



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 11:56 AM GMT

PDB ID : 3QH0
Title : X-ray crystal structure of palmitic acid bound to the cyclooxygenase channel of cyclooxygenase-2
Authors : Vecchio, A.J.; Malkowski, M.G.
Deposited on : 2011-01-25
Resolution : 2.10 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

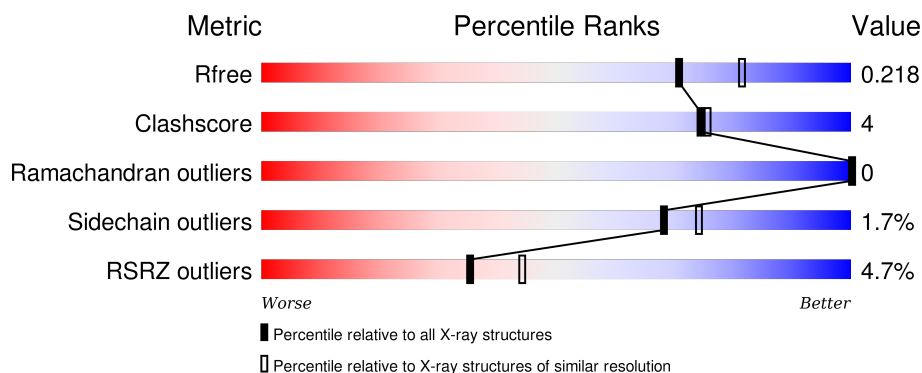
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	91344	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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	610	<div> <div>4%</div> <div>82%</div> <div>7%</div> <div>10%</div> </div>
1	B	610	<div> <div>4%</div> <div>85%</div> <div>5%</div> <div>10%</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	NAG	B	661	-	-	-	X
2	EDO	A	624	-	-	-	X
2	EDO	B	621	-	-	-	X
2	EDO	B	622	-	-	-	X
2	EDO	B	623	-	-	-	X
2	EDO	B	626	-	-	-	X
2	EDO	B	9	-	-	-	X
3	PLM	A	625	-	-	X	X
4	AKR	A	2	-	-	X	-
5	COH	A	626	-	-	-	X
5	COH	B	627	-	-	-	X
6	HSQ	A	661	X	-	-	-
8	NAG	A	681	-	-	-	X
8	NAG	B	681	-	-	-	X

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 10038 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 Prostaglandin G/H synthase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	552	Total	C	N	O	S	0	6	0
			4461	2878	744	814	25			
1	B	551	Total	C	N	O	S	0	8	0
			4447	2878	739	804	26			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	29	HIS	-	EXPRESSION TAG	UNP Q05769
A	30	HIS	-	EXPRESSION TAG	UNP Q05769
A	31	HIS	-	EXPRESSION TAG	UNP Q05769
A	32	HIS	-	EXPRESSION TAG	UNP Q05769
A	33	HIS	-	EXPRESSION TAG	UNP Q05769
A	34	HIS	-	EXPRESSION TAG	UNP Q05769
A	594	ALA	ASN	ENGINEERED MUTATION	UNP Q05769
B	29	HIS	-	EXPRESSION TAG	UNP Q05769
B	30	HIS	-	EXPRESSION TAG	UNP Q05769
B	31	HIS	-	EXPRESSION TAG	UNP Q05769
B	32	HIS	-	EXPRESSION TAG	UNP Q05769
B	33	HIS	-	EXPRESSION TAG	UNP Q05769
B	34	HIS	-	EXPRESSION TAG	UNP Q05769
B	594	ALA	ASN	ENGINEERED MUTATION	UNP Q05769

- Molecule 2 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



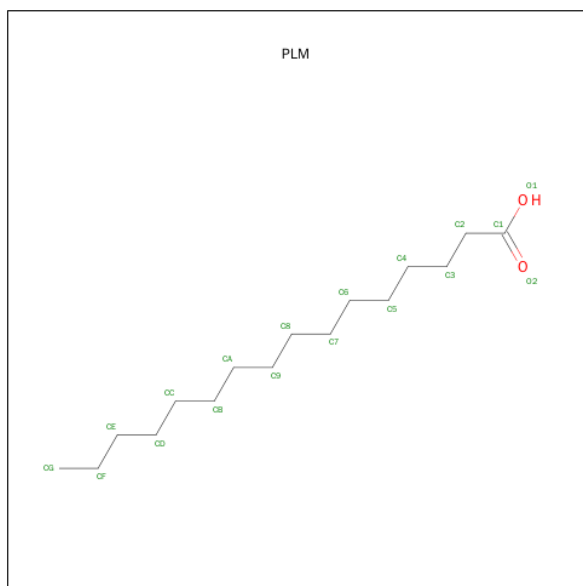
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 3 is PALMITIC ACID (three-letter code: PLM) (formula: C₁₆H₃₂O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			18	16	2		

- Molecule 4 is ACRYLIC ACID (three-letter code: AKR) (formula: C₃H₄O₂).



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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	B	1	Total	C	Co	N	O	0	0
			43	34	1	4	4		

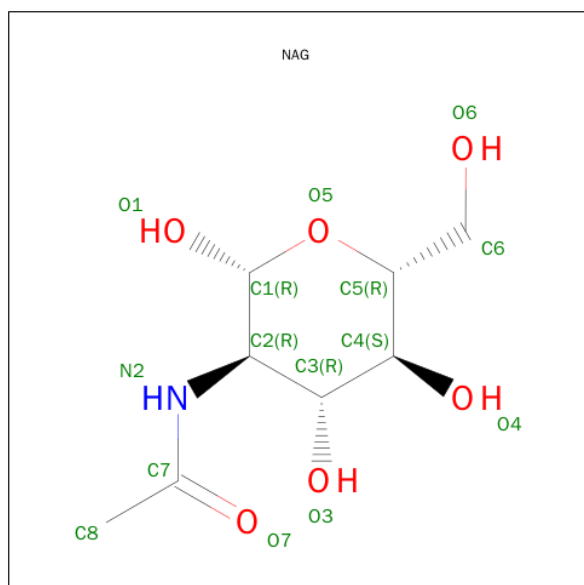
- Molecule 6 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 7 is a polymer of unknown type called SUGAR (3-MER).

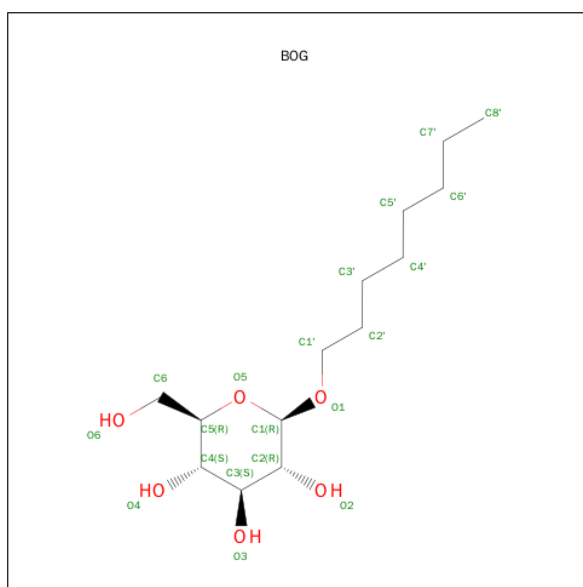
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 8 is SUGAR (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	B	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 9 is SUGAR (B-OCTYLGLUCOSIDE) (three-letter code: BOG) (formula: $C_{14}H_{28}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	C	O	0	0
			20	14	6		

- Molecule 10 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	B	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 11 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
11	B	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	370	Total	O	0	0
			370	370		
12	B	383	Total	O	0	0
			383	383		

4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	121.91Å 130.89Å 179.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.10 20.00 – 2.10	Depositor EDS
% Data completeness (in resolution range)	97.9 (20.00-2.10) 97.9 (20.00-2.10)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.40 (at 2.09Å)	Xtriage
Refinement program	REFMAC 5.5.0088	Depositor
R, R_{free}	0.159 , 0.199 0.187 , 0.218	Depositor DCC
R_{free} test set	4122 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	25.9	Xtriage
Anisotropy	0.014	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 56.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 82051 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10038	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.71% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: NAG, AKR, EDO, NDG, HSQ, COH, PLM, BOG, 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	0.56	0/4606	0.60	2/6258 (0.0%)
1	B	0.54	0/4599	0.58	0/6247
All	All	0.55	0/9205	0.59	2/12505 (0.0%)

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
6	A	1	0
All	All	1	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	456	ARG	NE-CZ-NH1	6.27	123.44	120.30
1	A	456	ARG	NE-CZ-NH2	-6.02	117.29	120.30

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	A	661	HSQ	C1

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	581	ASN	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	4461	0	4261	42	0
1	B	4447	0	4259	24	0
2	A	36	0	54	1	0
2	B	56	0	84	5	0
3	A	18	0	31	10	0
4	A	10	0	6	3	0
5	A	43	0	30	2	0
5	B	43	0	30	2	0
6	A	28	0	25	1	0
7	A	39	0	34	4	0
8	A	14	0	13	0	0
8	B	14	0	13	1	0
9	A	20	0	28	1	0
10	B	28	0	25	0	0
11	B	28	0	25	5	0
12	A	370	0	0	2	0
12	B	383	0	0	2	0
All	All	10038	0	8918	72	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 72 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:B:216:ARG:NH1	11:B:672:NAG:H83	1.78	0.99
1:B:216:ARG:HH11	11:B:672:NAG:H83	1.32	0.94
1:A:216:ARG:NH1	7:A:672:NAG:H83	1.95	0.81
1:A:161:THR:HG21	1:A:166:LYS:O	1.81	0.80
1:A:456:ARG:HD3	1:A:502:GLU:OE1	1.84	0.77

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	556/610 (91%)	547 (98%)	9 (2%)	0	100	100
1	B	557/610 (91%)	545 (98%)	12 (2%)	0	100	100
All	All	1113/1220 (91%)	1092 (98%)	21 (2%)	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	477/542 (88%)	467 (98%)	10 (2%)	61	66
1	B	474/542 (88%)	468 (99%)	6 (1%)	76	82
All	All	951/1084 (88%)	935 (98%)	16 (2%)	68	74

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	471	SER
1	A	484	GLU
1	B	289	GLN
1	A	444	VAL
1	B	385	TYR

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

Mol	Chain	Res	Type
1	A	214	HIS
1	B	278	HIS
1	B	581	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

9 carbohydrates 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	$\# Z > 2$
6	HSQ	A	661	1,6	14,14,15	0.47	0	15,19,21	1.81	1 (6%)
6	NAG	A	662	6	14,14,15	0.50	0	15,19,21	1.76	2 (13%)
7	NAG	A	671	1,7	14,14,15	0.54	0	15,19,21	1.36	2 (13%)
7	NAG	A	672	7	14,14,15	0.58	0	15,19,21	0.83	0
7	MAN	A	673	7	11,11,12	0.46	0	14,15,17	1.99	3 (21%)
10	NAG	B	661	1,10	14,14,15	1.70	1 (7%)	15,19,21	2.07	2 (13%)
10	NDG	B	662	10	14,14,15	0.56	0	15,19,21	1.03	1 (6%)
11	NAG	B	671	11,1	14,14,15	0.52	0	15,19,21	1.33	2 (13%)
11	NAG	B	672	11	14,14,15	0.66	0	15,19,21	1.06	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
6	HSQ	A	661	1,6	1/1/5/7	0/6/23/26	0/1/1/1
6	NAG	A	662	6	-	0/6/23/26	0/1/1/1
7	NAG	A	671	1,7	-	0/6/23/26	0/1/1/1
7	NAG	A	672	7	-	0/6/23/26	0/1/1/1
7	MAN	A	673	7	-	0/2/19/22	1/1/1/1
10	NAG	B	661	1,10	-	0/6/23/26	0/1/1/1
10	NDG	B	662	10	-	0/6/23/26	0/1/1/1
11	NAG	B	671	11,1	-	0/6/23/26	0/1/1/1
11	NAG	B	672	11	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	B	661	NAG	O5-C1	-6.00	1.33	1.43

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	B	661	NAG	C1-O5-C5	-7.26	103.04	112.25
7	A	671	NAG	C2-N2-C7	-3.10	119.06	123.04
11	B	671	NAG	C2-N2-C7	-3.07	119.09	123.04
7	A	673	MAN	C2-C3-C4	-2.39	106.98	111.04
6	A	662	NAG	C3-C4-C5	2.12	113.89	110.20

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	A	661	HSQ	C1

There are no torsion outliers.

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	A	673	MAN	C1-C2-C3-C4-C5-O5

4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	661	HSQ	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	672	NAG	4	0
7	A	673	MAN	1	0
11	B	672	NAG	5	0

5.6 Ligand geometry [i](#)

31 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	$\# Z > 2$
2	EDO	A	1	-	3,3,3	0.55	0	2,2,2	0.33	0
4	AKR	A	2	-	1,4,4	1.50	0	0,4,4	0.00	-
4	AKR	A	3	-	1,4,4	1.63	0	0,4,4	0.00	-
2	EDO	A	4	-	3,3,3	0.43	0	2,2,2	0.73	0
2	EDO	A	5	-	3,3,3	0.50	0	2,2,2	0.43	0
2	EDO	A	619	-	3,3,3	0.43	0	2,2,2	0.51	0
2	EDO	A	620	-	3,3,3	0.50	0	2,2,2	0.29	0
2	EDO	A	621	-	3,3,3	0.39	0	2,2,2	0.46	0
2	EDO	A	622	-	3,3,3	0.39	0	2,2,2	0.60	0
2	EDO	A	623	-	3,3,3	0.39	0	2,2,2	0.56	0
2	EDO	A	624	-	3,3,3	0.44	0	2,2,2	0.53	0
3	PLM	A	625	-	14,17,17	0.25	0	14,17,17	0.58	0
5	COH	A	626	-	28,50,50	2.27	9 (32%)	19,82,82	1.64	5 (26%)
8	NAG	A	681	1	14,14,15	0.59	0	15,19,21	1.15	1 (6%)
9	BOG	A	703	-	20,20,20	0.49	0	25,25,25	0.55	0
2	EDO	B	2	-	3,3,3	0.52	0	2,2,2	0.42	0
2	EDO	B	3	-	3,3,3	0.45	0	2,2,2	0.57	0
2	EDO	B	6	-	3,3,3	0.40	0	2,2,2	0.86	0
2	EDO	B	619	-	3,3,3	0.19	0	2,2,2	0.88	0
2	EDO	B	620	-	3,3,3	0.59	0	2,2,2	0.19	0
2	EDO	B	621	-	3,3,3	0.36	0	2,2,2	0.58	0
2	EDO	B	622	-	3,3,3	0.47	0	2,2,2	0.49	0
2	EDO	B	623	-	3,3,3	0.51	0	2,2,2	0.36	0
2	EDO	B	624	-	3,3,3	0.41	0	2,2,2	0.69	0
2	EDO	B	625	-	3,3,3	0.22	0	2,2,2	0.77	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	EDO	B	626	-	3,3,3	0.45	0	2,2,2	0.51	0
5	COH	B	627	-	28,50,50	2.25	8 (28%)	19,82,82	1.53	3 (15%)
8	NAG	B	681	1	14,14,15	0.82	0	15,19,21	1.15	1 (6%)
2	EDO	B	7	-	3,3,3	0.36	0	2,2,2	0.60	0
2	EDO	B	8	-	3,3,3	0.46	0	2,2,2	0.54	0
2	EDO	B	9	-	3,3,3	0.41	0	2,2,2	0.46	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
2	EDO	A	1	-	-	0/1/1/1	0/0/0/0
4	AKR	A	2	-	-	0/0/2/2	0/0/0/0
4	AKR	A	3	-	-	0/0/2/2	0/0/0/0
2	EDO	A	4	-	-	0/1/1/1	0/0/0/0
2	EDO	A	5	-	-	0/1/1/1	0/0/0/0
2	EDO	A	619	-	-	0/1/1/1	0/0/0/0
2	EDO	A	620	-	-	0/1/1/1	0/0/0/0
2	EDO	A	621	-	-	0/1/1/1	0/0/0/0
2	EDO	A	622	-	-	0/1/1/1	0/0/0/0
2	EDO	A	623	-	-	0/1/1/1	0/0/0/0
2	EDO	A	624	-	-	0/1/1/1	0/0/0/0
3	PLM	A	625	-	-	0/13/15/15	0/0/0/0
5	COH	A	626	-	-	0/6/54/54	0/0/8/8
8	NAG	A	681	1	-	0/6/23/26	0/1/1/1
9	BOG	A	703	-	-	0/11/31/31	0/1/1/1
2	EDO	B	2	-	-	0/1/1/1	0/0/0/0
2	EDO	B	3	-	-	0/1/1/1	0/0/0/0
2	EDO	B	6	-	-	0/1/1/1	0/0/0/0
2	EDO	B	619	-	-	0/1/1/1	0/0/0/0
2	EDO	B	620	-	-	0/1/1/1	0/0/0/0
2	EDO	B	621	-	-	0/1/1/1	0/0/0/0
2	EDO	B	622	-	-	0/1/1/1	0/0/0/0
2	EDO	B	623	-	-	0/1/1/1	0/0/0/0
2	EDO	B	624	-	-	0/1/1/1	0/0/0/0
2	EDO	B	625	-	-	0/1/1/1	0/0/0/0
2	EDO	B	626	-	-	0/1/1/1	0/0/0/0
5	COH	B	627	-	-	0/6/54/54	0/0/8/8
8	NAG	B	681	1	-	0/6/23/26	0/1/1/1
2	EDO	B	7	-	-	0/1/1/1	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	EDO	B	8	-	-	0/1/1/1	0/0/0/0
2	EDO	B	9	-	-	0/1/1/1	0/0/0/0

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	627	COH	C3B-C2B	-4.40	1.34	1.40
5	A	626	COH	C3B-C2B	-4.33	1.34	1.40
5	B	627	COH	C3C-C2C	-4.26	1.34	1.40
5	A	626	COH	C3C-C2C	-4.08	1.34	1.40
5	A	626	COH	CO-NC	2.23	2.09	1.97

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	627	COH	C3C-CAC-CBC	-3.61	118.93	126.32
5	A	626	COH	C3C-CAC-CBC	-3.11	119.96	126.32
5	B	627	COH	C3B-CAB-CBB	-2.79	120.61	126.32
5	A	626	COH	CBD-CAD-C3D	-2.74	107.62	112.53
5	A	626	COH	CAA-CBA-CGA	-2.38	108.38	112.75

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

11 monomers are involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	2	AKR	3	0
2	A	621	EDO	1	0
3	A	625	PLM	10	0
5	A	626	COH	2	0
9	A	703	BOG	1	0
2	B	620	EDO	1	0
2	B	625	EDO	2	0
5	B	627	COH	2	0
8	B	681	NAG	1	0
2	B	7	EDO	1	0
2	B	9	EDO	1	0

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	552/610 (90%)	0.03	27 (4%) 33 42	13, 26, 39, 47	0
1	B	551/610 (90%)	0.06	25 (4%) 37 46	11, 27, 43, 52	0
All	All	1103/1220 (90%)	0.04	52 (4%) 35 44	11, 27, 40, 52	0

The worst 5 of 52 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	279	ILE	5.8
1	A	583	GLN	5.8
1	B	277	PRO	5.2
1	B	283	LEU	4.7
1	B	278	HIS	4.6

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](#)

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
10	NAG	B	661	14/15	0.81	0.28	2.75	47,52,56,61	0
6	HSQ	A	661	14/15	0.85	0.22	1.24	43,52,55,60	0
11	NAG	B	672	14/15	0.86	0.22	0.24	36,40,42,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
7	NAG	A	671	14/15	0.95	0.09	-0.70	20,25,30,33	0
11	NAG	B	671	14/15	0.97	0.08	-1.60	22,25,27,32	0
7	NAG	A	672	14/15	0.89	0.19	-	38,42,47,52	0
7	MAN	A	673	11/12	0.55	0.39	-	57,60,61,62	0
6	NAG	A	662	14/15	0.70	0.49	-	65,69,70,71	0
10	NDG	B	662	14/15	0.68	0.47	-	65,68,68,68	0

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
5	COH	A	626	43/43	0.55	0.35	8.95	60,71,74,76	43
2	EDO	B	622	4/4	0.83	0.28	7.87	49,49,49,50	0
5	COH	B	627	43/43	0.36	0.44	7.79	66,77,79,80	43
3	PLM	A	625	18/18	0.74	0.25	7.64	34,51,61,61	0
8	NAG	A	681	14/15	0.83	0.28	5.13	44,50,54,56	0
2	EDO	B	9	4/4	0.80	0.17	4.95	50,51,51,52	0
2	EDO	B	623	4/4	0.68	0.22	4.88	57,57,57,57	0
2	EDO	B	621	4/4	0.95	0.18	3.78	45,46,46,47	0
2	EDO	B	626	4/4	0.73	0.15	2.63	60,60,60,62	0
8	NAG	B	681	14/15	0.75	0.28	2.41	47,54,58,60	0
2	EDO	A	624	4/4	0.85	0.14	2.30	50,51,51,52	0
2	EDO	A	5	4/4	0.79	0.18	1.50	58,59,59,60	0
2	EDO	B	3	4/4	0.95	0.11	1.45	21,22,22,23	0
2	EDO	B	625	4/4	0.86	0.17	1.41	50,50,50,51	0
9	BOG	A	703	20/20	0.91	0.15	1.33	35,38,41,41	0
2	EDO	A	4	4/4	0.94	0.14	1.30	29,29,32,35	0
2	EDO	B	2	4/4	0.96	0.15	1.08	34,34,36,36	0
2	EDO	A	619	4/4	0.96	0.14	0.94	27,29,31,31	0
2	EDO	B	7	4/4	0.85	0.16	0.79	58,58,59,60	0
4	AKR	A	2	5/5	0.88	0.19	0.53	49,50,50,50	0
2	EDO	B	8	4/4	0.98	0.10	0.49	24,28,29,29	0
2	EDO	B	619	4/4	0.84	0.18	0.18	40,40,41,42	0
2	EDO	A	1	4/4	0.95	0.12	0.14	38,38,38,38	0
2	EDO	B	6	4/4	0.92	0.14	0.13	32,33,33,35	0
4	AKR	A	3	5/5	0.94	0.18	0.06	38,38,38,39	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	EDO	A	623	4/4	0.87	0.13	-0.16	59,60,60,61	0
2	EDO	A	621	4/4	0.94	0.12	-0.18	44,44,45,48	0
2	EDO	A	620	4/4	0.97	0.09	-0.51	25,25,26,26	0
2	EDO	B	620	4/4	0.48	0.24	-	62,63,63,64	0
2	EDO	A	622	4/4	0.96	0.09	-	45,45,45,45	0
2	EDO	B	624	4/4	0.90	0.13	-	37,41,42,45	0

6.5 Other polymers [i](#)

There are no such residues in this entry.