



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 3KLS
Title : Structure of complement C5 in complex with SSL7
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Jensen, L.; Fraser, J.D.; Andersen, G.R.
Deposited on : 2009-11-09
Resolution : 3.60 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

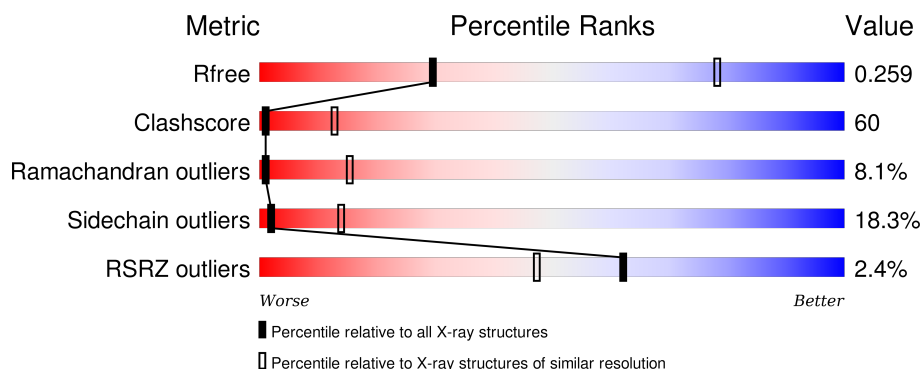
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.60 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	1408 (3.80-3.40)
Clashscore	102246	1010 (3.74-3.46)
Ramachandran outliers	100387	1007 (3.76-3.44)
Sidechain outliers	100360	1007 (3.76-3.44)
RSRZ outliers	91569	1003 (3.78-3.42)

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	1676	<div> <div>2%</div> <div>25% 53% 17% . .</div> </div>
1	B	1676	<div> <div>%</div> <div>23% 48% 16% • 12%</div> </div>
2	X	231	<div> <div>8%</div> <div>29% 42% 10% • 17%</div> </div>
2	Y	231	<div> <div>6%</div> <div>29% 42% 10% • 17%</div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 27683 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 Complement C5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1622	Total	C	N	O	S	0	0	0
			12836	8224	2107	2452	53			
1	B	1478	Total	C	N	O	S	0	0	0
			11676	7478	1926	2226	46			

- Molecule 2 is a protein called Exotoxin 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	X	191	Total	C	N	O	S	0	0	0
			1539	965	267	306	1			
2	Y	191	Total	C	N	O	S	0	0	0
			1539	965	267	306	1			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	35	GLY	GLU	ENGINEERED	UNP Q6GJP2
Y	35	GLY	GLU	ENGINEERED	UNP Q6GJP2

- Molecule 3 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	4	Total	Cd	0	0
			4	4		
3	A	5	Total	Cd	0	0
			5	5		

- Molecule 4 is a polymer of unknown type called SUGAR (2-MER).

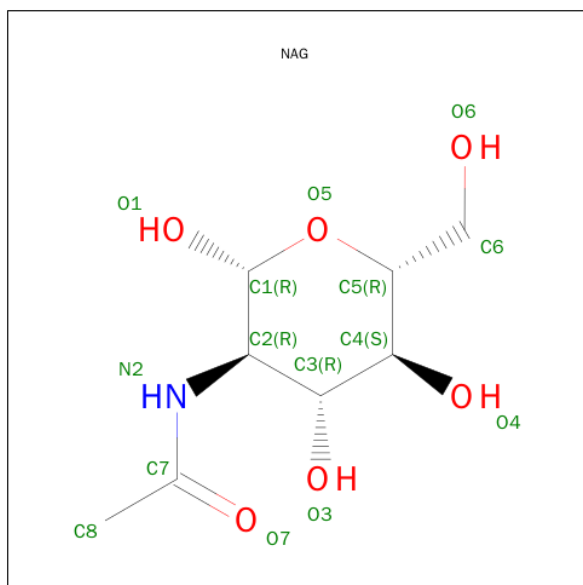
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	2	Total	C	N	O	0	0
			28	16	2	10		

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

- Molecule 5 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).

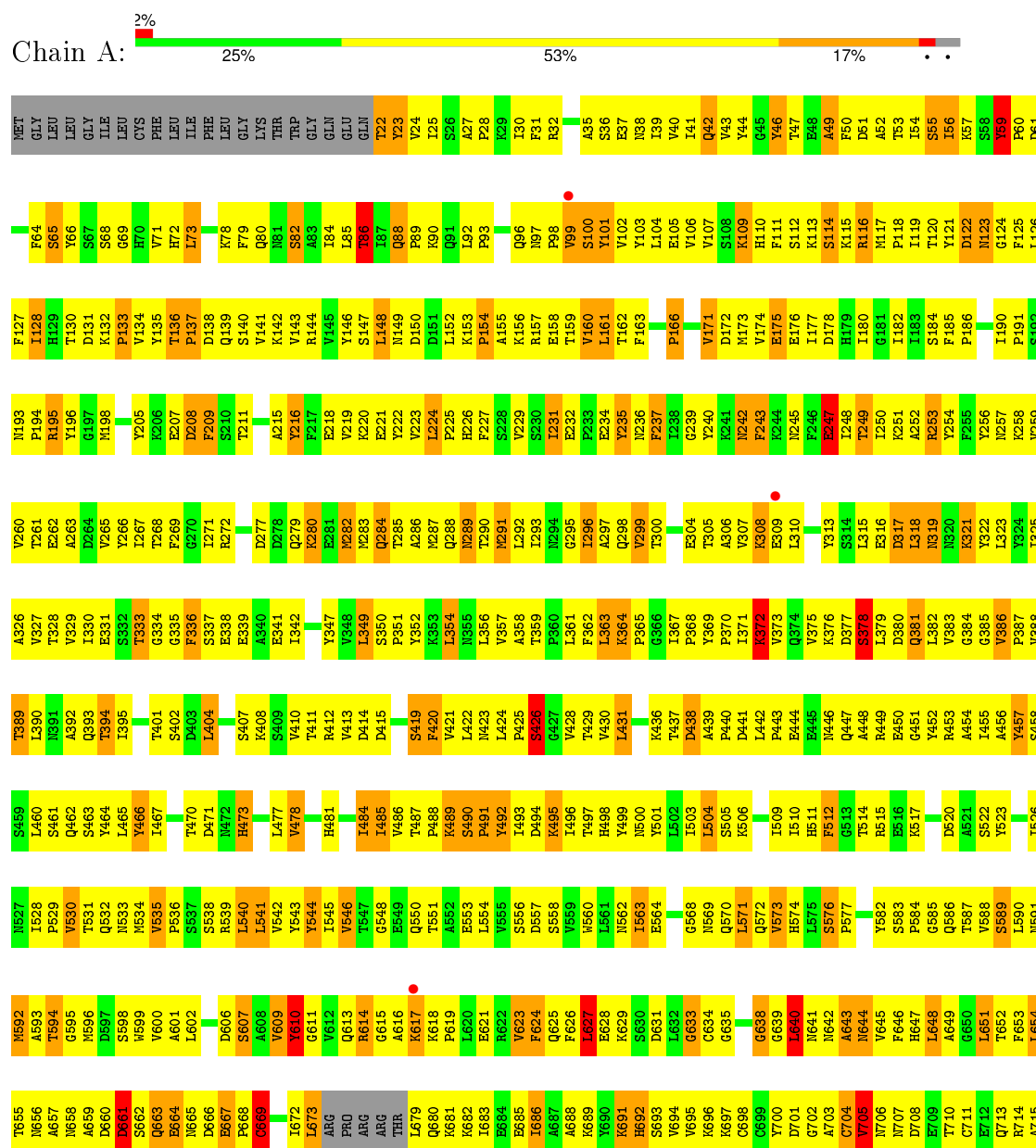


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	B	1	Total	C	N	O	0	0
			14	8	1	5		

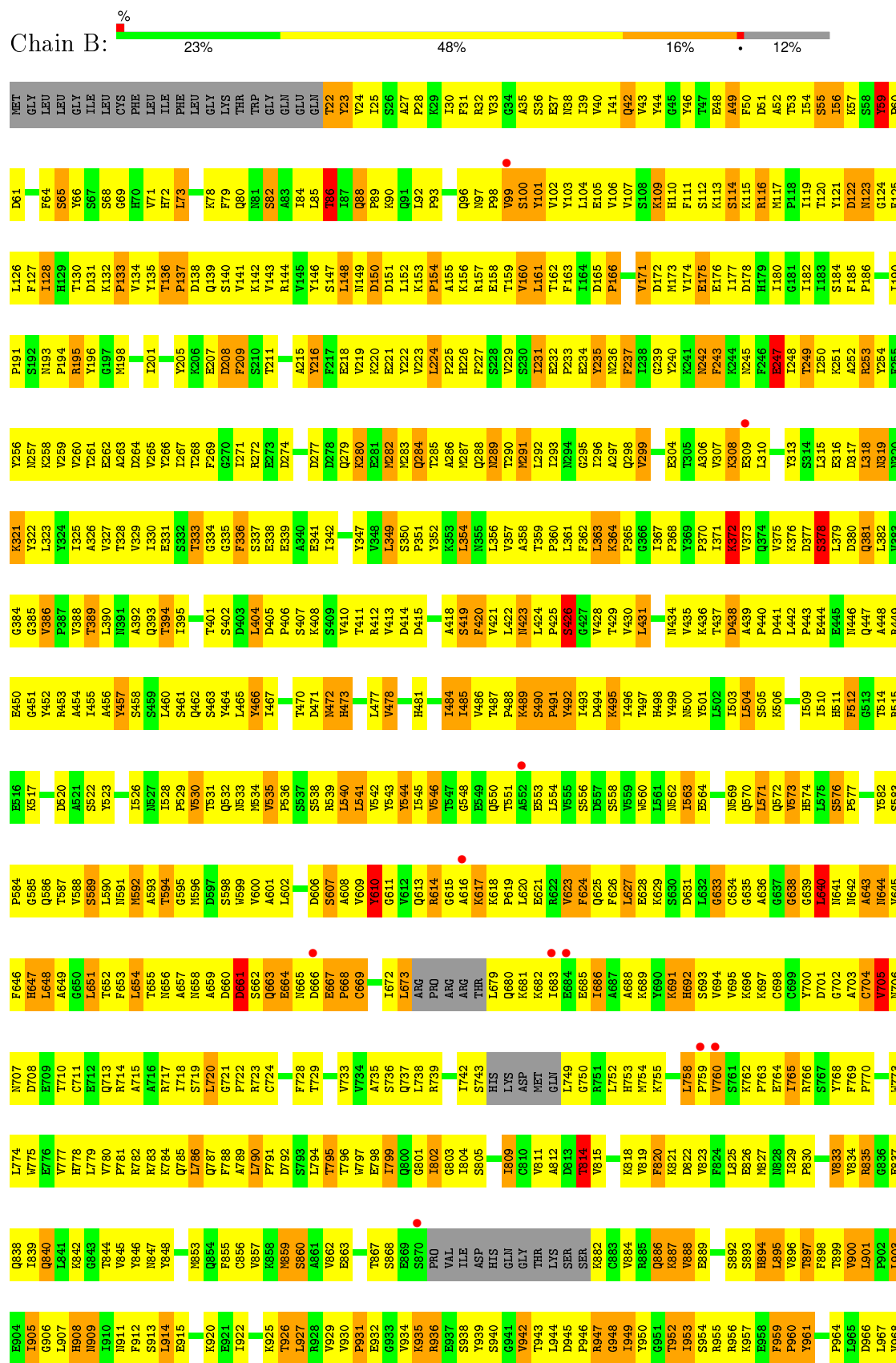
3 Residue-property plots

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.

• Molecule 1: Complement C5

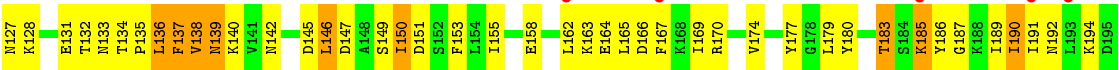
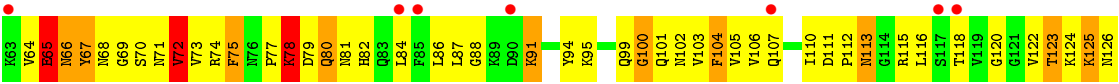


- Molecule 1: Complement C5





• Molecule 2: Exotoxin 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α , β , γ	143.88Å 143.88Å 241.24Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.05 – 3.60 29.31 – 3.60	Depositor EDS
% Data completeness (in resolution range)	99.5 (29.05-3.60) 99.6 (29.31-3.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.39 (at 3.65Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.5_2)	Depositor
R, R_{free}	0.198 , 0.263 0.192 , 0.259	Depositor DCC
R_{free} test set	3205 reflections (4.99%)	DCC
Wilson B-factor (Å ²)	111.0	Xtriage
Anisotropy	0.346	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 120.3	EDS
Estimated twinning fraction	0.025 for -h,-k,l 0.410 for h,-h-k,-l 0.028 for -k,-h,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 64555 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	27683	wwPDB-VP
Average B, all atoms (Å ²)	156.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.55% 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, CD

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	0.59	1/13111 (0.0%)	0.82	7/17784 (0.0%)
1	B	0.60	2/11928 (0.0%)	0.83	6/16183 (0.0%)
2	X	0.33	0/1560	0.56	0/2096
2	Y	0.33	0/1560	0.57	1/2096 (0.0%)
All	All	0.57	3/28159 (0.0%)	0.80	14/38159 (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	A	0	4
1	B	0	2
All	All	0	6

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	247	GLU	CB-CG	5.75	1.63	1.52
1	B	247	GLU	CG-CD	5.70	1.60	1.51
1	A	247	GLU	CB-CG	5.40	1.62	1.52

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1487	PHE	N-CA-CB	7.79	124.62	110.60
1	A	1303	LEU	CA-CB-CG	6.25	129.68	115.30
1	B	1303	LEU	CA-CB-CG	6.20	129.56	115.30
1	A	1283	GLY	N-CA-C	5.75	127.47	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	1283	GLY	N-CA-C	5.71	127.37	113.10

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1179	THR	Peptide
1	A	1633	PHE	Peptide
1	A	1635	TYR	Peptide
1	A	651	LEU	Peptide
1	B	651	LEU	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	12836	0	12796	1596	1
1	B	11676	0	11649	1413	1
2	X	1539	0	1530	162	0
2	Y	1539	0	1530	163	0
3	A	5	0	0	0	0
3	B	4	0	0	0	0
4	A	28	0	25	3	0
4	B	28	0	25	2	0
5	A	14	0	13	0	0
5	B	14	0	13	0	0
All	All	27683	0	27581	3288	1

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 60.

The worst 5 of 3288 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:1279:ARG:HG3	1:B:1284:PHE:CB	1.60	1.32

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1488:LEU:O	1:B:1488:LEU:HD12	1.31	1.30
1:A:1279:ARG:HG3	1:A:1284:PHE:CB	1.60	1.29
1:A:1486:GLY:O	1:A:1487:PHE:CD2	1.86	1.27
1:B:1323:LEU:HD12	1:B:1324:HIS:H	1.04	1.15

All (1) 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)
1:A:955:ARG:NH2	1:B:434:ASN:OD1[3_454]	2.19	0.01

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	1612/1676 (96%)	1199 (74%)	273 (17%)	140 (9%)	1	14
1	B	1468/1676 (88%)	1126 (77%)	224 (15%)	118 (8%)	1	16
2	X	189/231 (82%)	150 (79%)	28 (15%)	11 (6%)	2	25
2	Y	189/231 (82%)	150 (79%)	29 (15%)	10 (5%)	2	27
All	All	3458/3814 (91%)	2625 (76%)	554 (16%)	279 (8%)	1	15

5 of 279 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	46	TYR
1	A	59	TYR
1	A	97	ASN
1	A	209	PHE
1	A	243	PHE

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	1438/1484 (97%)	1168 (81%)	270 (19%)	2	13
1	B	1311/1484 (88%)	1055 (80%)	256 (20%)	2	12
2	X	175/205 (85%)	155 (89%)	20 (11%)	7	36
2	Y	175/205 (85%)	154 (88%)	21 (12%)	6	33
All	All	3099/3378 (92%)	2532 (82%)	567 (18%)	2	14

5 of 567 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1561	TYR
1	B	160	VAL
1	B	1464	LEU
1	A	1629	TYR
2	X	190	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 100 such sidechains are listed below:

Mol	Chain	Res	Type
2	X	80	GLN
1	B	123	ASN
2	Y	59	ASN
2	X	81	ASN
2	X	176	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 ⓘ

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$
4	NAG	A	2001	1,4	14,14,15	0.55	0	15,19,21	1.63	2 (13%)
4	NAG	A	2002	4	14,14,15	0.42	0	15,19,21	1.18	1 (6%)
4	NAG	B	2001	1,4	14,14,15	0.54	0	15,19,21	1.17	1 (6%)
4	NAG	B	2002	4	14,14,15	0.38	0	15,19,21	1.09	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
4	NAG	A	2001	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	2002	4	-	0/6/23/26	0/1/1/1
4	NAG	B	2001	1,4	-	0/6/23/26	0/1/1/1
4	NAG	B	2002	4	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	2001	NAG	C2-N2-C7	-3.86	118.08	123.04
4	B	2001	NAG	C3-C4-C5	-2.73	105.44	110.20
4	B	2002	NAG	C1-O5-C5	3.53	116.73	112.25
4	A	2002	NAG	C1-O5-C5	3.69	116.93	112.25
4	A	2001	NAG	C1-O5-C5	3.95	117.27	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	2001	NAG	3	0
4	B	2001	NAG	2	0

5.6 Ligand geometry

Of 11 ligands modelled in this entry, 9 are monoatomic - leaving 2 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	$\# Z > 2$
5	NAG	A	1682	1	14,14,15	0.66	0	15,19,21	0.97	0
5	NAG	B	1681	1	14,14,15	0.72	0	15,19,21	1.08	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
5	NAG	A	1682	1	-	0/6/23/26	0/1/1/1
5	NAG	B	1681	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	1681	NAG	C1-O5-C5	2.32	115.19	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 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	1622/1676 (96%)	-0.08	37 (2%) 64 48	60, 136, 275, 372	0
1	B	1478/1676 (88%)	-0.16	13 (0%) 85 75	61, 129, 232, 340	0
2	X	191/231 (82%)	0.31	19 (9%) 9 7	150, 242, 308, 342	0
2	Y	191/231 (82%)	0.31	15 (7%) 15 10	149, 242, 308, 342	0
All	All	3482/3814 (91%)	-0.07	84 (2%) 62 47	60, 140, 279, 372	0

The worst 5 of 84 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1594	LYS	9.5
1	A	1593	GLU	8.7
1	A	1542	THR	6.7
1	A	1630	ASN	5.5
1	A	1522	GLY	5.4

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(\AA^2)	Q<0.9
4	NAG	B	2002	14/15	0.84	0.28	-	309,312,314,314	0
4	NAG	A	2001	14/15	0.82	0.46	-	304,306,310,312	0
4	NAG	B	2001	14/15	0.84	0.49	-	315,318,321,323	0
4	NAG	A	2002	14/15	0.81	0.35	-	302,303,305,305	0

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. 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
3	CD	A	1678	1/1	0.93	0.07	-2.60	261,261,261,261	0
3	CD	B	1678	1/1	0.39	0.09	-	271,271,271,271	0
5	NAG	A	1682	14/15	0.65	0.58	-	285,301,311,313	0
3	CD	A	1677	1/1	0.96	0.42	-	137,137,137,137	1
3	CD	A	1681	1/1	0.64	0.15	-	263,263,263,263	0
5	NAG	B	1681	14/15	0.81	0.36	-	268,294,323,333	0
3	CD	B	1677	1/1	0.93	0.06	-	255,255,255,255	0
3	CD	B	1680	1/1	0.67	0.13	-	252,252,252,252	0
3	CD	A	1680	1/1	0.81	0.10	-	241,241,241,241	0
3	CD	B	1679	1/1	0.95	0.12	-	240,240,240,240	0
3	CD	A	1679	1/1	0.91	0.08	-	270,270,270,270	0

6.5 Other polymers [i](#)

There are no such residues in this entry.