



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 11, 2019 – 01:18 PM EST

PDB ID : 2VC2
Title : Re-refinement of Integrin AlphaIIbBeta3 Headpiece Bound to Antagonist L-739758
Authors : Springer, T.A.; Zhu, J.; Xiao, T.
Deposited on : 2007-09-18
Resolution : 3.10 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 : 1.8.0 (224370), CSD as540be (2019)
Xtriage (Phenix) : 1.13
EDS : 2.4
buster-report : 1.1.7 (2018)
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.4

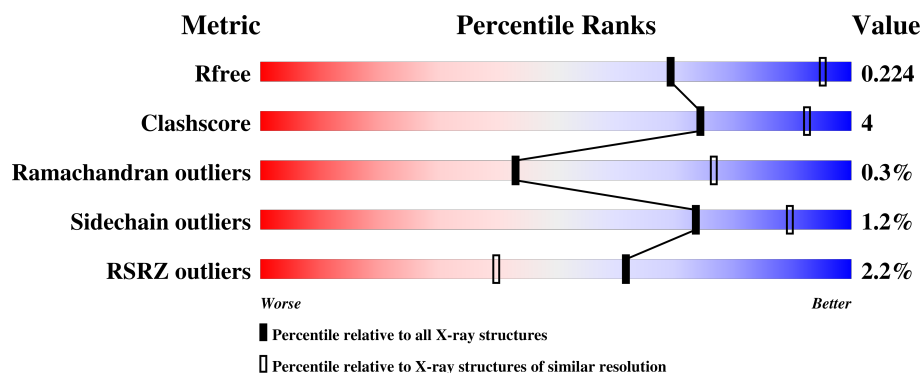
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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}	111664	1115 (3.12-3.08)
Clashscore	122126	1042 (3.10-3.10)
Ramachandran outliers	120053	1010 (3.10-3.10)
Sidechain outliers	120020	1010 (3.10-3.10)
RSRZ outliers	108989	1089 (3.12-3.08)

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. 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	452	<div> <div>%</div> <div> <div></div> <div>91%</div> <div>9%</div> </div> </div>
2	B	461	<div> <div>5%</div> <div> <div></div> <div>87%</div> <div>11%</div> <div>.</div> </div> </div>
3	H	221	<div> <div>%</div> <div> <div></div> <div>90%</div> <div>10%</div> <div>.</div> </div> </div>
4	L	214	<div> <div></div> <div> <div></div> <div>94%</div> <div>6%</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
10	MAN	B	3322	X	-	-	-
10	MAN	B	3324	-	-	-	X
10	MAN	B	3373	X	-	-	-
8	NAG	A	3015	-	-	-	X
8	NAG	A	3249	-	-	-	X
9	180	B	1477	X	-	-	-

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 10686 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 INTEGRIN ALPHA-IIB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	452	Total	C	N	O	S	0	3	0
			3493	2218	606	661	8			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	282	GLY	ALA	SEE REMARK 999	UNP P08514

- Molecule 2 is a protein called INTEGRIN BETA-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	457	Total	C	N	O	S	0	2	0
			3543	2208	606	697	32			

- Molecule 3 is a protein called MONOCLONAL ANTIBODY 10E5 HEAVY CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	219	Total	C	N	O	S	0	2	0
			1675	1061	271	337	6			

- Molecule 4 is a protein called MONOCLONAL ANTIBODY 10E5 LIGHT CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	L	214	Total	C	N	O	S	0	1	0
			1637	1019	268	341	9			

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

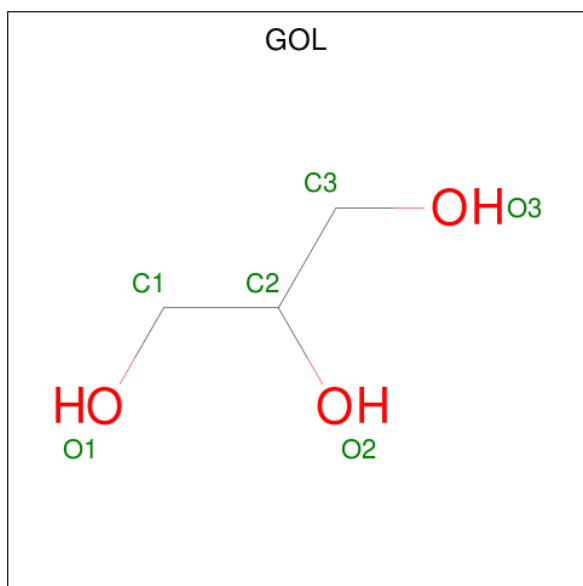
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Mg	0	0
			1	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Mg	0	0
			1	1		

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).

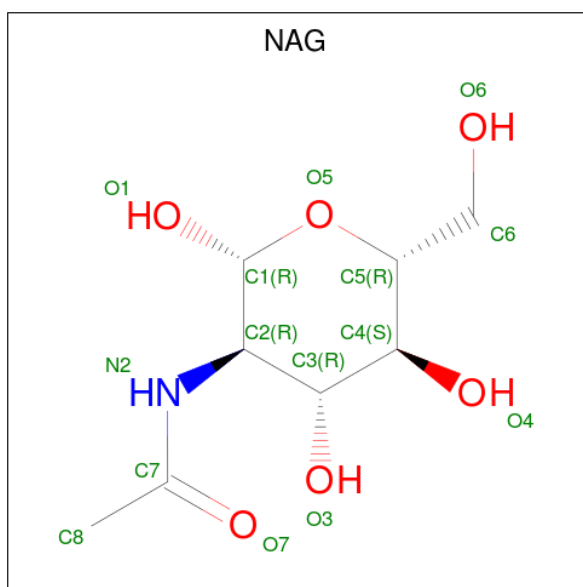


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			6	3	3		
6	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 7 is CALCIUM ION (three-letter code: CA) (formula: Ca).

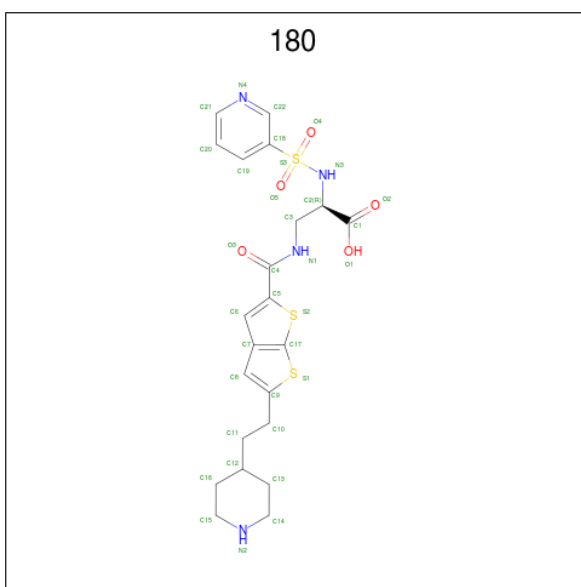
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	2	Total	Ca	0	0
			2	2		
7	A	4	Total	Ca	0	0
			4	4		

- Molecule 8 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



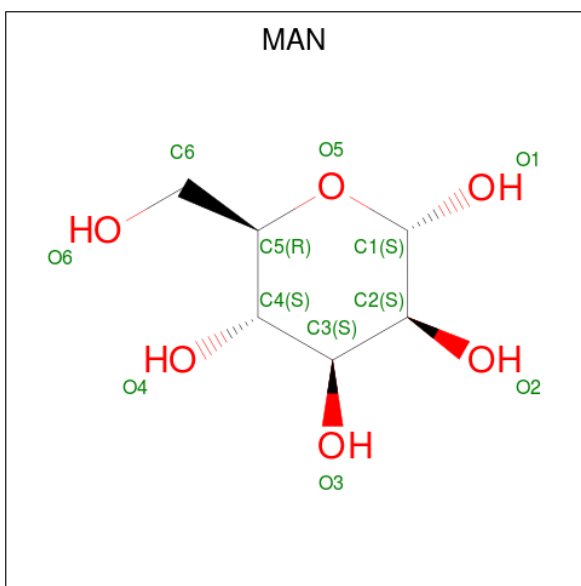
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	N	O	0	0
			14	8	1	5		
8	A	1	Total	C	N	O	0	0
			14	8	1	5		
8	B	1	Total	C	N	O	0	0
			14	8	1	5		
8	B	1	Total	C	N	O	0	0
			14	8	1	5		
8	B	1	Total	C	N	O	0	0
			14	8	1	5		
8	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 9 is 2-(S)-[N-(3-PYRIDYLSULFONYL)AMINO]-3-[[2-CARBONYL-5-[2-(PIPERIDIN-4-YL)ETHYL]-THIENO[2,3-B]THIOPHENYL]AMINO]-PROPIONIC ACID (three-letter code: 180) (formula: C₂₂H₂₆N₄O₅S₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
9	B	1	Total	C	N	O	S	0	0
			34	22	4	5	3		

- Molecule 10 is ALPHA-D-MANNOSE (three-letter code: MAN) (formula: $\text{C}_6\text{H}_{12}\text{O}_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	B	1	Total 11	C 6	O 5	0	0
10	B	1	Total 11	C 6	O 5	0	0
10	B	1	Total 11	C 6	O 5	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	B	1	Total	C	O	0	0
			11	6	5		
10	B	1	Total	C	O	0	0
			11	6	5		
10	B	1	Total	C	O	0	0
			11	6	5		
10	B	1	Total	C	O	0	0
			11	6	5		
10	B	1	Total	C	O	0	0
			11	6	5		

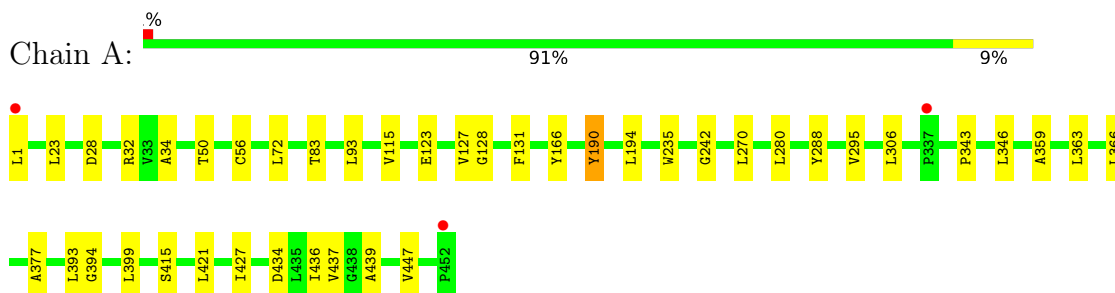
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	33	Total	O	0	0
			33	33		
11	B	26	Total	O	0	0
			26	26		
11	H	22	Total	O	0	0
			22	22		
11	L	17	Total	O	0	0
			17	17		

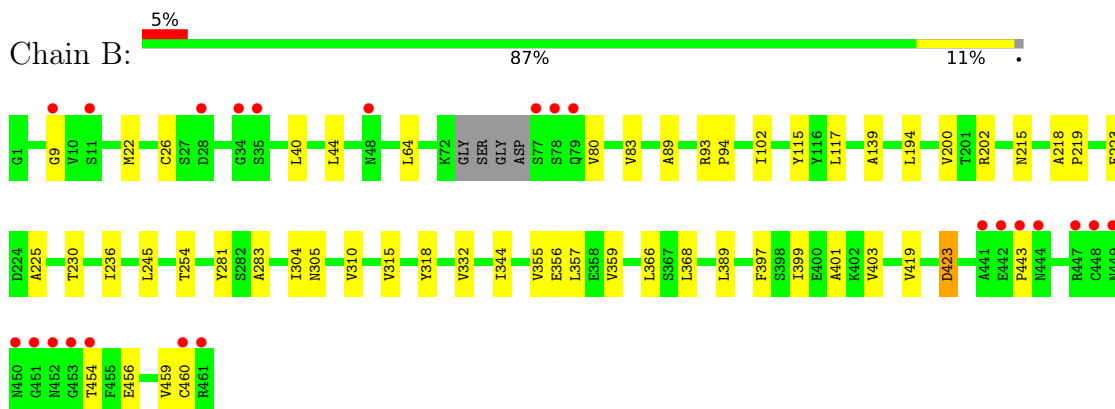
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

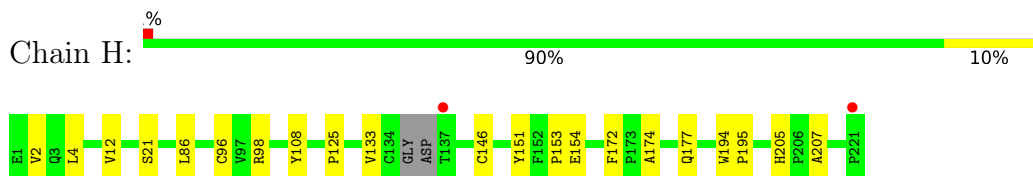
• Molecule 1: INTEGRIN ALPHA-IIB



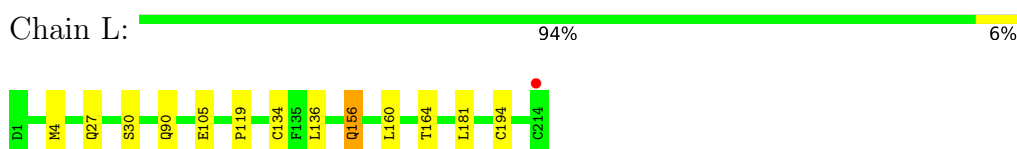
• Molecule 2: INTEGRIN BETA-3



• Molecule 3: MONOCLONAL ANTIBODY 10E5 HEAVY CHAIN



• Molecule 4: MONOCLONAL ANTIBODY 10E5 LIGHT CHAIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	149.15Å 149.15Å 176.22Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	42.72 – 3.10 42.70 – 3.10	Depositor EDS
% Data completeness (in resolution range)	97.7 (42.72-3.10) 94.8 (42.70-3.10)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.85 (at 3.12Å)	Xtriage
Refinement program	REFMAC 5.3.0037	Depositor
R, R_{free}	0.177 , 0.217 0.190 , 0.224	Depositor DCC
R_{free} test set	1985 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	46.4	Xtriage
Anisotropy	0.119	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 24.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.027 for -h,-k,l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	10686	wwPDB-VP
Average B, all atoms (Å ²)	3.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.93% 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: GOL, MG, NAG, CA, 180, MAN

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	0.33	0/3596	0.52	0/4899
2	B	0.32	0/3607	0.49	0/4889
3	H	0.33	0/1721	0.49	0/2356
4	L	0.32	0/1673	0.52	0/2269
All	All	0.32	0/10597	0.51	0/14413

There are no bond length outliers.

There are no bond angle outliers.

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	3493	0	3329	24	0
2	B	3543	0	3470	30	0
3	H	1675	0	1630	16	0
4	L	1637	0	1551	6	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	6	0	8	0	0
6	B	6	0	7	0	0
7	A	4	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	2	0	0	0	0
8	A	28	0	26	0	0
8	B	70	0	61	0	0
9	B	34	0	25	2	0
10	B	88	0	74	0	0
11	A	33	0	0	0	0
11	B	26	0	0	0	0
11	H	22	0	0	1	0
11	L	17	0	0	0	0
All	All	10686	0	10181	73	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 4.

The worst 5 of 73 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)
2:B:230:THR:HG23	2:B:304:ILE:HD12	1.65	0.77
2:B:359:VAL:HG21	2:B:368:LEU:HD12	1.74	0.69
2:B:117:LEU:HD22	2:B:225:ALA:HB1	1.76	0.67
2:B:26:CYS:HB2	2:B:44:LEU:HD22	1.80	0.63
1:A:190:TYR:CE1	9:B:1477:180:H8	2.37	0.59

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	453/452 (100%)	436 (96%)	16 (4%)	1 (0%)	49 81
2	B	454/461 (98%)	425 (94%)	27 (6%)	2 (0%)	36 72

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	H	217/221 (98%)	211 (97%)	6 (3%)	0	100	100
4	L	212/214 (99%)	202 (95%)	9 (4%)	1 (0%)	31	68
All	All	1336/1348 (99%)	1274 (95%)	58 (4%)	4 (0%)	43	77

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	9	GLY
4	L	30	SER
1	A	123	GLU
2	B	80	VAL

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	363/360 (101%)	359 (99%)	4 (1%)	76	90
2	B	408/409 (100%)	406 (100%)	2 (0%)	90	95
3	H	191/190 (100%)	189 (99%)	2 (1%)	78	91
4	L	188/188 (100%)	182 (97%)	6 (3%)	42	74
All	All	1150/1147 (100%)	1136 (99%)	14 (1%)	74	89

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	H	21	SER
3	H	146	CYS
4	L	136	LEU
2	B	423	ASP
4	L	134	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	342	GLN
2	B	428	GLN
4	L	156	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 26 ligands modelled in this entry, 8 are monoatomic - leaving 18 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	$\# Z > 2$
6	GOL	A	1461	-	5,5,5	0.37	0	5,5,5	0.19	0
8	NAG	A	3015	1	14,14,15	0.67	0	17,19,21	2.13	2 (11%)
8	NAG	A	3249	1	14,14,15	0.61	0	17,19,21	0.85	0
9	180	B	1477	5	27,37,37	2.27	5 (18%)	29,52,52	2.31	5 (17%)
6	GOL	B	1478	7	5,5,5	0.36	0	5,5,5	0.27	0
8	NAG	B	3099	2	14,14,15	0.58	0	17,19,21	0.87	1 (5%)
8	NAG	B	3320	8,2	14,14,15	0.60	0	17,19,21	0.70	0
8	NAG	B	3321	8,10	14,14,15	0.65	0	17,19,21	0.96	0
10	MAN	B	3322	8,10	11,11,12	0.63	0	15,15,17	0.80	0
10	MAN	B	3323	10	11,11,12	0.52	0	15,15,17	0.85	1 (6%)
10	MAN	B	3324	10	11,11,12	0.59	0	15,15,17	1.42	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	NAG	B	3371	8,2	14,14,15	0.61	0	17,19,21	0.74	0
8	NAG	B	3372	8,10	14,14,15	0.50	0	17,19,21	0.95	1 (5%)
10	MAN	B	3373	8,10	11,11,12	0.66	0	15,15,17	0.97	1 (6%)
10	MAN	B	3374	10	11,11,12	0.58	0	15,15,17	0.82	0
10	MAN	B	3375	10	11,11,12	0.59	0	15,15,17	1.10	1 (6%)
10	MAN	B	3376	10	11,11,12	0.57	0	15,15,17	1.50	3 (20%)
10	MAN	B	3377	10	11,11,12	0.63	0	15,15,17	1.33	2 (13%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	GOL	A	1461	-	-	2/4/4/4	-
8	NAG	A	3015	1	-	2/6/23/26	0/1/1/1
8	NAG	A	3249	1	-	0/6/23/26	0/1/1/1
9	180	B	1477	5	1/1/5/8	1/22/37/37	0/4/4/4
6	GOL	B	1478	7	-	0/4/4/4	-
8	NAG	B	3099	2	-	2/6/23/26	0/1/1/1
8	NAG	B	3320	8,2	-	0/6/23/26	0/1/1/1
8	NAG	B	3321	8,10	-	2/6/23/26	0/1/1/1
10	MAN	B	3322	8,10	1/1/4/5	2/2/19/22	0/1/1/1
10	MAN	B	3323	10	-	0/2/19/22	0/1/1/1
10	MAN	B	3324	10	-	2/2/19/22	0/1/1/1
8	NAG	B	3371	8,2	-	0/6/23/26	0/1/1/1
8	NAG	B	3372	8,10	-	0/6/23/26	0/1/1/1
10	MAN	B	3373	8,10	1/1/4/5	2/2/19/22	0/1/1/1
10	MAN	B	3374	10	-	0/2/19/22	0/1/1/1
10	MAN	B	3375	10	-	0/2/19/22	0/1/1/1
10	MAN	B	3376	10	-	2/2/19/22	0/1/1/1
10	MAN	B	3377	10	-	2/2/19/22	0/1/1/1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	B	1477	180	C5-S2	-6.11	1.64	1.72
9	B	1477	180	O5-S3	5.93	1.49	1.43
9	B	1477	180	O4-S3	5.49	1.49	1.43

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	B	1477	180	C9-S1	-5.05	1.64	1.74
9	B	1477	180	C18-S3	-2.10	1.73	1.76

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	B	1477	180	O5-S3-O4	-8.84	108.52	119.56
8	A	3015	NAG	C1-O5-C5	5.70	119.95	112.20
9	B	1477	180	C2-N3-S3	-5.68	111.96	121.83
8	A	3015	NAG	O5-C1-C2	5.56	120.10	111.36
10	B	3324	MAN	C1-C2-C3	3.60	114.08	109.66

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
9	B	1477	180	C2
10	B	3373	MAN	C1
10	B	3322	MAN	C1

5 of 19 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	1461	GOL	O1-C1-C2-O2
6	A	1461	GOL	O1-C1-C2-C3
10	B	3324	MAN	O5-C5-C6-O6
8	B	3099	NAG	O5-C5-C6-O6
10	B	3324	MAN	C4-C5-C6-O6

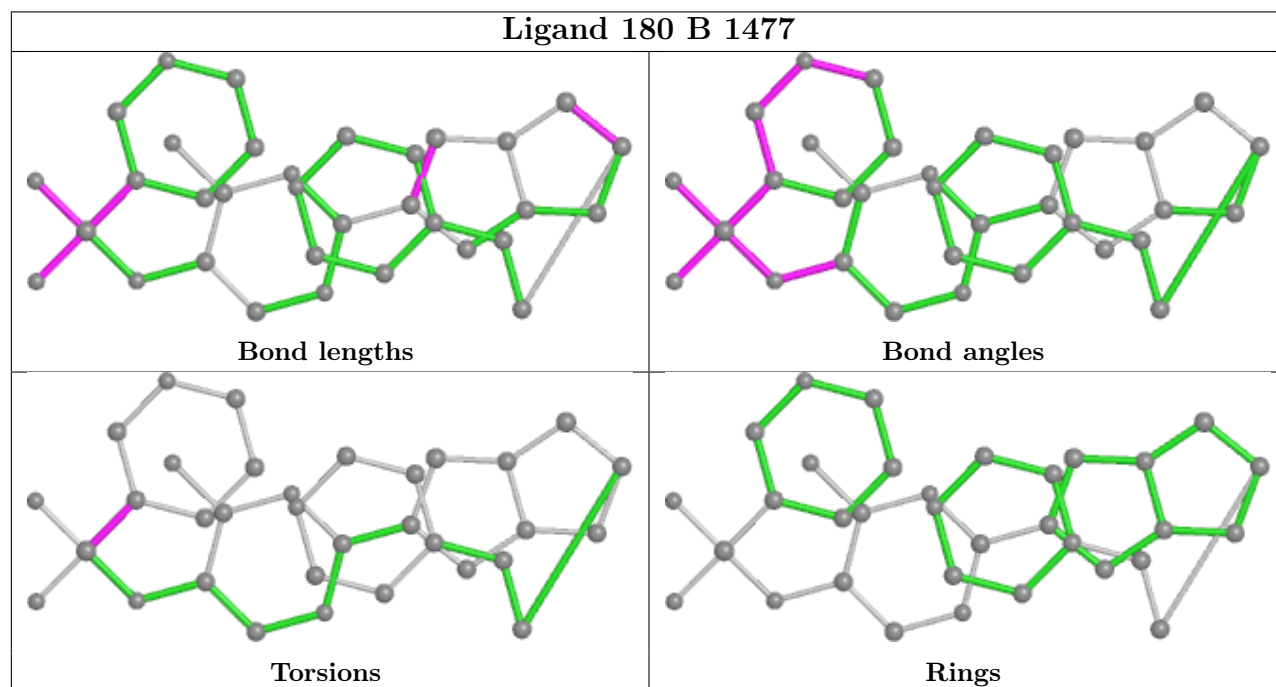
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	B	1477	180	2	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	452/452 (100%)	-0.58	3 (0%) 87 75	2, 2, 7, 19	1 (0%)
2	B	457/461 (99%)	-0.07	23 (5%) 29 13	2, 2, 9, 17	1 (0%)
3	H	219/221 (99%)	-0.46	2 (0%) 84 70	2, 2, 8, 23	0
4	L	214/214 (100%)	-0.56	1 (0%) 90 81	2, 2, 7, 11	1 (0%)
All	All	1342/1348 (99%)	-0.38	29 (2%) 62 40	2, 2, 8, 23	3 (0%)

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	444	ASN	4.4
3	H	137	THR	4.0
1	A	337	PRO	3.9
2	B	443	PRO	3.7
2	B	11	SER	3.5

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 carbohydrates in this entry.

6.4 Ligands [i](#)

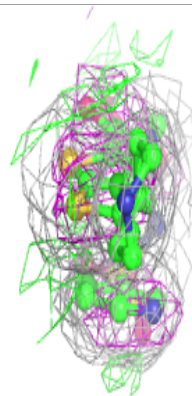
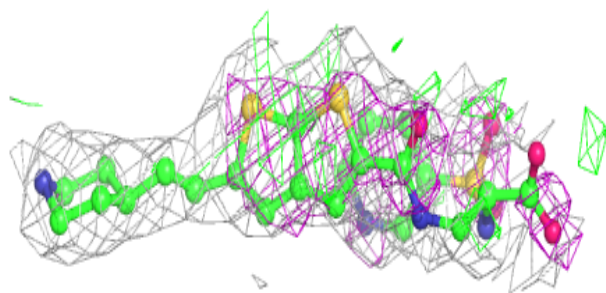
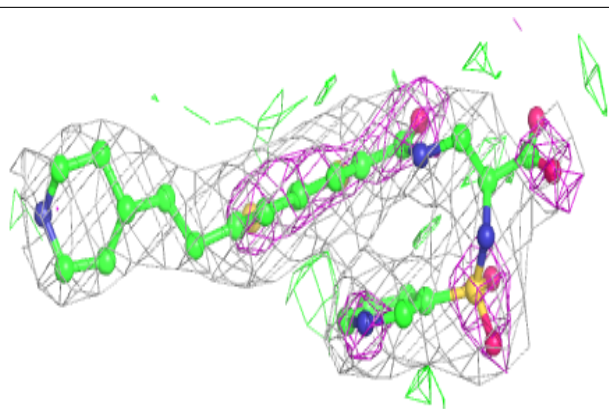
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
8	NAG	B	3099	14/15	0.72	0.34	43,48,53,54	0
8	NAG	A	3249	14/15	0.74	0.51	23,26,27,28	14
8	NAG	A	3015	14/15	0.76	0.50	40,44,46,47	0
10	MAN	B	3324	11/12	0.78	0.41	54,56,57,57	0
10	MAN	B	3322	11/12	0.84	0.33	38,43,50,54	0
10	MAN	B	3374	11/12	0.88	0.31	27,29,31,32	11
10	MAN	B	3323	11/12	0.89	0.29	35,37,39,40	0
8	NAG	B	3371	14/15	0.90	0.29	16,22,26,28	0
5	MG	A	1460	1/1	0.91	0.21	2,2,2,2	0
8	NAG	B	3321	14/15	0.92	0.30	18,21,28,35	0
8	NAG	B	3372	14/15	0.92	0.27	18,31,34,36	0
10	MAN	B	3376	11/12	0.92	0.20	17,19,20,21	0
10	MAN	B	3377	11/12	0.92	0.35	31,33,34,34	0
10	MAN	B	3373	11/12	0.92	0.27	30,35,36,37	0
6	GOL	A	1461	6/6	0.93	0.19	15,16,17,17	0
7	CA	A	2005	1/1	0.95	0.05	4,4,4,4	0
7	CA	A	2004	1/1	0.96	0.06	7,7,7,7	0
10	MAN	B	3375	11/12	0.96	0.20	20,23,26,27	0
8	NAG	B	3320	14/15	0.96	0.14	3,6,9,14	0
9	180	B	1477	34/34	0.97	0.10	2,2,2,2	0
7	CA	A	2007	1/1	0.98	0.06	3,3,3,3	0
6	GOL	B	1478	6/6	0.98	0.18	29,29,29,30	0
5	MG	B	2001	1/1	0.98	0.04	2,2,2,2	0
7	CA	B	2002	1/1	0.98	0.04	2,2,2,2	0
7	CA	A	2006	1/1	0.99	0.05	12,12,12,12	0
7	CA	B	2003	1/1	0.99	0.04	2,2,2,2	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 180 B 1477:

$2mF_o-DF_c$ (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.