Full wwPDB X-ray Structure Validation Report (i)

Jan 31, 2016 – 06:58 PM GMT

PDB ID	:	1DHK
Title	:	STRUCTURE OF PORCINE PANCREATIC ALPHA-AMYLASE
Authors	:	Bompard-Gilles, C.; Payan, F.
Deposited on	:	1996-10-14
Resolution	:	1.85 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

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

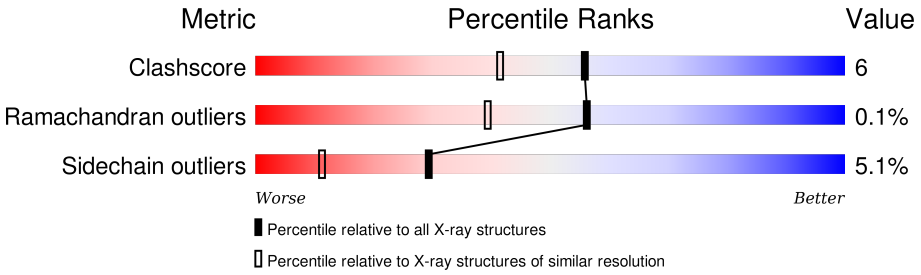
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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))
Clashscore	102246	1898 (1.86-1.86)
Ramachandran outliers	100387	1875 (1.86-1.86)
Sidechain outliers	100360	1875 (1.86-1.86)

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 <=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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	496	86% 12% •
2	B	223	71% 13% • • 13%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 7712 atoms, of which 1887 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 PORCINE PANCREATIC ALPHA-AMYLASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	496	Total	C	H	N	O	S	0	0	0
			4791	2468	885	687	730	21			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	49	VAL	ILE	CONFLICT	UNP P00690
A	404	GLN	GLU	CONFLICT	UNP P00690

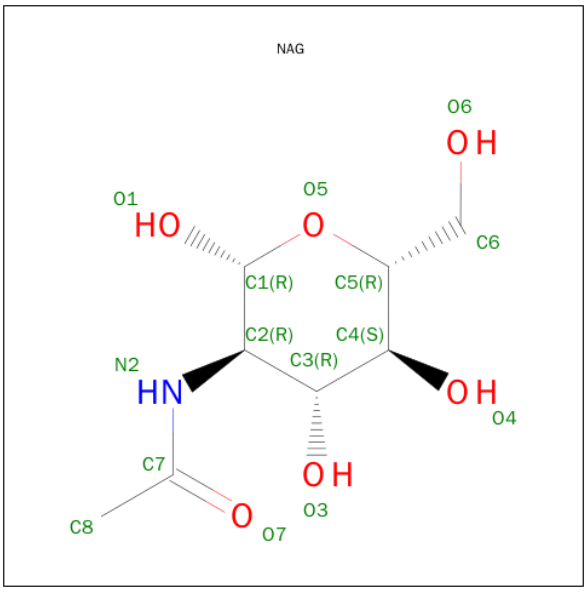
- Molecule 2 is a protein called BEAN LECTIN-LIKE INHIBITOR.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	195	Total	C	H	N	O	S	0	0	0
			1863	957	340	247	317	2			

- Molecule 3 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	2	Total	C	H	N	O	0	0
			35	16	7	2	10		
3	B	2	Total	C	H	N	O	0	0
			35	16	7	2	10		

- Molecule 4 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C H N O 18 8 4 1 5	0	0

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total Cl 1 1	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	257	Total H O 771 514 257	0	0
7	B	65	Total H O 195 130 65	0	0

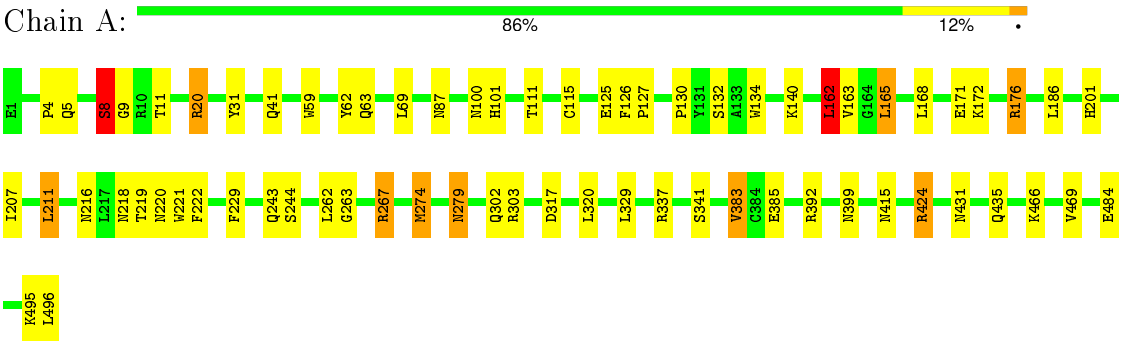
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

Note EDS was not executed.

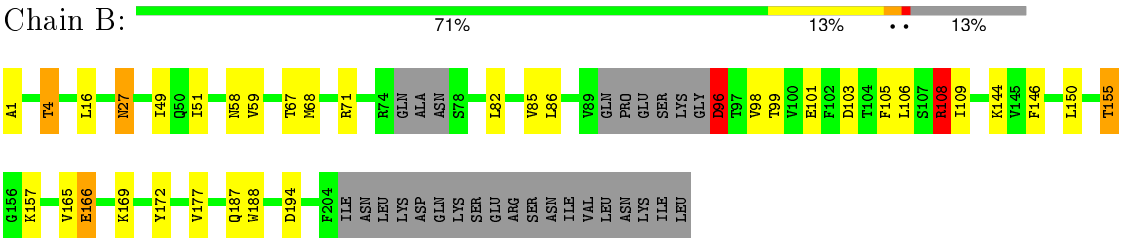
- Molecule 1: PORCINE PANCREATIC ALPHA-AMYLASE

Chain A:



- Molecule 2: BEAN LECTIN-LIKE INHIBITOR

Chain B:



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	151.60Å 79.40Å 68.00Å 90.00° 91.54° 90.00°	Depositor
Resolution (Å)	8.00 – 1.85	Depositor
% Data completeness (in resolution range)	(Not available) (8.00-1.85)	Depositor
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.183 , 0.220	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	7712	wwPDB-VP
Average B, all atoms (Å^2)	17.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, PCA, NAG, CL

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	0.42	4/4009 (0.1%)	0.88	13/5450 (0.2%)
2	B	0.58	2/1555 (0.1%)	1.21	12/2120 (0.6%)
All	All	0.47	6/5564 (0.1%)	0.98	25/7570 (0.3%)

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	A	0	1
2	B	1	1
All	All	1	2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	96	ASP	CA-CB	-12.48	1.26	1.53
2	B	108	ARG	CD-NE	-8.99	1.31	1.46
1	A	424	ARG	CD-NE	-8.03	1.32	1.46
1	A	216	ASN	CA-CB	-7.02	1.34	1.53
1	A	8	SER	CA-C	-5.75	1.38	1.52
1	A	8	SER	CB-OG	-5.66	1.34	1.42

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	108	ARG	NE-CZ-NH1	22.14	131.37	120.30
2	B	96	ASP	CA-CB-CG	19.86	157.09	113.40
1	A	176	ARG	NE-CZ-NH2	18.73	129.66	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	176	ARG	NE-CZ-NH1	-18.73	110.94	120.30
2	B	108	ARG	NE-CZ-NH2	-18.48	111.06	120.30
1	A	165	LEU	CB-CG-CD2	16.05	138.29	111.00
2	B	67	THR	CA-CB-CG2	15.26	133.76	112.40
1	A	469	VAL	CA-CB-CG1	13.07	130.51	110.90
2	B	96	ASP	CB-CA-C	12.89	136.18	110.40
1	A	162	LEU	CB-CG-CD2	12.40	132.08	111.00
1	A	162	LEU	CB-CG-CD1	-11.34	91.72	111.00
1	A	424	ARG	CD-NE-CZ	10.23	137.92	123.60
2	B	71	ARG	CG-CD-NE	-9.22	92.44	111.80
2	B	98	VAL	CA-CB-CG1	7.61	122.32	110.90
1	A	9	GLY	CA-C-O	-7.25	107.55	120.60
2	B	108	ARG	CD-NE-CZ	7.07	133.50	123.60
1	A	8	SER	CA-C-N	6.74	129.67	116.20
1	A	8	SER	CA-C-O	-6.29	106.88	120.10
2	B	59	VAL	CA-CB-CG2	6.13	120.09	110.90
1	A	9	GLY	O-C-N	5.77	131.94	122.70
1	A	267	ARG	CG-CD-NE	5.53	123.42	111.80
2	B	108	ARG	CG-CD-NE	-5.45	100.35	111.80
2	B	96	ASP	CA-C-O	5.41	131.45	120.10
2	B	96	ASP	CA-C-N	-5.27	105.61	117.20
1	A	20	ARG	CG-CD-NE	5.06	122.44	111.80

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	67	THR	CB

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	424	ARG	Sidechain
2	B	108	ARG	Sidechain

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	3906	885	3680	44	1
2	B	1523	340	1424	21	1
3	B	56	14	50	0	0
4	B	14	4	13	0	0
5	A	1	0	0	0	0
5	B	2	0	0	0	0
6	A	1	0	0	1	0
7	A	257	514	0	12	1
7	B	65	130	0	1	1
All	All	5825	1887	5167	64	2

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 6.

All (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:A:125:GLU:HB3	7:A:741:HOH:O	1.34	1.26
1:A:132:SER:OG	1:A:134:TRP:CE2	2.25	0.90
2:B:155:THR:HG22	2:B:157:LYS:HG2	1.55	0.88
1:A:127:PRO:HD3	7:A:741:HOH:O	1.74	0.87
2:B:155:THR:CG2	2:B:157:LYS:HG2	2.11	0.80
1:A:100:ASN:HD22	1:A:101:HIS:HD2	1.30	0.79
2:B:4:THR:CG2	2:B:49:ILE:HD12	2.19	0.72
1:A:279:ASN:HD22	1:A:279:ASN:H	1.39	0.69
1:A:41:GLN:HE22	1:A:337:ARG:HH11	1.41	0.68
2:B:4:THR:HG23	2:B:49:ILE:HD12	1.78	0.66
1:A:317:ASP:OD2	7:A:750:HOH:O	2.13	0.66
1:A:172:LYS:O	1:A:176:ARG:HG3	1.95	0.66
1:A:484:GLU:HG2	7:A:706:HOH:O	1.96	0.64
2:B:27:ASN:HD22	2:B:27:ASN:H	1.47	0.62
2:B:86:LEU:HD22	2:B:177:VAL:HG12	1.81	0.60
1:A:125:GLU:CB	7:A:741:HOH:O	2.15	0.60
1:A:140:LYS:HE3	7:A:654:HOH:O	2.01	0.60
1:A:302:GLN:HE21	1:A:303:ARG:HH12	1.49	0.59
1:A:125:GLU:CA	7:A:741:HOH:O	2.49	0.57
2:B:4:THR:HG21	2:B:49:ILE:HD12	1.87	0.55
1:A:41:GLN:HE22	1:A:337:ARG:NH1	2.02	0.55
1:A:162:LEU:HD13	1:A:163:VAL:HG22	1.89	0.55
1:A:337:ARG:NH2	6:A:498:CL:CL	2.74	0.54
1:A:263:GLY:O	1:A:267:ARG:HG3	2.09	0.53
1:A:302:GLN:HE21	1:A:303:ARG:NH1	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:85:VAL:HG12	2:B:99:THR:HG23	1.91	0.53
1:A:383:VAL:HG22	1:A:385:GLU:OE1	2.10	0.52
2:B:86:LEU:CD2	2:B:177:VAL:HG12	2.41	0.52
1:A:100:ASN:HD22	1:A:101:HIS:CD2	2.20	0.51
2:B:96:ASP:O	2:B:172:TYR:HE1	1.94	0.51
1:A:140:LYS:HZ1	1:A:171:GLU:CD	2.15	0.49
2:B:4:THR:HG22	7:B:526:HOH:O	2.13	0.48
2:B:51:ILE:HB	2:B:172:TYR:O	2.13	0.48
1:A:11:THR:H	1:A:399:ASN:HD21	1.61	0.48
1:A:126:PHE:O	1:A:130:PRO:HA	2.13	0.48
1:A:62:TYR:O	1:A:101:HIS:HE1	1.96	0.48
1:A:125:GLU:C	7:A:741:HOH:O	2.52	0.47
1:A:274:MET:HG3	7:A:554:HOH:O	2.14	0.47
1:A:31:TYR:OH	1:A:392:ARG:HG3	2.15	0.47
2:B:169:LYS:HD2	2:B:172:TYR:HE2	1.80	0.46
1:A:207:ILE:HG22	1:A:211:LEU:HD22	1.98	0.46
1:A:132:SER:OG	1:A:134:TRP:NE1	2.49	0.45
1:A:63:GLN:HG2	1:A:165:LEU:HD22	1.97	0.45
2:B:187:GLN:HG2	2:B:188:TRP:CD1	2.51	0.45
1:A:59:TRP:CE2	2:B:187:GLN:HB3	2.52	0.44
1:A:5:GLN:NE2	1:A:5:GLN:HA	2.32	0.44
1:A:5:GLN:HE21	1:A:5:GLN:HA	1.83	0.44
1:A:466:LYS:HE2	7:A:735:HOH:O	2.17	0.44
1:A:4:PRO:HA	1:A:229:PHE:CG	2.53	0.44
1:A:132:SER:OG	1:A:134:TRP:CD2	2.67	0.43
1:A:218:ASN:OD1	1:A:220:ASN:HB2	2.17	0.43
2:B:68:MET:SD	2:B:82:LEU:HD23	2.58	0.43
2:B:146:PHE:HB2	2:B:165:VAL:HG22	2.01	0.43
2:B:105:PHE:HD2	2:B:106:LEU:HD22	1.84	0.43
2:B:144:LYS:HE2	2:B:166:GLU:HG2	2.00	0.43
1:A:162:LEU:HD23	1:A:201:HIS:CE1	2.54	0.42
1:A:219:THR:HA	1:A:222:PHE:O	2.19	0.42
1:A:392:ARG:NH2	7:A:599:HOH:O	2.43	0.42
2:B:103:ASP:OD2	2:B:106:LEU:HD23	2.20	0.42
1:A:87:ASN:HB3	1:A:221:TRP:CD1	2.55	0.41
1:A:415:ASN:HB3	1:A:431:ASN:HB3	2.02	0.41
2:B:101:GLU:O	2:B:109:ILE:HA	2.21	0.41
1:A:140:LYS:CE	7:A:654:HOH:O	2.65	0.41
1:A:279:ASN:HD22	1:A:279:ASN:N	2.10	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1:ALA:H2	7:B:527:HOH:H1[2_655]	1.13	0.47
1:A:495:LYS:HZ1	7:A:751:HOH:H2[4_655]	1.14	0.46

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	494/496 (100%)	479 (97%)	14 (3%)	1 (0%)	52 36
2	B	189/223 (85%)	184 (97%)	5 (3%)	0	100 100
All	All	683/719 (95%)	663 (97%)	19 (3%)	1 (0%)	56 39

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	8	SER

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	411/411 (100%)	391 (95%)	20 (5%)	31 12
2	B	176/203 (87%)	166 (94%)	10 (6%)	25 9
All	All	587/614 (96%)	557 (95%)	30 (5%)	29 11

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	SER
1	A	20	ARG
1	A	69	LEU
1	A	111	THR
1	A	115	CYS
1	A	162	LEU
1	A	168	LEU
1	A	186	LEU
1	A	211	LEU
1	A	243	GLN
1	A	244	SER
1	A	262	LEU
1	A	274	MET
1	A	279	ASN
1	A	320	LEU
1	A	329	LEU
1	A	341	SER
1	A	383	VAL
1	A	435	GLN
1	A	496	LEU
2	B	4	THR
2	B	16	LEU
2	B	27	ASN
2	B	58	ASN
2	B	96	ASP
2	B	108	ARG
2	B	150	LEU
2	B	155	THR
2	B	166	GLU
2	B	194	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	GLN
1	A	15	HIS
1	A	41	GLN
1	A	101	HIS
1	A	279	ASN
1	A	302	GLN
1	A	355	ASN
1	A	399	ASN
2	B	27	ASN

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Mol	Chain	Res	Type
2	B	29	ASN
2	B	31	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)

1 non-standard protein/DNA/RNA residue is 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	$\#\|Z\| > 2$
1	PCA	A	1	1	7,8,9	1.07	1 (14%)	9,10,12	3.69	7 (77%)

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
1	PCA	A	1	1	-	0/0/11/13	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1	PCA	CG-CD	2.14	1.57	1.50

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1	PCA	CG-CD-N	-4.62	91.42	108.04
1	A	1	PCA	CB-CA-C	-3.81	107.56	112.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1	PCA	OE-CD-CG	-2.39	121.47	126.81
1	A	1	PCA	CG-CB-CA	-2.27	94.57	104.25
1	A	1	PCA	CB-CG-CD	2.59	109.48	104.22
1	A	1	PCA	CA-N-CD	3.27	124.77	113.81
1	A	1	PCA	OE-CD-N	7.36	147.10	124.85

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

4 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	$\#\|Z\| > 2$
3	NAG	B	508	3	14,14,15	0.82	0	15,19,21	1.19	1 (6%)
3	NAG	B	509	3,2	14,14,15	0.64	1 (7%)	15,19,21	1.07	1 (6%)
3	NAG	B	510	3	14,14,15	0.73	1 (7%)	15,19,21	2.76	2 (13%)
3	NAG	B	511	3,2	14,14,15	0.68	1 (7%)	15,19,21	1.00	1 (6%)

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	NAG	B	508	3	-	0/6/23/26	0/1/1/1
3	NAG	B	509	3,2	-	0/6/23/26	0/1/1/1
3	NAG	B	510	3	-	0/6/23/26	0/1/1/1
3	NAG	B	511	3,2	-	0/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	509	NAG	C1-C2	2.00	1.55	1.52
3	B	511	NAG	C1-C2	2.17	1.55	1.52
3	B	510	NAG	C1-C2	2.32	1.55	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	510	NAG	C2-N2-C7	-9.86	110.37	123.04
3	B	508	NAG	C1-O5-C5	-3.97	107.21	112.25
3	B	509	NAG	C1-O5-C5	-3.57	107.72	112.25
3	B	510	NAG	C1-O5-C5	-3.48	107.83	112.25
3	B	511	NAG	C1-O5-C5	-3.11	108.30	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.6 Ligand geometry

Of 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 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	$\#\|Z\| > 2$
4	NAG	B	512	2	14,14,15	0.87	1 (7%)	15,19,21	1.19	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
4	NAG	B	512	2	-	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)
4	B	512	NAG	C1-C2	2.87	1.56	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	B	512	NAG	C1-O5-C5	-3.07	108.35	112.25
4	B	512	NAG	C3-C4-C5	-2.85	105.23	110.20

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates

EDS was not executed - this section will therefore be empty.

6.4 Ligands

EDS was not executed - this section will therefore be empty.

6.5 Other polymers

EDS was not executed - this section will therefore be empty.