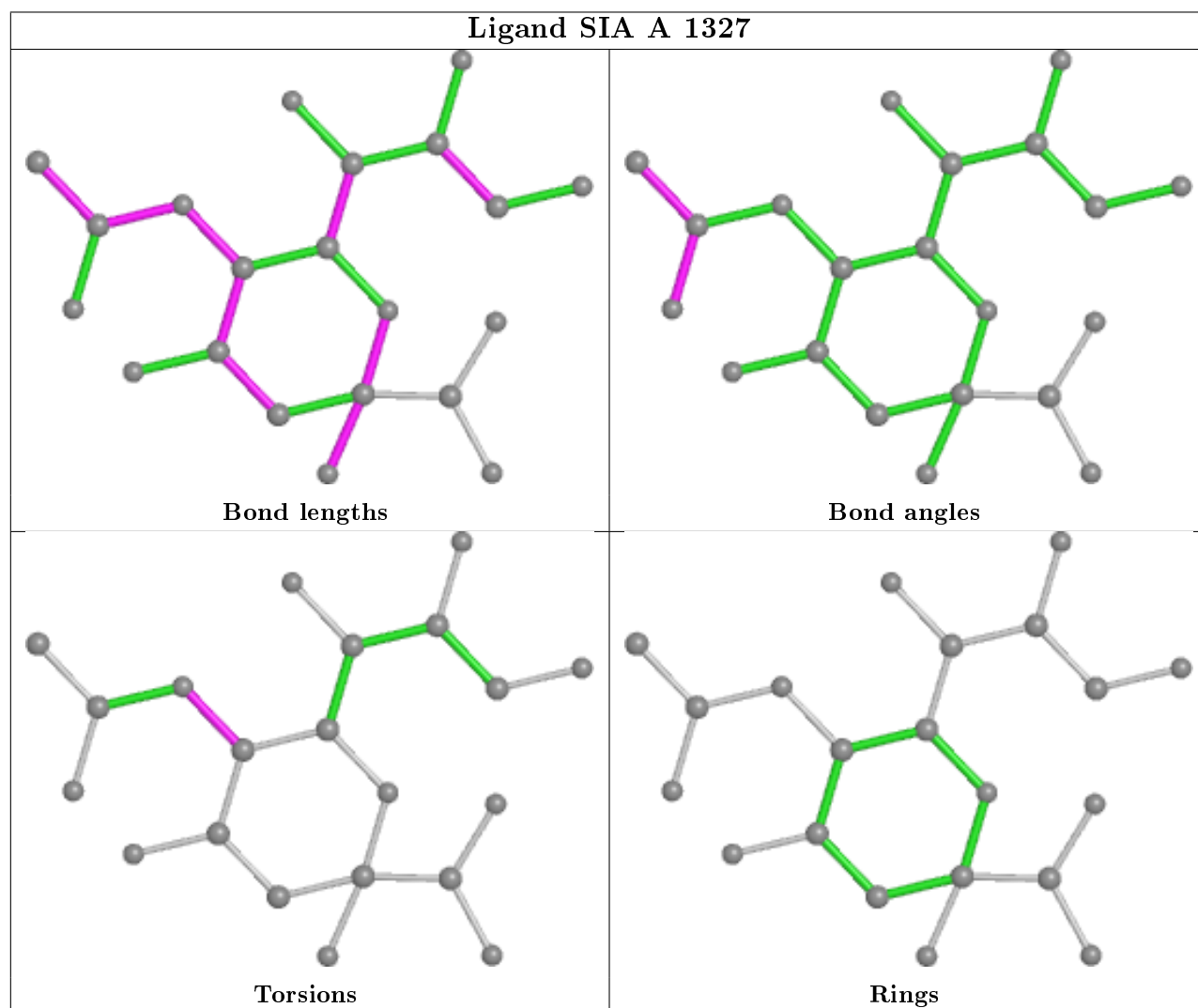
There are no ring outliers.

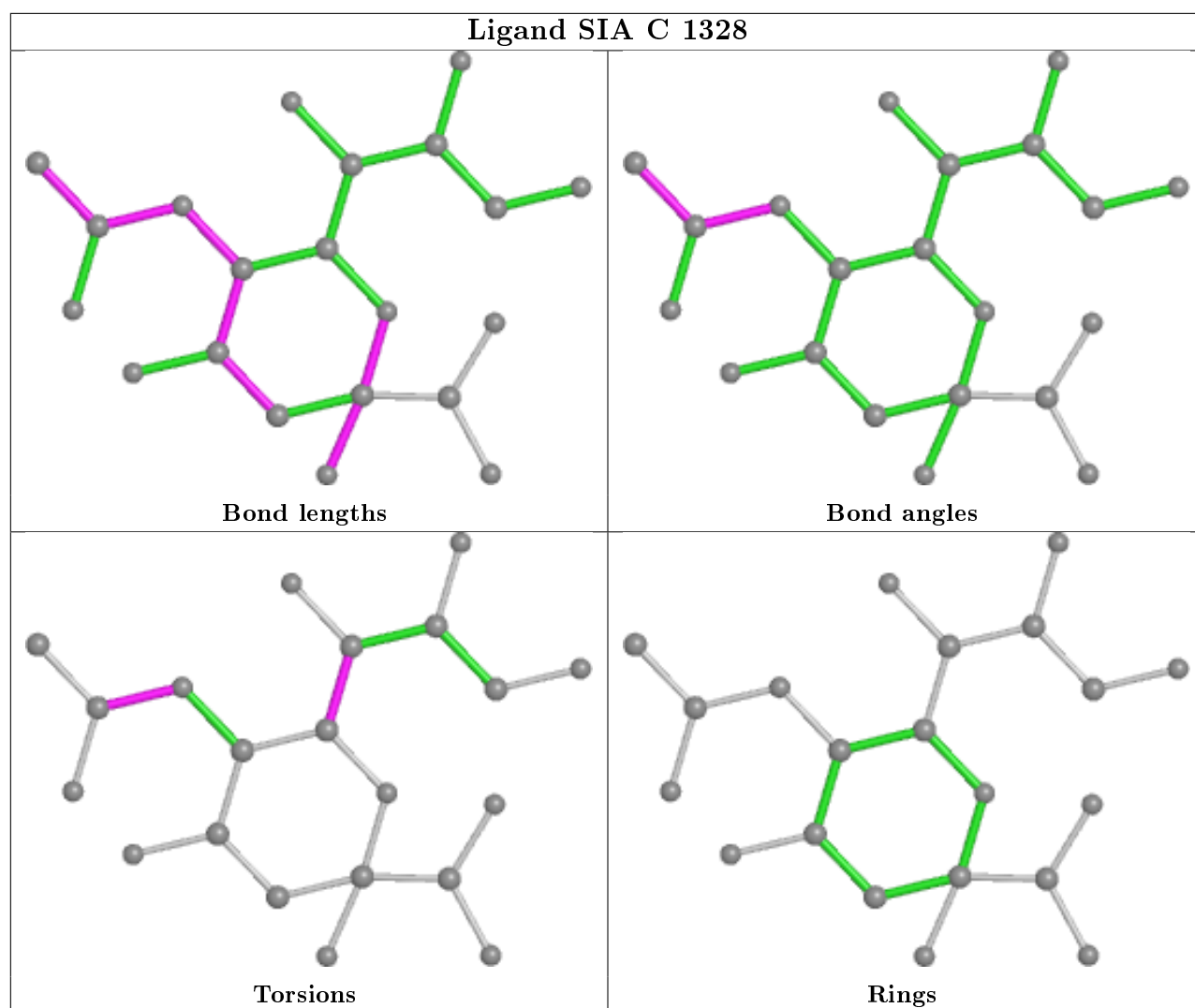
6 monomers are involved in 8 short contacts:

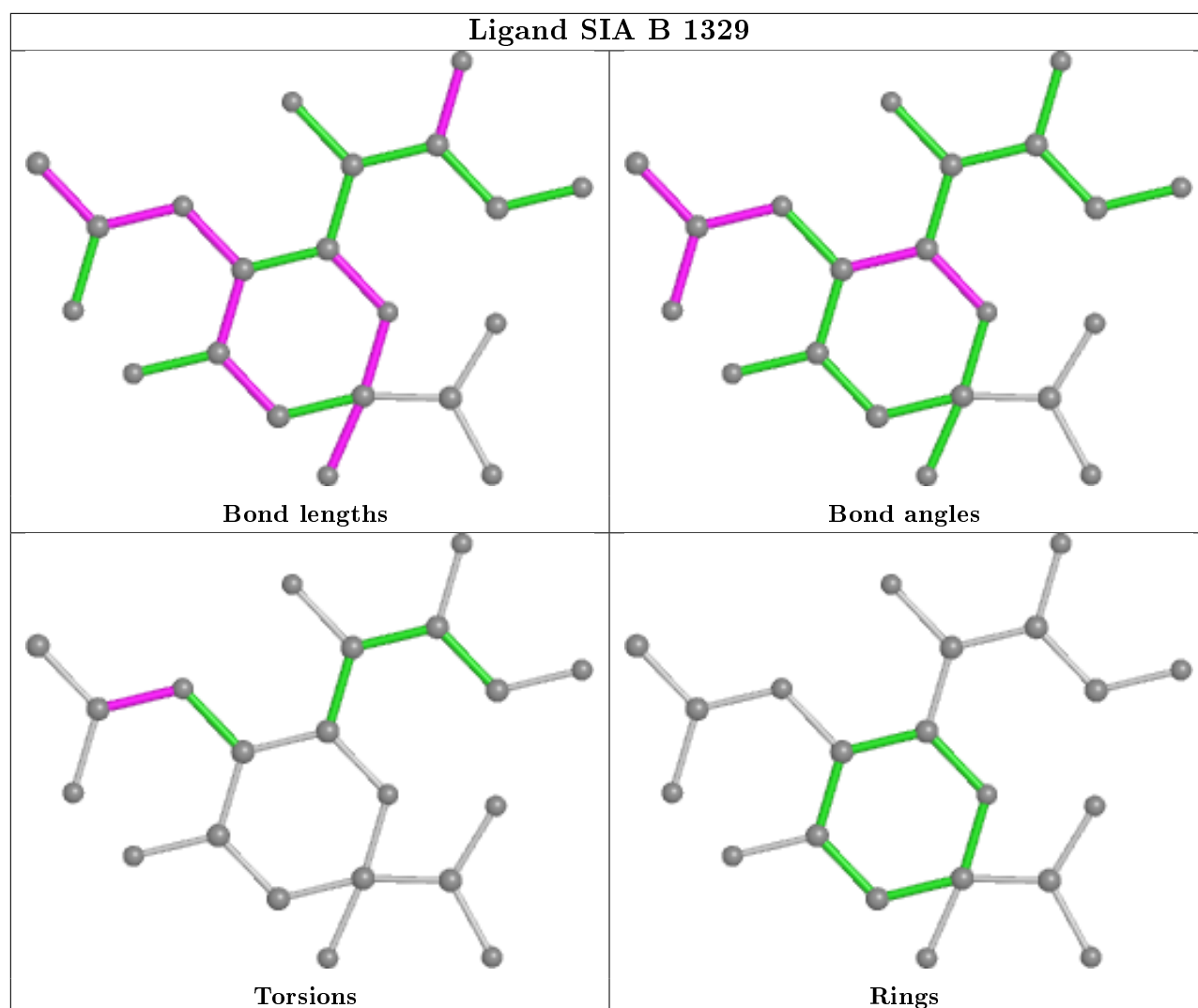
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1325	SO4	1	0
3	A	1332	SO4	1	0
4	A	1327	SIA	1	0
3	A	1326	SO4	1	0
3	D	1325	SO4	1	0
3	C	1327	SO4	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be

highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	131/158 (82%)	-0.56	0 100 100	28, 46, 86, 120	0
1	B	133/158 (84%)	-0.60	0 100 100	31, 47, 85, 116	0
1	C	132/158 (83%)	-0.53	0 100 100	27, 45, 84, 122	0
1	D	132/158 (83%)	-0.59	0 100 100	28, 47, 84, 113	0
All	All	528/632 (83%)	-0.57	0 100 100	27, 46, 85, 122	0

There are no RSRZ outliers to report.

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	SIA	A	1327	21/21	0.89	0.15	46,84,158,176	0
3	SO4	D	1327	5/5	0.89	0.11	107,119,134,135	0
3	SO4	A	1329	5/5	0.91	0.15	106,121,131,136	0
3	SO4	B	1334	5/5	0.91	0.14	99,113,134,144	0

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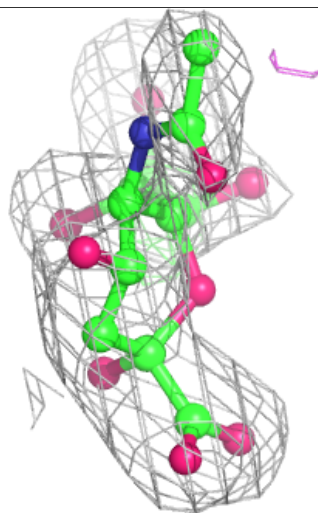
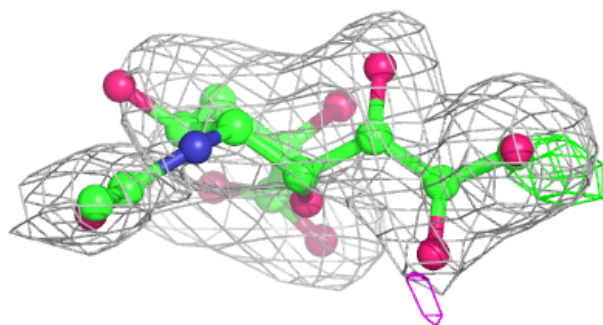
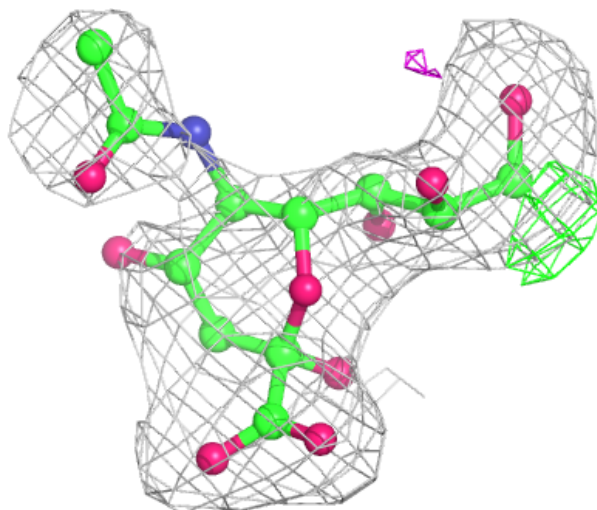
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	SO4	A	1332	5/5	0.92	0.11	69,101,108,113	0
3	SO4	C	1331	5/5	0.92	0.10	83,118,133,135	0
3	SO4	C	1332	5/5	0.92	0.12	69,131,144,149	0
4	SIA	B	1329	21/21	0.93	0.15	49,139,190,195	0
3	SO4	A	1330	5/5	0.94	0.09	85,107,124,130	0
3	SO4	D	1328	5/5	0.95	0.11	69,102,120,125	0
3	SO4	D	1326	5/5	0.95	0.17	59,107,115,133	0
2	CA	D	1323	1/1	0.96	0.06	80,80,80,80	0
3	SO4	B	1328	5/5	0.96	0.11	58,92,109,113	0
3	SO4	A	1324	5/5	0.96	0.14	54,102,116,121	0
4	SIA	C	1328	21/21	0.96	0.17	42,122,147,225	0
3	SO4	C	1330	5/5	0.97	0.12	105,114,124,130	0
5	CL	C	1329	1/1	0.97	0.13	75,75,75,75	0
3	SO4	B	1332	5/5	0.97	0.09	50,123,127,146	0
3	SO4	B	1326	5/5	0.97	0.09	37,68,101,102	0
3	SO4	B	1331	5/5	0.97	0.10	94,116,121,132	0
3	SO4	C	1326	5/5	0.97	0.09	55,79,95,96	0
3	SO4	A	1333	5/5	0.97	0.10	63,64,96,136	0
2	CA	C	1323	1/1	0.97	0.07	76,76,76,76	0
3	SO4	D	1325	5/5	0.98	0.11	32,61,78,95	0
3	SO4	A	1326	5/5	0.98	0.12	37,75,88,105	0
3	SO4	A	1331	5/5	0.98	0.11	37,71,92,132	0
2	CA	A	1323	1/1	0.98	0.06	55,55,55,55	0
3	SO4	B	1327	5/5	0.98	0.10	32,49,92,99	0
5	CL	A	1328	1/1	0.98	0.06	54,54,54,54	0
2	CA	B	1325	1/1	0.98	0.03	75,75,75,75	0
3	SO4	B	1330	5/5	0.98	0.07	80,103,111,113	0
3	SO4	D	1324	5/5	0.98	0.10	39,55,92,104	0
3	SO4	C	1327	5/5	0.98	0.09	68,89,91,104	0
3	SO4	A	1325	5/5	0.98	0.06	83,92,94,120	0
3	SO4	C	1333	5/5	0.99	0.10	25,84,87,107	0
3	SO4	D	1329	5/5	0.99	0.09	25,35,39,91	0
3	SO4	C	1325	5/5	0.99	0.08	70,85,104,115	0
3	SO4	B	1324	5/5	0.99	0.10	28,42,54,79	0
3	SO4	C	1324	5/5	0.99	0.12	62,68,82,85	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.

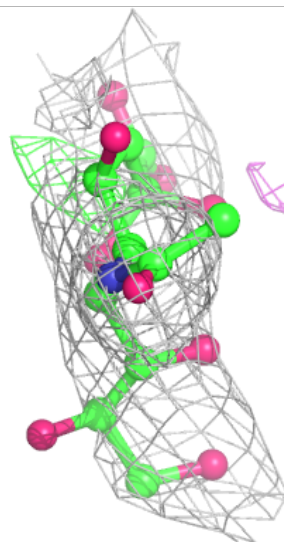
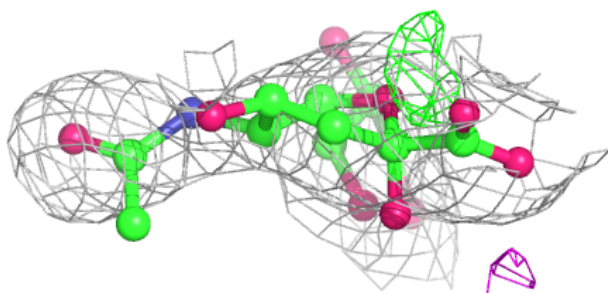
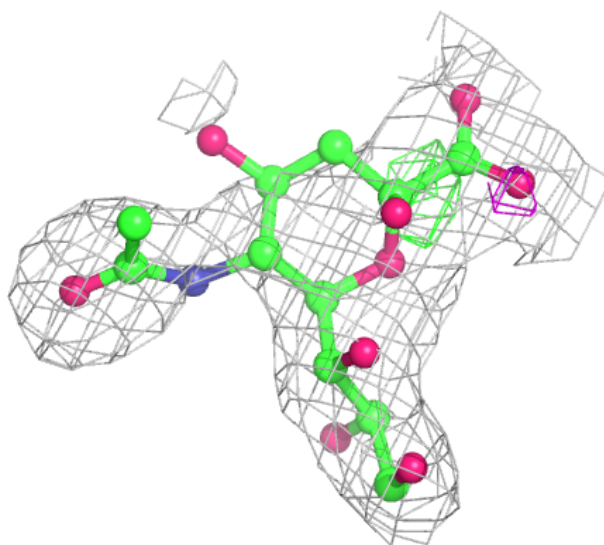
Electron density around SIA A 1327:

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



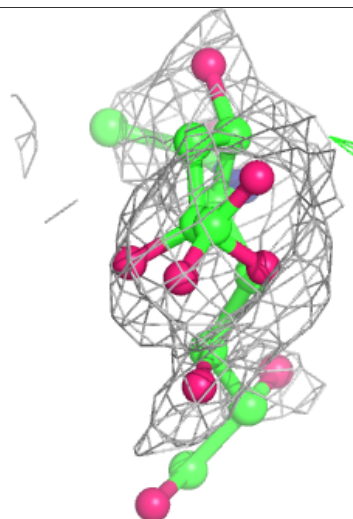
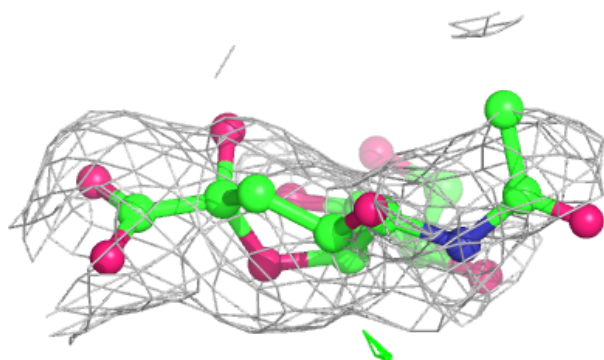
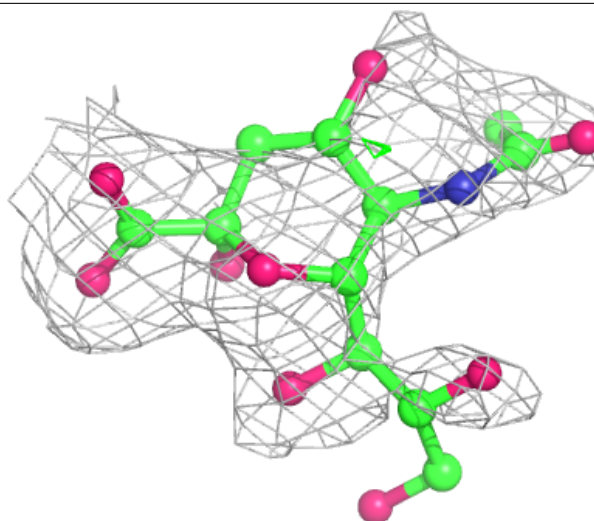
Electron density around SIA B 1329:

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



Electron density around SIA C 1328:

$2mF_o-DF_c$ (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.