



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 02:39 am GMT

PDB ID : 4LSX  
Title : Plant steroid receptor ectodomain bound to brassinolide and SERK1 co-receptor ectodomain  
Authors : Santiago, J.; Henzler, C.; Hothorn, M.  
Deposited on : 2013-07-23  
Resolution : 3.30 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : recalc28949

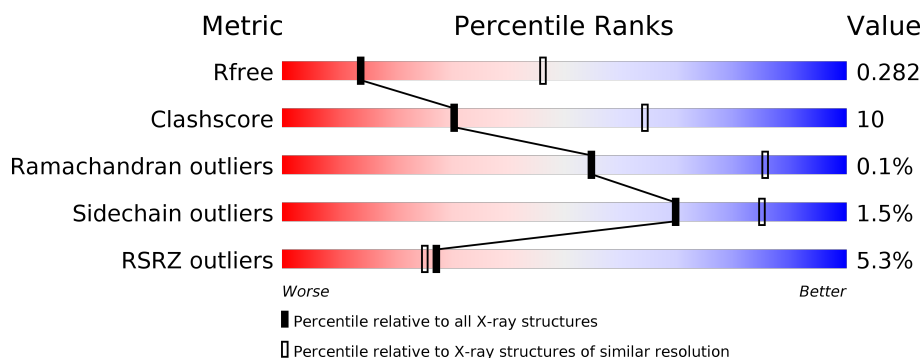
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.30 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))
$R_{free}$	100719	1034 (3.36-3.24)
Clashscore	112137	1100 (3.36-3.24)
Ramachandran outliers	110173	1081 (3.36-3.24)
Sidechain outliers	110143	1080 (3.36-3.24)
RSRZ outliers	101464	1039 (3.36-3.24)

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  $\geq 3$ , 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	774	<div> <div>3%</div> <div> <div></div> <div>72%</div> <div>23%</div> <div>• •</div> </div> </div>
1	B	774	<div> <div>3%</div> <div> <div></div> <div>69%</div> <div>22%</div> <div>• 8%</div> </div> </div>
2	C	203	<div> <div>9%</div> <div> <div></div> <div>66%</div> <div>25%</div> <div>9%</div> </div> </div>
2	D	203	<div> <div>16%</div> <div> <div></div> <div>67%</div> <div>23%</div> <div>9%</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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	BLD	B	801	-	-	-	X
6	NAG	A	807	-	-	-	X

## 2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 13920 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 Protein BRASSINOSTEROID INSENSITIVE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	740	Total	C	N	O	S	0	0	0
			5454	3421	914	1088	31			
1	B	710	Total	C	N	O	S	0	0	0
			5217	3283	868	1037	29			

There are 30 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	24	GLY	-	EXPRESSION TAG	UNP O22476
A	25	SER	-	EXPRESSION TAG	UNP O22476
A	26	SER	-	EXPRESSION TAG	UNP O22476
A	27	MET	-	EXPRESSION TAG	UNP O22476
A	28	GLY	-	EXPRESSION TAG	UNP O22476
A	643	GLU	GLY	ENGINEERED MUTATION	UNP O22476
A	789	LEU	-	EXPRESSION TAG	UNP O22476
A	790	GLU	-	EXPRESSION TAG	UNP O22476
A	791	ASN	-	EXPRESSION TAG	UNP O22476
A	792	LEU	-	EXPRESSION TAG	UNP O22476
A	793	TYR	-	EXPRESSION TAG	UNP O22476
A	794	PHE	-	EXPRESSION TAG	UNP O22476
A	795	GLN	-	EXPRESSION TAG	UNP O22476
A	796	GLY	-	EXPRESSION TAG	UNP O22476
A	797	ALA	-	EXPRESSION TAG	UNP O22476
B	24	GLY	-	EXPRESSION TAG	UNP O22476
B	25	SER	-	EXPRESSION TAG	UNP O22476
B	26	SER	-	EXPRESSION TAG	UNP O22476
B	27	MET	-	EXPRESSION TAG	UNP O22476
B	28	GLY	-	EXPRESSION TAG	UNP O22476
B	643	GLU	GLY	ENGINEERED MUTATION	UNP O22476
B	789	LEU	-	EXPRESSION TAG	UNP O22476
B	790	GLU	-	EXPRESSION TAG	UNP O22476
B	791	ASN	-	EXPRESSION TAG	UNP O22476
B	792	LEU	-	EXPRESSION TAG	UNP O22476

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Chain	Residue	Modelled	Actual	Comment	Reference
B	793	TYR	-	EXPRESSION TAG	UNP O22476
B	794	PHE	-	EXPRESSION TAG	UNP O22476
B	795	GLN	-	EXPRESSION TAG	UNP O22476
B	796	GLY	-	EXPRESSION TAG	UNP O22476
B	797	ALA	-	EXPRESSION TAG	UNP O22476

- Molecule 2 is a protein called Somatic embryogenesis receptor kinase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	185	Total	C	N	O	S	0	0	0
			1397	881	238	273	5			
2	D	185	Total	C	N	O	S	0	0	0
			1380	871	234	271	4			

There are 26 discrepancies between the modelled and reference sequences:

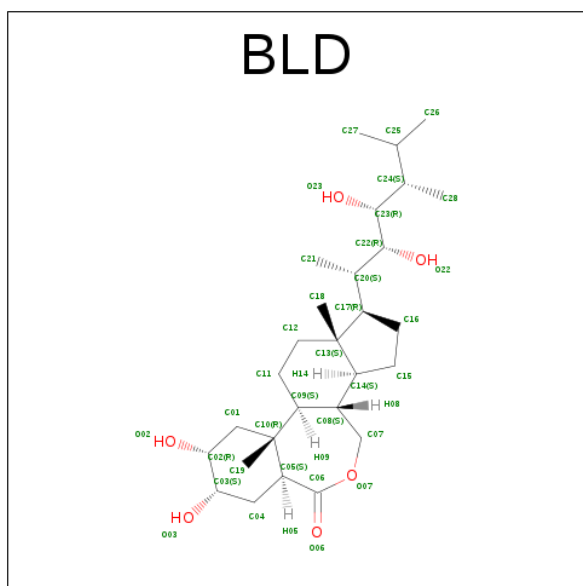
Chain	Residue	Modelled	Actual	Comment	Reference
C	20	GLY	-	EXPRESSION TAG	UNP Q94AG2
C	21	SER	-	EXPRESSION TAG	UNP Q94AG2
C	22	SER	-	EXPRESSION TAG	UNP Q94AG2
C	23	MET	-	EXPRESSION TAG	UNP Q94AG2
C	214	LEU	-	EXPRESSION TAG	UNP Q94AG2
C	215	GLU	-	EXPRESSION TAG	UNP Q94AG2
C	216	ASN	-	EXPRESSION TAG	UNP Q94AG2
C	217	LEU	-	EXPRESSION TAG	UNP Q94AG2
C	218	TYR	-	EXPRESSION TAG	UNP Q94AG2
C	219	PHE	-	EXPRESSION TAG	UNP Q94AG2
C	220	GLN	-	EXPRESSION TAG	UNP Q94AG2
C	221	GLY	-	EXPRESSION TAG	UNP Q94AG2
C	222	ALA	-	EXPRESSION TAG	UNP Q94AG2
D	20	GLY	-	EXPRESSION TAG	UNP Q94AG2
D	21	SER	-	EXPRESSION TAG	UNP Q94AG2
D	22	SER	-	EXPRESSION TAG	UNP Q94AG2
D	23	MET	-	EXPRESSION TAG	UNP Q94AG2
D	214	LEU	-	EXPRESSION TAG	UNP Q94AG2
D	215	GLU	-	EXPRESSION TAG	UNP Q94AG2
D	216	ASN	-	EXPRESSION TAG	UNP Q94AG2
D	217	LEU	-	EXPRESSION TAG	UNP Q94AG2
D	218	TYR	-	EXPRESSION TAG	UNP Q94AG2
D	219	PHE	-	EXPRESSION TAG	UNP Q94AG2
D	220	GLN	-	EXPRESSION TAG	UNP Q94AG2
D	221	GLY	-	EXPRESSION TAG	UNP Q94AG2

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Chain	Residue	Modelled	Actual	Comment	Reference
D	222	ALA	-	EXPRESSION TAG	UNP Q94AG2

- Molecule 3 is BRASSINOLIDE (three-letter code: BLD) (formula:  $C_{28}H_{48}O_6$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 34 28 6	0	0
3	B	1	Total C O 34 28 6	0	0

- 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	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	A	1	Total	C	N	O	0	0
			14	8	1	5		
4	B	1	Total	C	N	O	0	0
			14	8	1	5		
4	C	1	Total	C	N	O	0	0
			14	8	1	5		
4	C	1	Total	C	N	O	0	0
			14	8	1	5		
4	D	1	Total	C	N	O	0	0
			14	8	1	5		
4	D	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 5 is a polymer of unknown type called SUGAR (4-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	4	Total	C	N	O	0	0
			50	28	2	20		
5	B	4	Total	C	N	O	0	0
			50	28	2	20		
5	B	4	Total	C	N	O	0	0
			50	28	2	20		

- 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		
6	B	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 7 is a polymer of unknown type called SUGAR (5-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	5	Total	C	N	O	0	0
			61	34	2	25		

- Molecule 8 is a polymer of unknown type called SUGAR (3-MER).

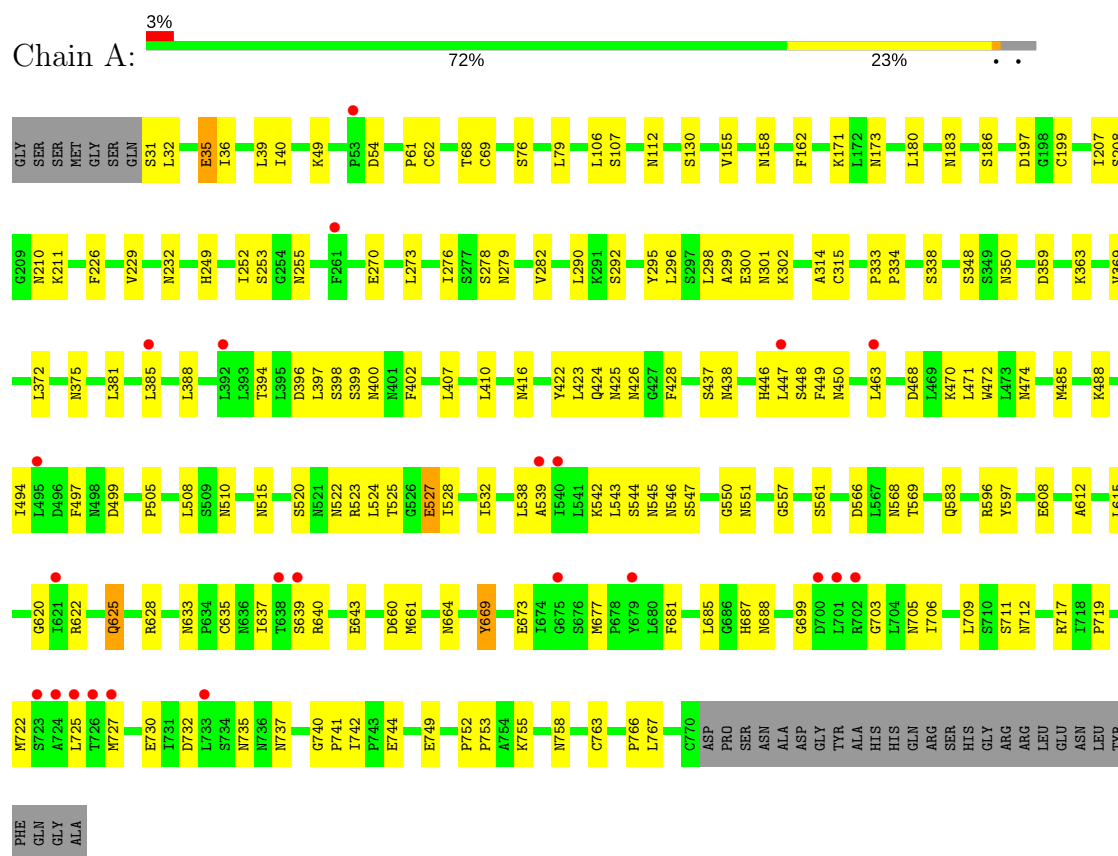
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	B	3	Total	C	N	O	0	0
			39	22	2	15		



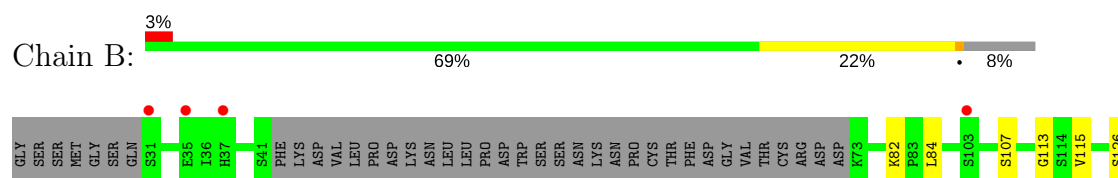
### 3 Residue-property plots

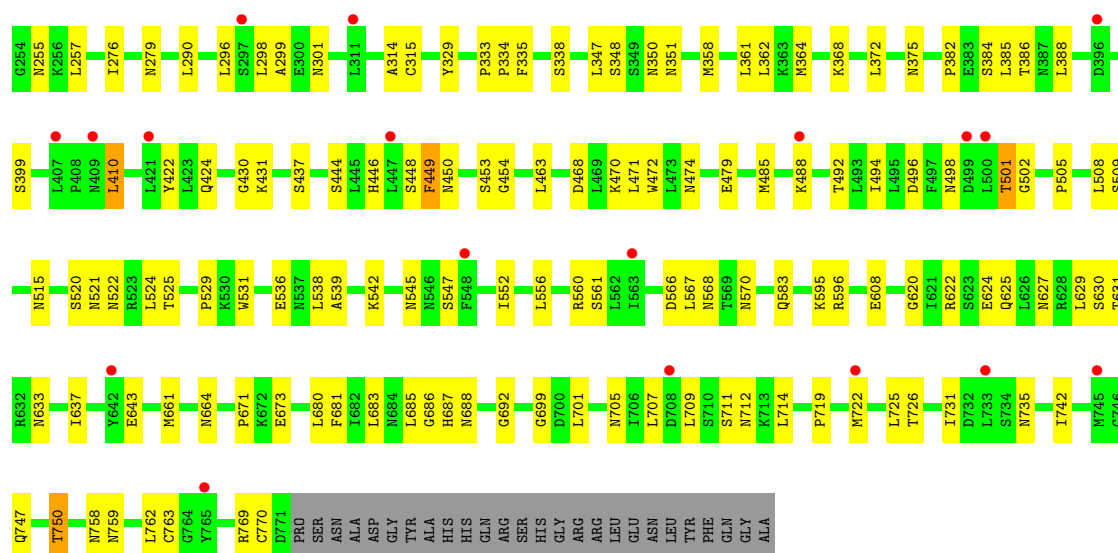
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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 ( $\text{RSRZ} > 2$ ). 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: Protein BRASSINOSTEROID INSENSITIVE 1

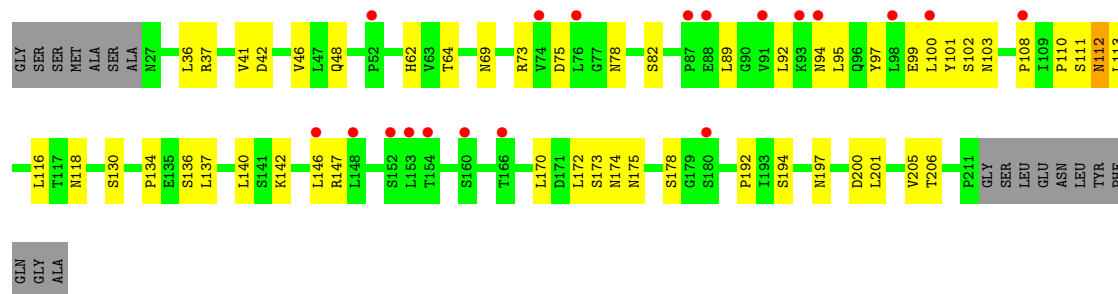


#### • Molecule 1: Protein BRASSINOSTEROID INSENSITIVE 1

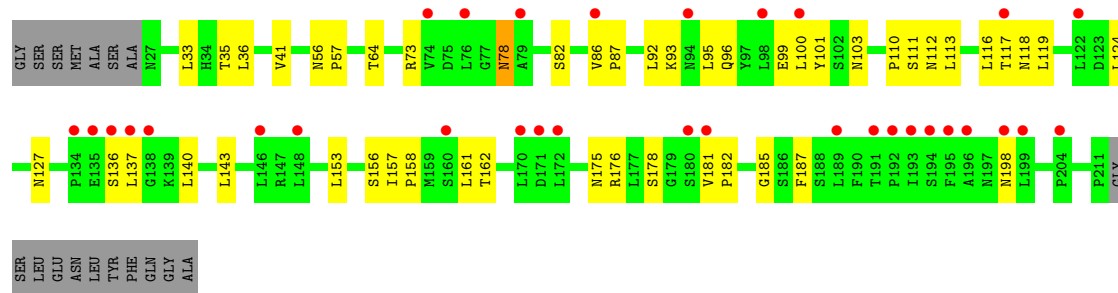




• Molecule 2: Somatic embryogenesis receptor kinase 1



• Molecule 2: Somatic embryogenesis receptor kinase 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	69.90Å 69.90Å 873.55Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.53 – 3.30 48.53 – 3.30	Depositor EDS
% Data completeness (in resolution range)	98.2 (48.53-3.30) 96.4 (48.53-3.30)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	0.11	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.38 (at 3.33Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1334)	Depositor
R, $R_{free}$	0.246 , 0.285 0.243 , 0.282	Depositor DCC
$R_{free}$ test set	1982 reflections (6.07%)	DCC
Wilson B-factor (Å <sup>2</sup> )	85.8	Xtriage
Anisotropy	0.182	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 75.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.42$ , $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	0.457 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	13920	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	122.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.17% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: BLD, BMA, NAG, 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	0.23	0/5553	0.45	0/7543
1	B	0.22	0/5311	0.44	0/7218
2	C	0.25	0/1427	0.47	0/1959
2	D	0.24	0/1410	0.47	0/1940
All	All	0.23	0/13701	0.45	0/18660

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	5454	0	5251	113	0
1	B	5217	0	5032	109	0
2	C	1397	0	1366	31	0
2	D	1380	0	1332	30	0
3	A	34	0	47	5	0
3	B	34	0	47	5	0
4	A	28	0	26	3	0
4	B	14	0	13	1	0
4	C	28	0	26	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	28	0	26	0	0
5	A	50	0	43	1	0
5	B	100	0	86	4	0
6	A	28	0	25	2	0
6	B	28	0	25	0	0
7	A	61	0	52	1	0
8	B	39	0	34	0	0
All	All	13920	0	13431	286	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 10.

The worst 5 of 286 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:551:ASN:HD21	4:A:814:NAG:H82	1.39	0.86
1:A:290:LEU:HB3	1:A:314:ALA:HB2	1.71	0.73
2:C:64:THR:HB	2:C:73:ARG:HB2	1.72	0.72
2:D:140:LEU:HD12	2:D:143:LEU:HD22	1.72	0.71
1:B:198:GLY:HA2	1:B:220:ARG:HH12	1.56	0.71

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	738/774 (95%)	710 (96%)	27 (4%)	1 (0%)	55 85
1	B	706/774 (91%)	680 (96%)	25 (4%)	1 (0%)	55 85
2	C	183/203 (90%)	176 (96%)	7 (4%)	0	100 100
2	D	183/203 (90%)	177 (97%)	6 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1810/1954 (93%)	1743 (96%)	65 (4%)	2 (0%)	55 85

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	637	ILE
1	B	637	ILE

### 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	611/680 (90%)	600 (98%)	11 (2%)	64 83
1	B	580/680 (85%)	571 (98%)	9 (2%)	68 84
2	C	165/182 (91%)	164 (99%)	1 (1%)	89 93
2	D	161/182 (88%)	160 (99%)	1 (1%)	89 93
All	All	1517/1724 (88%)	1495 (98%)	22 (2%)	70 85

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	625	GLN
1	B	162	PHE
2	C	112	ASN
1	A	669	TYR
1	B	107	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	78	ASN
2	D	118	ASN
2	C	112	ASN

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Mol	Chain	Res	Type
1	A	551	ASN
2	D	94	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 ⓘ

24 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	$\# Z  > 2$
5	NAG	A	803	1,5	14,14,15	0.25	0	15,19,21	0.52	0
5	NAG	A	804	5	14,14,15	0.46	0	15,19,21	1.33	1 (6%)
5	BMA	A	805	5	11,11,12	0.70	0	13,15,17	1.03	0
5	MAN	A	806	5	11,11,12	0.73	0	13,15,17	1.02	1 (7%)
6	NAG	A	807	1,6	14,14,15	0.35	0	15,19,21	0.58	0
6	NAG	A	808	6	14,14,15	0.40	0	15,19,21	0.69	1 (6%)
7	NAG	A	809	1,7	14,14,15	0.30	0	15,19,21	0.45	0
7	NAG	A	810	7	14,14,15	0.21	0	15,19,21	0.44	0
7	BMA	A	811	7	11,11,12	0.99	1 (9%)	13,15,17	0.95	0
7	MAN	A	812	7	11,11,12	0.73	0	13,15,17	1.03	2 (15%)
7	MAN	A	813	7	11,11,12	0.77	0	13,15,17	1.77	4 (30%)
5	NAG	B	803	1,5	14,14,15	0.31	0	15,19,21	0.50	0
5	NAG	B	804	5	14,14,15	0.47	0	15,19,21	1.32	1 (6%)
5	BMA	B	805	5	11,11,12	0.63	0	13,15,17	0.98	1 (7%)
5	MAN	B	806	5	11,11,12	0.77	1 (9%)	13,15,17	1.05	2 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
8	NAG	B	807	1,8	14,14,15	0.63	1 (7%)	15,19,21	0.64	0
8	NAG	B	808	8	14,14,15	0.65	1 (7%)	15,19,21	0.66	0
8	BMA	B	809	8	11,11,12	0.64	0	13,15,17	1.10	2 (15%)
5	NAG	B	810	1,5	14,14,15	0.22	0	15,19,21	0.52	0
5	NAG	B	811	5	14,14,15	0.49	0	15,19,21	0.53	0
5	BMA	B	812	5	11,11,12	1.37	3 (27%)	13,15,17	1.58	2 (15%)
5	MAN	B	813	5	11,11,12	0.81	1 (9%)	13,15,17	1.11	2 (15%)
6	NAG	B	814	1,6	14,14,15	0.41	0	15,19,21	0.46	0
6	NAG	B	815	6	14,14,15	0.24	0	15,19,21	0.44	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
5	NAG	A	803	1,5	-	0/6/23/26	0/1/1/1
5	NAG	A	804	5	-	0/6/23/26	0/1/1/1
5	BMA	A	805	5	-	0/2/19/22	0/1/1/1
5	MAN	A	806	5	-	0/2/19/22	0/1/1/1
6	NAG	A	807	1,6	-	0/6/23/26	0/1/1/1
6	NAG	A	808	6	-	0/6/23/26	0/1/1/1
7	NAG	A	809	1,7	-	0/6/23/26	0/1/1/1
7	NAG	A	810	7	-	0/6/23/26	0/1/1/1
7	BMA	A	811	7	-	0/2/19/22	0/1/1/1
7	MAN	A	812	7	-	0/2/19/22	0/1/1/1
7	MAN	A	813	7	-	0/2/19/22	0/1/1/1
5	NAG	B	803	1,5	-	0/6/23/26	0/1/1/1
5	NAG	B	804	5	-	0/6/23/26	0/1/1/1
5	BMA	B	805	5	-	0/2/19/22	0/1/1/1
5	MAN	B	806	5	-	0/2/19/22	0/1/1/1
8	NAG	B	807	1,8	-	0/6/23/26	0/1/1/1
8	NAG	B	808	8	-	0/6/23/26	0/1/1/1
8	BMA	B	809	8	-	0/2/19/22	0/1/1/1
5	NAG	B	810	1,5	-	0/6/23/26	0/1/1/1
5	NAG	B	811	5	-	0/6/23/26	0/1/1/1
5	BMA	B	812	5	-	0/2/19/22	0/1/1/1
5	MAN	B	813	5	-	0/2/19/22	0/1/1/1
6	NAG	B	814	1,6	-	0/6/23/26	0/1/1/1
6	NAG	B	815	6	-	0/6/23/26	0/1/1/1

The worst 5 of 8 bond length outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	812	BMA	O5-C1	-2.98	1.38	1.43
8	B	808	NAG	O5-C1	-2.29	1.40	1.43
8	B	807	NAG	O5-C1	-2.24	1.40	1.43
5	B	813	MAN	O5-C1	-2.21	1.40	1.43
5	B	806	MAN	O5-C1	-2.01	1.40	1.43

The worst 5 of 19 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	B	809	BMA	O2-C2-C3	-2.51	105.25	110.17
5	B	806	MAN	O2-C2-C3	-2.39	105.48	110.17
7	A	813	MAN	O2-C2-C3	-2.38	105.49	110.17
5	B	813	MAN	O2-C2-C3	-2.34	105.57	110.17
8	B	809	BMA	C1-C2-C3	-2.29	106.75	109.65

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	804	NAG	1	0
6	A	807	NAG	2	0
7	A	811	BMA	1	0
7	A	813	MAN	1	0
5	B	803	NAG	1	0
5	B	804	NAG	1	0
5	B	811	NAG	1	0
5	B	813	MAN	1	0

## 5.6 Ligand geometry

9 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
3	BLD	A	801	-	36,37,37	3.12	13 (36%)	46,59,59	1.96	13 (28%)
4	NAG	A	802	1	14,14,15	0.36	0	15,19,21	0.66	0
4	NAG	A	814	1	14,14,15	0.56	0	15,19,21	1.28	1 (6%)
3	BLD	B	801	-	36,37,37	3.10	12 (33%)	46,59,59	1.85	12 (26%)
4	NAG	B	802	1	14,14,15	0.24	0	15,19,21	0.49	0
4	NAG	C	1000	2	14,14,15	1.09	1 (7%)	15,19,21	0.64	0
4	NAG	C	1001	2	14,14,15	0.20	0	15,19,21	0.49	0
4	NAG	D	1001	2	14,14,15	0.37	0	15,19,21	0.46	0
4	NAG	D	1002	2	14,14,15	1.76	1 (7%)	15,19,21	1.41	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
3	BLD	A	801	-	-	0/20/85/85	0/4/4/4
4	NAG	A	802	1	-	0/6/23/26	0/1/1/1
4	NAG	A	814	1	-	0/6/23/26	0/1/1/1
3	BLD	B	801	-	-	0/20/85/85	0/4/4/4
4	NAG	B	802	1	-	0/6/23/26	0/1/1/1
4	NAG	C	1000	2	-	0/6/23/26	0/1/1/1
4	NAG	C	1001	2	-	0/6/23/26	0/1/1/1
4	NAG	D	1001	2	-	0/6/23/26	0/1/1/1
4	NAG	D	1002	2	-	0/6/23/26	0/1/1/1

The worst 5 of 27 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	801	BLD	O07-C07	-11.07	1.30	1.45
3	B	801	BLD	O07-C07	-10.91	1.30	1.45
3	B	801	BLD	C15-C14	-5.09	1.43	1.54
3	A	801	BLD	C15-C14	-5.05	1.43	1.54
3	B	801	BLD	O22-C22	-3.28	1.35	1.43

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	801	BLD	C15-C14-C08	-5.46	110.37	119.07
3	B	801	BLD	C15-C14-C08	-5.23	110.74	119.07
3	A	801	BLD	O07-C06-O06	-5.01	108.67	116.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	801	BLD	O07-C06-O06	-4.76	109.07	116.68
3	A	801	BLD	C17-C20-C22	-3.42	105.47	111.24

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	801	BLD	5	0
4	A	802	NAG	1	0
4	A	814	NAG	2	0
3	B	801	BLD	5	0
4	B	802	NAG	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q < 0.9
1	A	740/774 (95%)	0.03	23 (3%)	49 48	47, 114, 169, 224	0
1	B	710/774 (91%)	0.05	23 (3%)	48 46	57, 115, 166, 222	0
2	C	185/203 (91%)	0.41	19 (10%)	7 6	88, 145, 192, 210	0
2	D	185/203 (91%)	0.73	32 (17%)	2 1	105, 146, 225, 259	0
All	All	1820/1954 (93%)	0.15	97 (5%)	27 25	47, 121, 183, 259	0

The worst 5 of 97 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	726	THR	8.1
2	D	192	PRO	6.6
2	D	138	GLY	6.5
2	D	137	LEU	6.4
2	D	98	LEU	6.3

### 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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
6	NAG	A	807	14/15	0.92	0.26	2.21	92,102,111,111	0
7	NAG	A	809	14/15	0.90	0.24	0.34	111,121,148,149	0
5	NAG	B	803	14/15	0.92	0.20	-0.27	110,124,137,137	0
8	NAG	B	807	14/15	0.93	0.17	-0.40	72,85,96,100	0
5	NAG	B	810	14/15	0.83	0.19	-0.46	86,99,107,109	0
5	NAG	A	803	14/15	0.95	0.17	-0.68	48,61,73,95	0
5	NAG	B	811	14/15	0.93	0.16	-1.07	98,120,128,130	0
7	NAG	A	810	14/15	0.93	0.15	-1.61	88,102,106,111	0
8	NAG	B	808	14/15	0.93	0.13	-	93,114,124,132	0
6	NAG	A	808	14/15	0.88	0.17	-	107,112,122,127	0
5	BMA	A	805	11/12	0.89	0.13	-	77,110,116,116	0
5	NAG	A	804	14/15	0.94	0.12	-	108,114,118,120	0
8	BMA	B	809	11/12	0.81	0.19	-	136,138,139,143	0
6	NAG	B	815	14/15	0.93	0.26	-	72,85,107,107	0
5	BMA	B	805	11/12	0.79	0.18	-	125,136,149,156	0
5	MAN	B	813	11/12	0.95	0.13	-	84,92,96,99	0
5	MAN	A	806	11/12	0.90	0.13	-	83,104,121,128	0
7	MAN	A	812	11/12	0.87	0.17	-	128,135,139,143	0
5	MAN	B	806	11/12	0.77	0.27	-	150,157,165,169	0
7	BMA	A	811	11/12	0.91	0.13	-	101,118,146,149	0
5	NAG	B	804	14/15	0.93	0.19	-	109,116,136,136	0
6	NAG	B	814	14/15	0.85	0.20	-	93,107,121,122	0
7	MAN	A	813	11/12	0.87	0.21	-	76,87,117,130	0
5	BMA	B	812	11/12	0.85	0.16	-	98,131,145,150	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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
3	BLD	B	801	34/34	0.90	0.43	1.51	85,127,138,149	0
3	BLD	A	801	34/34	0.94	0.22	-0.72	61,109,134,140	0
4	NAG	D	1002	14/15	0.91	0.12	-	81,98,108,109	0
4	NAG	B	802	14/15	0.86	0.17	-	96,105,113,114	0
4	NAG	A	802	14/15	0.64	0.41	-	138,158,174,175	0
4	NAG	C	1001	14/15	0.84	0.18	-	77,91,108,109	0
4	NAG	C	1000	14/15	0.90	0.19	-	96,99,105,106	0
4	NAG	A	814	14/15	0.79	0.20	-	88,94,101,103	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	NAG	D	1001	14/15	0.85	0.20	-	102,115,132,134	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.