

Full wwPDB X-ray Structure Validation Report (i)

Jan 2, 2024 – 08:33 am GMT

PDB ID : 5L7D

Title: Structure of human Smoothened in complex with cholesterol

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Deposited on : 2016-06-03

Resolution : 3.20 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

MolProbity: 4.02b-467

Mogul : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : 1.13

EDS : 2.36

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)

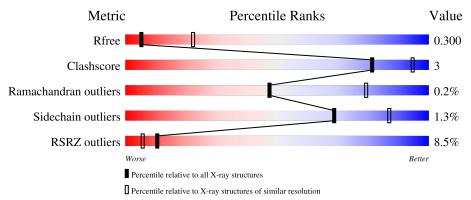
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY\ DIFFRACTION$

The reported resolution of this entry is 3.20 Å.

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



Metric	Whole archive $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\mathring{A})}) \end{array}$
R_{free}	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	638	84%	8%	8%
1	В	638	83%	7%	9%

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	1201	-	-	-	X
2	NAG	A	1202	-	-	-	X



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 9265 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 Smoothened homolog, Soluble cytochrome b562, Smoothened homolog.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	A	588	Total 4640	C 2985	N 792	O 830	S 33	0	0	0
1	В	578	Total 4567	C 2936	N 779	O 819	S 33	0	0	0

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	329	PHE	VAL	conflict	UNP Q99835
A	1011	ALA	-	linker	UNP Q99835
A	1012	ARG	-	linker	UNP Q99835
A	1013	ARG	-	linker	UNP Q99835
A	1014	GLN	-	linker	UNP Q99835
A	1015	LEU	-	linker	UNP Q99835
A	1022	TRP	MET	conflict	UNP P0ABE7
A	1117	ILE	HIS	conflict	UNP P0ABE7
A	1121	LEU	-	linker	UNP P0ABE7
A	1122	GLU	-	linker	UNP P0ABE7
A	1123	ARG	-	linker	UNP P0ABE7
A	1124	ALA	-	linker	UNP P0ABE7
A	1125	ARG	-	linker	UNP P0ABE7
A	1126	SER	-	linker	UNP P0ABE7
A	1127	THR	-	linker	UNP P0ABE7
A	1128	LEU	-	linker	UNP P0ABE7
A	556	GLY	-	expression tag	UNP Q99835
A	557	THR	-	expression tag	UNP Q99835
A	558	GLU	-	expression tag	UNP Q99835
A	559	THR	-	expression tag	UNP Q99835
A	560	SER	-	expression tag	UNP Q99835
A	561	GLN	-	expression tag	UNP Q99835
A	562	VAL	-	expression tag	UNP Q99835
A	563	ALA	-	expression tag	UNP Q99835

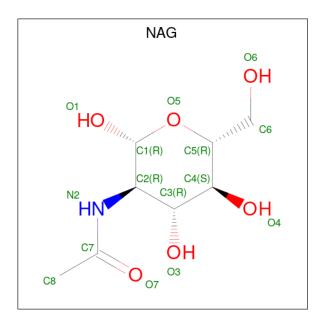


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Chain	Residue	Modelled	Actual	Comment	Reference
A	564	PRO	-	expression tag	UNP Q99835
A	565	ALA	-	expression tag	UNP Q99835
В	329	PHE	VAL	conflict	UNP Q99835
В	1011	ALA	-	linker	UNP Q99835
В	1012	ARG	-	linker	UNP Q99835
В	1013	ARG	-	linker	UNP Q99835
В	1014	GLN	-	linker	UNP Q99835
В	1015	LEU	-	linker	UNP Q99835
В	1022	TRP	MET	conflict	UNP P0ABE7
В	1117	ILE	HIS	conflict	UNP P0ABE7
В	1121	LEU	-	linker	UNP P0ABE7
В	1122	GLU	-	linker	UNP P0ABE7
В	1123	ARG	-	linker	UNP P0ABE7
В	1124	ALA	-	linker	UNP P0ABE7
В	1125	ARG	-	linker	UNP P0ABE7
В	1126	SER	-	linker	UNP P0ABE7
В	1127	THR	-	linker	UNP P0ABE7
В	1128	LEU	-	linker	UNP P0ABE7
В	556	GLY	-	expression tag	UNP Q99835
В	557	THR	-	expression tag	UNP Q99835
В	558	GLU	-	expression tag	UNP Q99835
В	559	THR	-	expression tag	UNP Q99835
В	560	SER	-	expression tag	UNP Q99835
В	561	GLN	-	expression tag	UNP Q99835
В	562	VAL	-	expression tag	UNP Q99835
В	563	ALA	-	expression tag	UNP Q99835
В	564	PRO	-	expression tag	UNP Q99835
В	565	ALA	-	expression tag	UNP Q99835

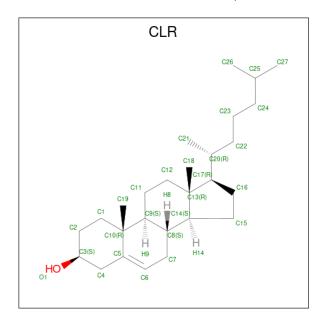
• Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).





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

 \bullet Molecule 3 is CHOLESTEROL (three-letter code: CLR) (formula: $\mathrm{C_{27}H_{46}O}).$



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total C	0	0	0
	_	_	28 27	1		

• Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).



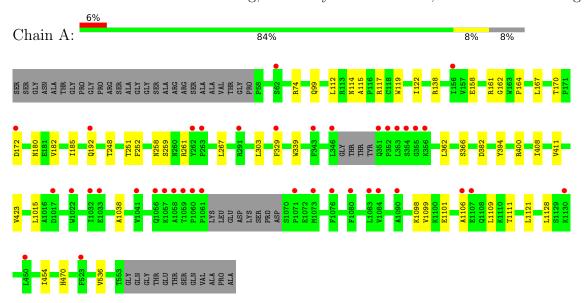
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	2	Total Na 2 2	0	0



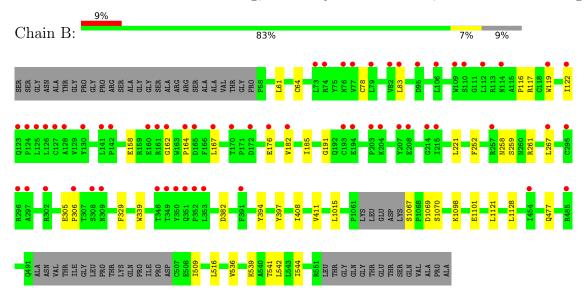
3 Residue-property plots (i)

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

• Molecule 1: Smoothened homolog, Soluble cytochrome b562, Smoothened homolog



• Molecule 1: Smoothened homolog, Soluble cytochrome b562, Smoothened homolog





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	122.90Å 63.02Å 208.59Å	Donositor
a, b, c, α , β , γ	90.00° 96.64° 90.00°	Depositor
Resolution (Å)	29.33 - 3.20	Depositor
rtesolution (A)	61.04 - 3.19	EDS
% Data completeness	94.6 (29.33-3.20)	Depositor
(in resolution range)	94.1 (61.04-3.19)	EDS
R_{merge}	0.30	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.08 (at 3.19Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
D D.	0.230 , 0.264	Depositor
R, R_{free}	0.268 , 0.300	DCC
R_{free} test set	1306 reflections (5.18%)	wwPDB-VP
Wilson B-factor $(Å^2)$	93.0	Xtriage
Anisotropy	0.310	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.31, 88.9	EDS
L-test for twinning ²	$ < L >=0.43, < L^2>=0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	9265	wwPDB-VP
Average B, all atoms (Å ²)	137.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.78% of the height of the origin peak. No significant pseudotranslation is detected.

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



¹Intensities estimated from amplitudes.

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: CLR, NAG, NA

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		
MIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.42	0/4757	0.56	0/6467	
1	В	0.42	0/4683	0.56	0/6364	
All	All	0.42	0/9440	0.56	0/12831	

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	4640	0	4584	24	0
1	В	4567	0	4494	24	0
2	A	28	0	26	0	0
3	A	28	0	46	1	0
4	A	2	0	0	0	0
All	All	9265	0	9150	47	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 3.

All (47) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



Atom-1	Atom-2	Interatomic	Clash
		distance (Å)	overlap (Å)
1:B:382:ASP:HB2	1:B:394:TYR:HB2	1.79	0.65
1:B:78:CYS:HB2	1:B:83:LEU:HD21	1.77	0.64
1:B:258:ASN:HA	1:B:261:ARG:HH21	1.63	0.63
1:A:258:ASN:HA	1:A:261:ARG:HH21	1.63	0.63
1:A:382:ASP:HB2	1:A:394:TYR:HB2	1.83	0.61
1:A:339:TRP:HH2	1:A:423:VAL:HG13	1.66	0.60
1:B:252:PHE:HD1	1:B:259:SER:HB3	1.71	0.55
1:A:182:VAL:HA	1:A:185:ILE:HD12	1.88	0.54
1:B:397:TYR:HB3	1:B:477:GLN:HG2	1.89	0.54
1:B:164:PRO:HD2	1:B:167:LEU:HB2	1.90	0.54
1:B:182:VAL:HA	1:B:185:ILE:HD12	1.89	0.54
1:B:305:GLU:HG2	1:B:306:PRO:HA	1.90	0.53
1:A:248:THR:HA	1:A:536:VAL:HG21	1.90	0.52
1:A:164:PRO:HD2	1:A:167:LEU:HB2	1.91	0.51
1:A:329:PHE:HB3	1:A:411:VAL:HG11	1.93	0.50
1:A:74:ARG:HH21	1:A:99:GLN:HB2	1.76	0.50
1:B:329:PHE:HB3	1:B:411:VAL:HG11	1.93	0.49
1:B:539:LYS:HA	1:B:542:LEU:HD12	1.93	0.49
1:A:1015:LEU:HD22	1:A:1128:LEU:HD22	1.97	0.46
1:B:1067:SER:HB3	1:B:1070:SER:HB2	1.98	0.45
1:B:541:THR:HA	1:B:544:ILE:HD12	1.98	0.45
1:A:454:ILE:HD11	1:B:516:LEU:HD21	1.98	0.45
1:A:112:LEU:HD11	3:A:1203:CLR:H17	1.99	0.45
1:A:119:TRP:HA	1:A:122:ILE:HG22	1.99	0.45
1:B:1015:LEU:HD22	1:B:1128:LEU:HD22	1.99	0.44
1:B:536:VAL:CG1	1:B:536:VAL:O	2.65	0.44
1:A:158:GLU:HA	1:A:162:GLY:HA2	1.99	0.43
1:A:252:PHE:HD1	1:A:259:SER:HB2	1.83	0.43
1:B:119:TRP:HA	1:B:122:ILE:HG22	2.01	0.43
1:B:158:GLU:HA	1:B:162:GLY:HA2	1.99	0.43
1:B:221:LEU:HD22	1:B:509:ILE:HG21	2.00	0.42
1:A:362:LEU:O	1:A:366:SER:HB3	2.20	0.42
1:A:408:ILE:HA	1:A:411:VAL:HG22	2.01	0.42
1:A:170:THR:HG22	1:A:172:ASP:H	1.83	0.41
1:B:408:ILE:HA	1:B:411:VAL:HG22	2.01	0.41
1:A:1038:ALA:HB2	1:A:1099:VAL:HG22	2.01	0.41
1:A:114:ASN:HA	1:A:192:GLN:O	2.21	0.41
1:A:1106:ALA:HA	1:A:1109:LEU:HG	2.02	0.41
1:B:536:VAL:O	1:B:536:VAL:HG12	2.21	0.41
1:B:61:LEU:HB2	1:B:64:CYS:HB2	2.02	0.41
1:B:1098:LYS:HB3	1:B:1101:GLU:HB2	2.03	0.41
1:A:180:ASN:HB3	1:A:182:VAL:HG22	2.03	0.41
1.71.100.71011.11D0	1.71.102. VIII.IIG22	2.00	0.40



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Atom-1	Atom-2	$egin{aligned} & ext{Interatomic} \ & ext{distance} \ & ext{(Å)} \end{aligned}$	$egin{aligned} ext{Clash} \ ext{overlap } (ext{Å}) \end{aligned}$
1:A:1098:LYS:HB3	1:A:1101:GLU:HB2	2.03	0.40
1:B:252:PHE:CD1	1:B:259:SER:HB3	2.53	0.40
1:A:252:PHE:CD1	1:A:259:SER:HB2	2.55	0.40
1:A:400:ARG:NH2	1:A:470:HIS:HD2	2.19	0.40
1:B:116:PRO:HA	1:B:191:GLY:HA3	2.03	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	Perce	ntiles
1	A	582/638 (91%)	561 (96%)	20 (3%)	1 (0%)	47	79
1	В	572/638 (90%)	553 (97%)	18 (3%)	1 (0%)	47	79
All	All	1154/1276 (90%)	1114 (96%)	38 (3%)	2 (0%)	47	79

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	В	176	GLU
1	A	115	ALA

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	Percent	iles
1	A	495/529 (94%)	487 (98%)	8 (2%)	62 8	4
1	В	486/529 (92%)	481 (99%)	5 (1%)	76 9	0
All	All	981/1058 (93%)	968 (99%)	13 (1%)	69 8	7

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	117	ARG
1	A	138	ARG
1	A	161	ARG
1	A	251	THR
1	A	267	LEU
1	A	303	LEU
1	A	1111	THR
1	A	1121	LEU
1	В	117	ARG
1	В	267	LEU
1	В	339	TRP
1	В	1069	ASP
1	В	1121	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	192	GLN
1	A	470	HIS
1	A	491	GLN
1	A	521	ASN
1	В	470	HIS
1	В	521	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)

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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		Bo	ond leng	$_{ m ths}$	В	ond ang	les
MIOI	туре	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	CLR	A	1203	-	31,31,31	0.65	0	48,48,48	1.42	7 (14%)
2	NAG	A	1201	1	14,14,15	0.34	0	17,19,21	0.57	0
2	NAG	A	1202	1	14,14,15	0.28	0	17,19,21	0.87	1 (5%)

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	CLR	A	1203	-	-	5/10/68/68	0/4/4/4
2	NAG	A	1201	1	-	0/6/23/26	0/1/1/1
2	NAG	A	1202	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\mathbf{Ideal}(^{o})$
3	A	1203	CLR	C4-C5-C10	3.80	121.47	116.42
2	A	1202	NAG	C1-O5-C5	3.20	116.53	112.19
3	A	1203	CLR	C4-C5-C6	-3.19	116.02	120.61
3	A	1203	CLR	C1-C2-C3	3.11	114.46	110.47
3	A	1203	CLR	C21-C20-C22	-3.05	105.58	110.36
3	A	1203	CLR	C7-C8-C14	2.63	114.72	110.91
3	A	1203	CLR	C12-C11-C9	2.32	117.13	113.11



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Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}({}^{o})$
3	A	1203	CLR	C21-C20-C17	2.26	116.39	112.92

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1203	CLR	C17-C20-C22-C23
3	A	1203	CLR	C21-C20-C22-C23
2	A	1202	NAG	O5-C5-C6-O6
3	A	1203	CLR	C22-C23-C24-C25
3	A	1203	CLR	C23-C24-C25-C26
3	A	1203	CLR	C23-C24-C25-C27
2	A	1202	NAG	C4-C5-C6-O6

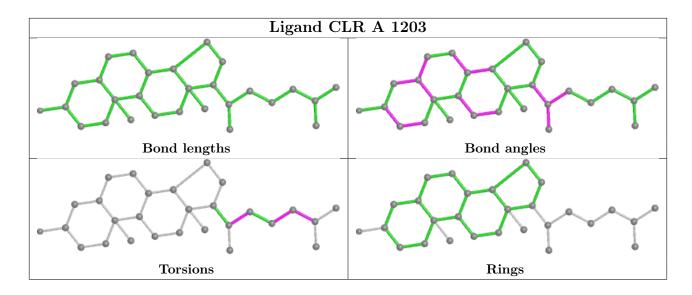
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1203	CLR	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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, 95^{th} 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>	# RSRZ > 2	$OWAB(Å^2)$	Q < 0.9
1	A	588/638~(92%)	0.48	39 (6%) 18 11	63, 116, 206, 272	0
1	В	578/638 (90%)	0.61	60 (10%) 6 4	58, 138, 208, 221	0
All	All	$1166/1276 \ (91\%)$	0.55	99 (8%) 10 6	58, 126, 207, 272	0

All (99) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1080	PHE	6.9
1	В	127	CYS	6.6
1	A	1058	ALA	6.5
1	В	128	ALA	6.3
1	A	353	LEU	6.0
1	A	1106	ALA	5.9
1	В	109	TRP	5.9
1	В	203	PRO	5.9
1	A	346	LEU	5.6
1	В	122	ILE	5.6
1	В	214	GLY	5.3
1	В	165	ASP	5.3
1	В	161	ARG	5.1
1	В	126	LEU	4.9
1	В	167	LEU	4.4
1	В	124	PRO	4.3
1	В	123	GLN	4.3
1	A	1073	MET	4.3
1	В	76	ASN	4.3
1	В	142	PRO	4.3
1	В	308	SER	4.2
1	A	1084	VAL	4.0
1	В	309	ASN	4.0
1	В	182	VAL	3.9



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Mol Chain Res Type RSR						
1	В	119	TRP	3.9		
1	В	74	ARG	3.8		
1	A	1076	PHE	3.8		
1	В	170	THR	3.8		
1	В	125	LEU	3.8		
1	В	353	LEU	3.8		
1	В	164	PRO	3.7		
1	A	1083	LEU	3.7		
1	В	130	TYR	3.6		
1	A	355	GLY	3.6		
1	A	351	GLN	3.6		
1	A	1061	PRO	3.5		
1	В	204	LYS	3.4		
1	В	297	ALA	3.4		
1	A	262	TYR	3.4		
1	В	83	LEU	3.2		
1	В	295	CYS	3.2		
1	В	77	VAL	3.2		
1	A	1032	ILE	3.2		
1	A	354	SER	3.2		
1	A	352	PRO	3.2		
1	A	1059	THR	3.2		
1	В	73	LEU	3.1		
1	A	343	PHE	3.1		
1	В	352	PRO	3.1		
1	A	1017	ASP	3.1		
1	В	194	GLU	3.0		
1	В	82	VAL	3.0		
1	В	349	THR	2.9		
1	A	1130	LYS	2.9		
1	В	391	PHE	2.9		
1	В	267	LEU	2.9		
1	A	356	LYS	2.8		
1	A	1090	ALA	2.8		
1	В	350	TYR	2.7		
1	В	79	LEU	2.7		
1	A	1107	GLU	2.7		
1	В	296	ARG	2.6		
1	A	263	PRO	2.6		
1	A	192	GLN	2.6		
1	В	454	ILE	2.6		
1	В	351	GLN	2.5		



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Mol	Chain	Res	Type	RSRZ
1	В	208	GLU	2.5
1	A	1056	GLN	2.5
1	В	141	LEU	2.5
1	A	1057	LYS	2.5
1	В	207	TYR	2.5
1	В	106	LEU	2.4
1	В	160	GLU	2.4
1	A	291	ARG	2.4
1	A	172	ASP	2.4
1	В	193	CYS	2.4
1	В	306	PRO	2.4
1	A	1071	PRO	2.3
1	В	112	LEU	2.3
1	В	302	ARG	2.3
1	В	95	ASP	2.3
1	В	176	GLU	2.2
1	A	1060	PRO	2.2
1	A	329	PHE	2.2
1	A	1033	GLU	2.2
1	В	348	THR	2.2
1	A	156	ILE	2.2
1	В	215	ILE	2.2
1	В	257	ARG	2.2
1	В	110	SER	2.1
1	В	114	ASN	2.1
1	В	162	GLY	2.1
1	A	62	SER	2.1
1	A	523	PHE	2.1
1	A	1041	VAL	2.1
1	В	172	ASP	2.1
1	A	450	LEU	2.0
1	В	485	ARG	2.0
1	A	1022	TRP	2.0

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.

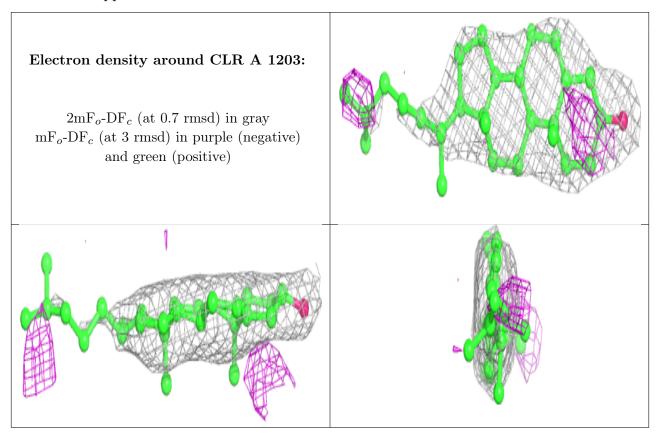


6.4 Ligands (i)

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, 95^{th} 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
2	NAG	A	1202	14/15	0.57	0.80	171,172,174,175	0
2	NAG	A	1201	14/15	0.68	0.57	148,151,153,153	0
4	NA	A	1205	1/1	0.91	0.14	71,71,71,71	0
3	CLR	A	1203	28/28	0.94	0.64	75,84,87,88	0
4	NA	A	1204	1/1	0.98	0.06	105,105,105,105	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.



6.5 Other polymers (i)

There are no such residues in this entry.

