



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 14, 2019 – 10:48 AM EDT

PDB ID : 2V5R
Title : Structural basis for Dscam isoform specificity
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Schmucker, D.; Wang, J.-H.
Deposited on : 2007-07-09
Resolution : 3.00 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.0 (224370), CSD as540be (2019)
Xtriage (Phenix) : 1.13
EDS : 2.4
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.4

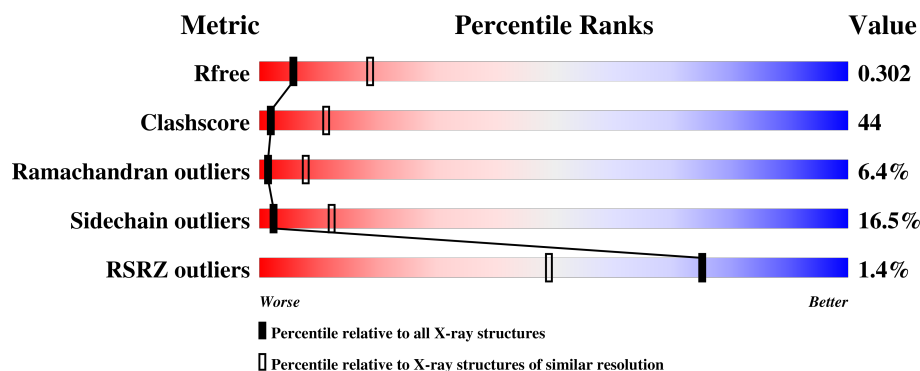
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	111664	1851 (3.00-3.00)
Clashscore	122126	2167 (3.00-3.00)
Ramachandran outliers	120053	2101 (3.00-3.00)
Sidechain outliers	120020	2104 (3.00-3.00)
RSRZ outliers	108989	1751 (3.00-3.00)

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	391	<div> <div>35%</div> <div>50%</div> <div>13%</div> <div>•</div> </div>
1	B	391	<div> <div>2%</div> <div>35%</div> <div>51%</div> <div>13%</div> <div>•</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	A	1392	-	-	X	-
2	NAG	B	1393	-	-	X	-

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 6232 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 DSCAM.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	391	Total	C	N	O	S	0	0	0
			3054	1920	530	591	13			
1	B	391	Total	C	N	O	S	0	0	0
			3054	1920	530	591	13			

There are 86 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	103	ILE	ALA	variant	UNP Q9NBA1
A	105	SER	TYR	variant	UNP Q9NBA1
A	108	SER	ALA	variant	UNP Q9NBA1
A	109	GLU	ASP	variant	UNP Q9NBA1
A	110	ALA	VAL	variant	UNP Q9NBA1
A	111	ASP	ASN	variant	UNP Q9NBA1
A	112	ASN	LYS	variant	UNP Q9NBA1
A	114	TYR	HIS	variant	UNP Q9NBA1
A	121	VAL	ALA	variant	UNP Q9NBA1
A	123	MET	ILE	variant	UNP Q9NBA1
A	126	GLU	LEU	variant	UNP Q9NBA1
A	130	TYR	PHE	variant	UNP Q9NBA1
A	136	PHE	GLU	variant	UNP Q9NBA1
A	138	ASP	VAL	variant	UNP Q9NBA1
A	139	LEU	SER	variant	UNP Q9NBA1
A	141	LEU	HIS	variant	UNP Q9NBA1
A	142	ASP	THR	variant	UNP Q9NBA1
A	143	SER	ASP	variant	UNP Q9NBA1
A	145	GLY	GLU	variant	UNP Q9NBA1
A	146	ARG	GLU	variant	UNP Q9NBA1
A	149	TYR	PHE	variant	UNP Q9NBA1
A	153	ALA	GLY	variant	UNP Q9NBA1
A	156	THR	TYR	variant	UNP Q9NBA1
A	210	GLY	SER	variant	UNP Q9NBA1
A	212	VAL	SER	variant	UNP Q9NBA1

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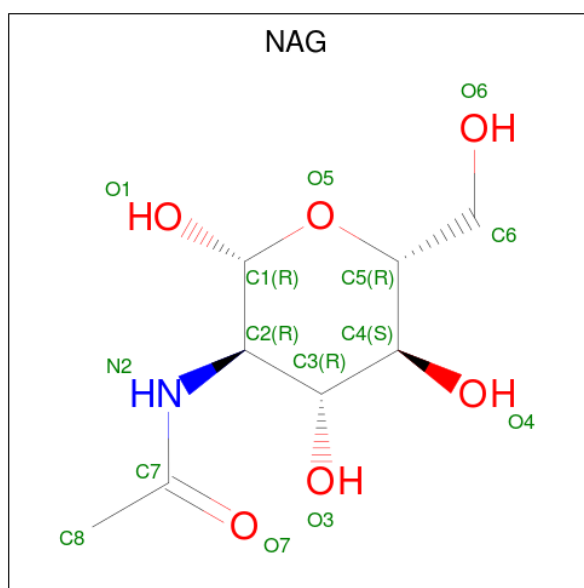
Chain	Residue	Modelled	Actual	Comment	Reference
A	213	ARG	PRO	variant	UNP Q9NBA1
A	216	VAL	ILE	variant	UNP Q9NBA1
A	218	PRO	THR	variant	UNP Q9NBA1
A	219	GLN	LEU	variant	UNP Q9NBA1
A	220	ASP	THR	variant	UNP Q9NBA1
A	221	LYS	TYR	variant	UNP Q9NBA1
A	222	HIS	LYS	variant	UNP Q9NBA1
A	223	GLN	PRO	variant	UNP Q9NBA1
A	224	PHE	ASN	variant	UNP Q9NBA1
A	229	LEU	SER	variant	UNP Q9NBA1
A	230	ALA	MET	variant	UNP Q9NBA1
A	231	SER	ALA	variant	UNP Q9NBA1
A	233	TYR	THR	variant	UNP Q9NBA1
A	234	SER	ALA	variant	UNP Q9NBA1
A	235	LEU	ILE	variant	UNP Q9NBA1
A	238	MET	PRO	variant	UNP Q9NBA1
A	241	SER	GLY	variant	UNP Q9NBA1
A	244	THR	ALA	variant	UNP Q9NBA1
B	103	ILE	ALA	variant	UNP Q9NBA1
B	105	SER	TYR	variant	UNP Q9NBA1
B	108	SER	ALA	variant	UNP Q9NBA1
B	109	GLU	ASP	variant	UNP Q9NBA1
B	110	ALA	VAL	variant	UNP Q9NBA1
B	111	ASP	ASN	variant	UNP Q9NBA1
B	112	ASN	LYS	variant	UNP Q9NBA1
B	114	TYR	HIS	variant	UNP Q9NBA1
B	121	VAL	ALA	variant	UNP Q9NBA1
B	123	MET	ILE	variant	UNP Q9NBA1
B	126	GLU	LEU	variant	UNP Q9NBA1
B	130	TYR	PHE	variant	UNP Q9NBA1
B	136	PHE	GLU	variant	UNP Q9NBA1
B	138	ASP	VAL	variant	UNP Q9NBA1
B	139	LEU	SER	variant	UNP Q9NBA1
B	141	LEU	HIS	variant	UNP Q9NBA1
B	142	ASP	THR	variant	UNP Q9NBA1
B	143	SER	ASP	variant	UNP Q9NBA1
B	145	GLY	GLU	variant	UNP Q9NBA1
B	146	ARG	GLU	variant	UNP Q9NBA1
B	149	TYR	PHE	variant	UNP Q9NBA1
B	153	ALA	GLY	variant	UNP Q9NBA1
B	156	THR	TYR	variant	UNP Q9NBA1
B	210	GLY	SER	variant	UNP Q9NBA1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	212	VAL	SER	variant	UNP Q9NBA1
B	213	ARG	PRO	variant	UNP Q9NBA1
B	216	VAL	ILE	variant	UNP Q9NBA1
B	218	PRO	THR	variant	UNP Q9NBA1
B	219	GLN	LEU	variant	UNP Q9NBA1
B	220	ASP	THR	variant	UNP Q9NBA1
B	221	LYS	TYR	variant	UNP Q9NBA1
B	222	HIS	LYS	variant	UNP Q9NBA1
B	223	GLN	PRO	variant	UNP Q9NBA1
B	224	PHE	ASN	variant	UNP Q9NBA1
B	229	LEU	SER	variant	UNP Q9NBA1
B	230	ALA	MET	variant	UNP Q9NBA1
B	231	SER	ALA	variant	UNP Q9NBA1
B	233	TYR	THR	variant	UNP Q9NBA1
B	234	SER	ALA	variant	UNP Q9NBA1
B	235	LEU	ILE	variant	UNP Q9NBA1
B	238	MET	PRO	variant	UNP Q9NBA1
B	241	SER	GLY	variant	UNP Q9NBA1
B	244	THR	ALA	variant	UNP Q9NBA1

- Molecule 2 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



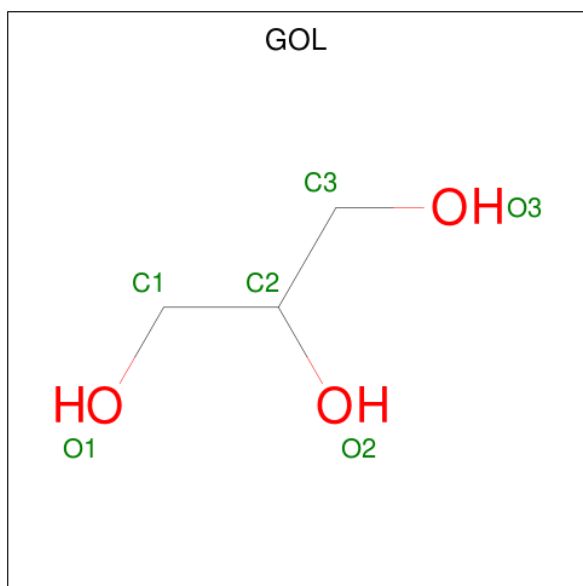
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

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

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).

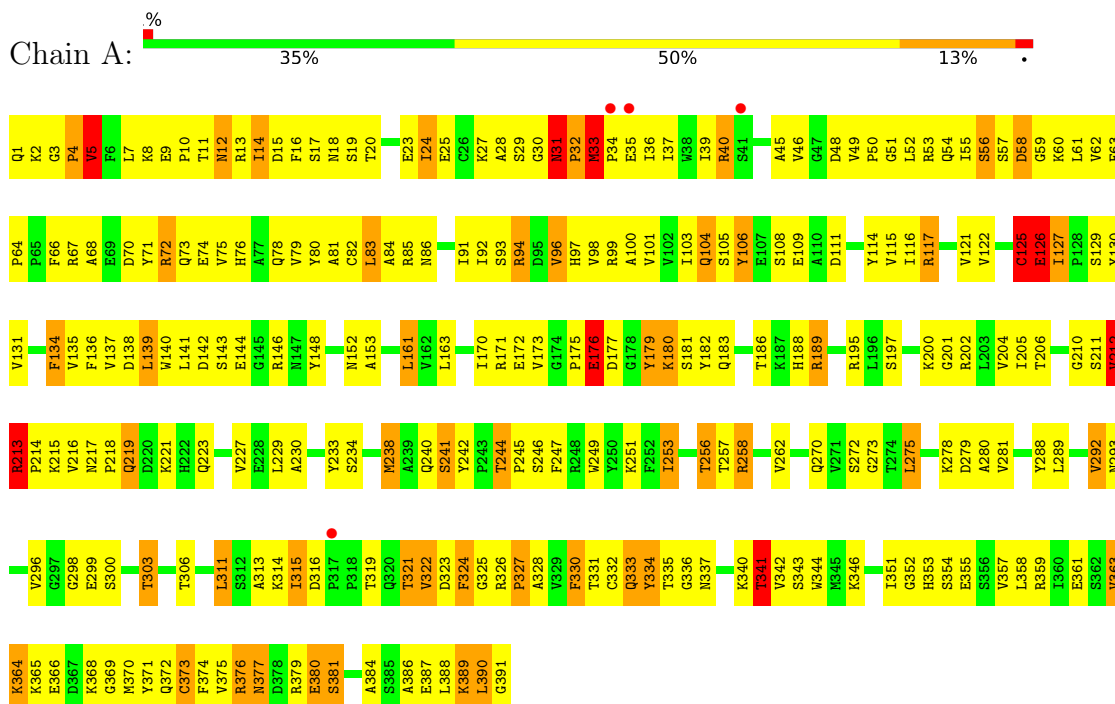


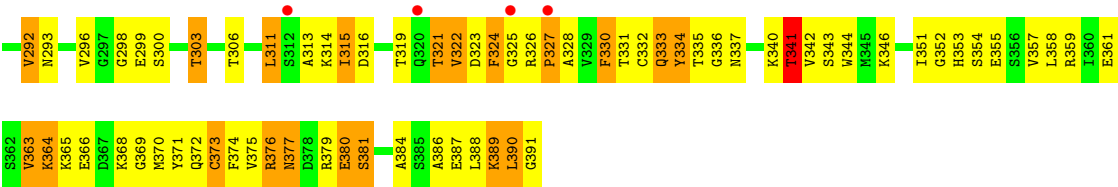
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		

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 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: DSCAM





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	277.78Å 70.55Å 72.77Å 90.00° 105.13° 90.00°	Depositor
Resolution (Å)	20.00 – 3.00 19.93 – 3.01	Depositor EDS
% Data completeness (in resolution range)	86.0 (20.00-3.00) 85.7 (19.93-3.01)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.71 (at 2.98Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.271 , 0.303 0.270 , 0.302	Depositor DCC
R_{free} test set	1162 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	56.6	Xtriage
Anisotropy	0.209	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 34.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.030 for -h+k-l,-l,-k 0.022 for -h-k-l,l,k 0.448 for -h-2*l,-k,l	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	6232	wwPDB-VP
Average B, all atoms (Å ²)	72.0	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.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

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	1.19	4/3117 (0.1%)	1.22	9/4226 (0.2%)
1	B	0.64	2/3117 (0.1%)	0.84	3/4226 (0.1%)
All	All	0.96	6/6234 (0.1%)	1.05	12/8452 (0.1%)

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	6
1	B	0	3
All	All	0	9

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	125	CYS	C-N	-45.17	0.30	1.34
1	A	126	GLU	C-N	-31.19	0.62	1.34
1	A	213	ARG	C-N	-24.45	0.87	1.34
1	B	213	ARG	C-N	-20.25	0.95	1.34
1	B	212	VAL	C-N	-16.25	0.96	1.34

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	126	GLU	O-C-N	-44.21	51.96	122.70
1	B	212	VAL	O-C-N	-31.24	72.71	122.70
1	A	212	VAL	O-C-N	-29.62	75.31	122.70
1	A	126	GLU	CA-C-N	23.48	168.86	117.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	125	CYS	O-C-N	-22.97	85.95	122.70

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	125	CYS	Mainchain
1	A	126	GLU	Mainchain
1	A	212	VAL	Mainchain,Peptide
1	A	213	ARG	Mainchain
1	A	31	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	3054	0	3014	271	0
1	B	3054	0	3016	270	0
2	A	56	0	52	12	0
2	B	56	0	52	11	0
3	B	12	0	16	4	0
All	All	6232	0	6150	546	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 44.

The worst 5 of 546 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:293:ASN:HD21	2:B:1396:NAG:C1	1.62	1.12
1:A:10:PRO:HB2	1:A:96:VAL:HG11	1.32	1.11
1:A:68:ALA:HB2	2:A:1392:NAG:H61	1.33	1.10
1:A:293:ASN:HD21	2:A:1395:NAG:C1	1.65	1.08
1:B:10:PRO:HB2	1:B:96:VAL:HG11	1.33	1.05

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	389/391 (100%)	310 (80%)	54 (14%)	25 (6%)	1	8
1	B	389/391 (100%)	313 (80%)	51 (13%)	25 (6%)	1	8
All	All	778/782 (100%)	623 (80%)	105 (14%)	50 (6%)	1	8

5 of 50 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	5	VAL
1	A	32	PRO
1	A	58	ASP
1	A	176	GLU
1	A	180	LYS

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	339/339 (100%)	283 (84%)	56 (16%)	2	12
1	B	339/339 (100%)	283 (84%)	56 (16%)	2	12
All	All	678/678 (100%)	566 (84%)	112 (16%)	2	12

5 of 112 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	341	THR

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Mol	Chain	Res	Type
1	B	58	ASP
1	B	330	PHE
1	A	364	LYS
1	B	5	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 25 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	353	HIS
1	B	31	ASN
1	B	353	HIS
1	A	372	GLN
1	B	54	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

10 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	NAG	A	1392	-	14,14,15	0.59	0	17,19,21	1.74	3 (17%)
2	NAG	A	1393	-	14,14,15	0.59	0	17,19,21	1.39	4 (23%)
2	NAG	A	1394	-	14,14,15	0.57	0	17,19,21	1.33	1 (5%)
2	NAG	A	1395	-	14,14,15	0.71	1 (7%)	17,19,21	1.47	4 (23%)
3	GOL	B	1392	-	5,5,5	0.39	0	5,5,5	0.36	0
2	NAG	B	1393	-	14,14,15	0.54	0	17,19,21	1.79	3 (17%)
2	NAG	B	1394	-	14,14,15	0.58	0	17,19,21	1.44	3 (17%)
2	NAG	B	1395	-	14,14,15	0.61	0	17,19,21	1.36	1 (5%)
2	NAG	B	1396	-	14,14,15	0.71	1 (7%)	17,19,21	1.48	5 (29%)
3	GOL	B	1397	-	5,5,5	0.36	0	5,5,5	0.39	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	NAG	A	1392	-	-	4/6/23/26	0/1/1/1
2	NAG	A	1393	-	-	3/6/23/26	0/1/1/1
2	NAG	A	1394	-	-	2/6/23/26	0/1/1/1
2	NAG	A	1395	-	-	2/6/23/26	0/1/1/1
3	GOL	B	1392	-	-	2/4/4/4	-
2	NAG	B	1393	-	-	4/6/23/26	0/1/1/1
2	NAG	B	1394	-	-	3/6/23/26	0/1/1/1
2	NAG	B	1395	-	-	2/6/23/26	0/1/1/1
2	NAG	B	1396	-	-	2/6/23/26	0/1/1/1
3	GOL	B	1397	-	-	2/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1395	NAG	O5-C1	-2.21	1.40	1.43
2	B	1396	NAG	O5-C1	-2.16	1.40	1.43

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1393	NAG	C1-O5-C5	4.73	118.64	112.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1392	NAG	C1-O5-C5	4.49	118.31	112.20
2	B	1395	NAG	C3-C4-C5	4.19	117.77	110.23
2	A	1394	NAG	C3-C4-C5	4.04	117.49	110.23
2	B	1393	NAG	C3-C4-C5	3.96	117.34	110.23

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1395	NAG	C8-C7-N2-C2
2	A	1395	NAG	O7-C7-N2-C2
3	B	1397	GOL	O1-C1-C2-C3
3	B	1392	GOL	O1-C1-C2-C3
2	B	1396	NAG	C8-C7-N2-C2

There are no ring outliers.

10 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1392	NAG	7	0
2	A	1393	NAG	2	0
2	A	1394	NAG	2	0
2	A	1395	NAG	3	0
3	B	1392	GOL	2	0
2	B	1393	NAG	7	0
2	B	1394	NAG	2	0
2	B	1395	NAG	2	0
2	B	1396	NAG	2	0
3	B	1397	GOL	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	4

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Mol	Chain	Number of breaks
1	B	2

The worst 5 of 6 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	212:VAL	C	213:ARG	N	1.00
1	B	212:VAL	C	213:ARG	N	0.96
1	B	213:ARG	C	214:PRO	N	0.95
1	A	213:ARG	C	214:PRO	N	0.87
1	A	126:GLU	C	127:ILE	N	0.62

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	391/391 (100%)	-0.37	4 (1%) 82 59	9, 67, 134, 163	0
1	B	391/391 (100%)	-0.36	7 (1%) 68 39	8, 69, 132, 168	0
All	All	782/782 (100%)	-0.36	11 (1%) 75 49	8, 68, 133, 168	0

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	34	PRO	5.3
1	B	59	GLY	3.6
1	A	34	PRO	3.6
1	B	35	GLU	2.9
1	B	312	SER	2.6

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](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	NAG	A	1394	14/15	0.74	0.16	97,97,97,97	0
2	NAG	B	1395	14/15	0.76	0.16	95,95,95,95	0
2	NAG	A	1393	14/15	0.79	0.17	74,74,74,74	0
2	NAG	B	1394	14/15	0.85	0.14	75,75,75,75	0
2	NAG	A	1395	14/15	0.88	0.17	53,53,53,53	0
2	NAG	A	1392	14/15	0.88	0.14	54,54,54,54	0
2	NAG	B	1396	14/15	0.89	0.17	51,51,51,51	0
3	GOL	B	1397	6/6	0.90	0.20	63,63,63,63	0
3	GOL	B	1392	6/6	0.91	0.16	64,64,64,64	0
2	NAG	B	1393	14/15	0.92	0.14	62,62,62,62	0

6.5 Other polymers [i](#)

There are no such residues in this entry.