



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 05:15 am GMT

PDB ID : 4D11
Title : GalNAc-T2 crystal soaked with UDP-5SGalNAc, mEA2 peptide and manganese (Lower resolution dataset)
Authors : Lira-Navarrete, E.; Iglesias-Fernandez, J.; Zandberg, W.F.; Companon, I.; Kong, Y.; Corzana, F.; Pinto, B.M.; Clausen, H.; Peregrina, J.M.; Vocadlo, D.; Rovira, C.; Hurtado-Guerrero, R.
Deposited on : 2014-05-01
Resolution : 2.85 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:

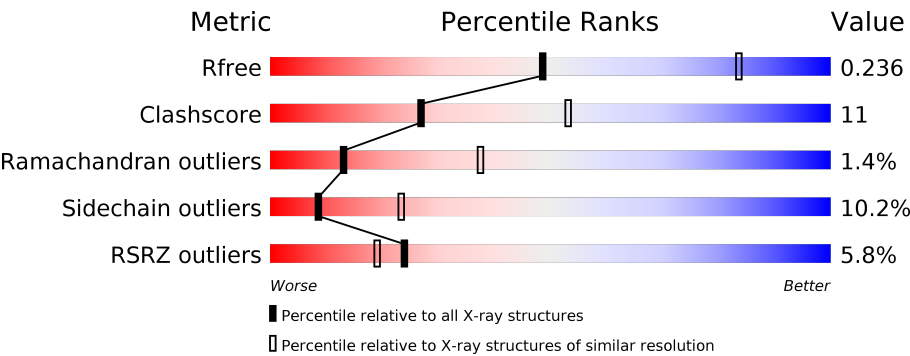
MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.85 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))
R_{free}	100719	2469 (2.90-2.82)
Clashscore	112137	2749 (2.90-2.82)
Ramachandran outliers	110173	2687 (2.90-2.82)
Sidechain outliers	110143	2690 (2.90-2.82)
RSRZ outliers	101464	2487 (2.90-2.82)

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	571	<div><div>2%</div><div><div></div><div>71%</div><div>11%</div><div>•</div><div>14%</div></div></div>
1	B	571	<div><div>2%</div><div><div></div><div>65%</div><div>16%</div><div>• •</div><div>16%</div></div></div>
1	D	571	<div><div>3%</div><div><div></div><div>65%</div><div>15%</div><div>• •</div><div>15%</div></div></div>
1	E	571	<div><div>3%</div><div><div></div><div>68%</div><div>14%</div><div>•</div><div>15%</div></div></div>
1	F	571	<div><div>7%</div><div><div></div><div>36%</div><div>10%</div><div>•</div><div>52%</div></div></div>
2	C	571	<div><div>9%</div><div><div></div><div>56%</div><div>16%</div><div>• •</div><div>24%</div></div></div>

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Mol	Chain	Length	Quality of chain
3	L	6	
3	O	6	
3	P	6	
3	X	6	
3	Z	6	

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
5	BBK	B	1572	-	-	-	X
5	BBK	D	1572	-	-	-	X
5	BBK	E	1571	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 21829 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 POLYPEPTIDE GALNAC-TRANSFERASE T2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	491	Total	C	N	O	S	20	0	0
			3938	2477	715	722	24			
1	B	482	Total	C	N	O	S	20	1	0
			3877	2441	703	710	23			
1	D	487	Total	C	N	O	S	20	0	0
			3916	2465	711	716	24			
1	E	487	Total	C	N	O	S	20	0	0
			3917	2465	711	717	24			
1	F	276	Total	C	N	O	S	8	0	0
			2246	1419	406	407	14			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	516	ASP	ASN	ENGINEERED MUTATION	UNP Q10471
B	516	ASP	ASN	ENGINEERED MUTATION	UNP Q10471
D	516	ASP	ASN	ENGINEERED MUTATION	UNP Q10471
E	516	ASP	ASN	ENGINEERED MUTATION	UNP Q10471
F	516	ASP	ASN	ENGINEERED MUTATION	UNP Q10471

- Molecule 2 is a protein called POLYPEPTIDE GALNAC-TRANSFERASE T2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	436	Total	C	N	O	S	20	0	0
			3560	2249	646	644	21			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	74	SER	GLY	CONFLICT	UNP Q10471
C	516	ASP	ASN	ENGINEERED MUTATION	UNP Q10471

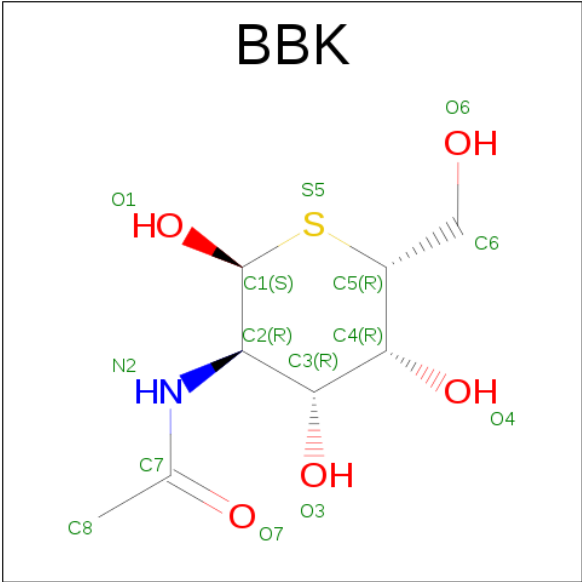
- Molecule 3 is a protein called PEPTIDE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	6	Total	C	N	O	S	0	0	1
			32	18	6	7	1			
3	O	6	Total	C	N	O	S	0	0	1
			32	18	6	7	1			
3	P	6	Total	C	N	O	S	0	0	1
			32	18	6	7	1			
3	X	6	Total	C	N	O	S	0	0	1
			32	18	6	7	1			
3	Z	5	Total	C	N	O	S	0	0	0
			31	18	5	7	1			

- Molecule 4 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

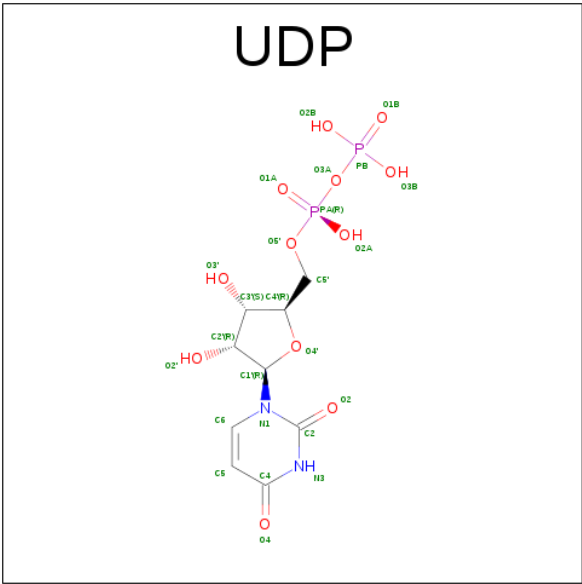
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	1	Total	Mn	0	0
			1	1		
4	E	1	Total	Mn	0	0
			1	1		
4	B	1	Total	Mn	0	0
			1	1		
4	C	1	Total	Mn	0	0
			1	1		
4	A	1	Total	Mn	0	0
			1	1		
4	F	1	Total	Mn	0	0
			1	1		

- Molecule 5 is SUGAR (2-(ACETYLAMINO)-2-DEOXY-5-THIO-ALPHA-D-GALACTOPYRANOSE) (three-letter code: BBK) (formula: C₈H₁₅NO₅S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
5	A	1	Total 15	8	1	5	1	0	0
5	B	1	Total 15	8	1	5	1	0	0
5	D	1	Total 15	8	1	5	1	0	0
5	E	1	Total 15	8	1	5	1	0	0

- Molecule 6 is URIDINE-5'-DIPHOSPHATE (three-letter code: UDP) (formula: C₉H₁₄N₂O₁₂P₂).

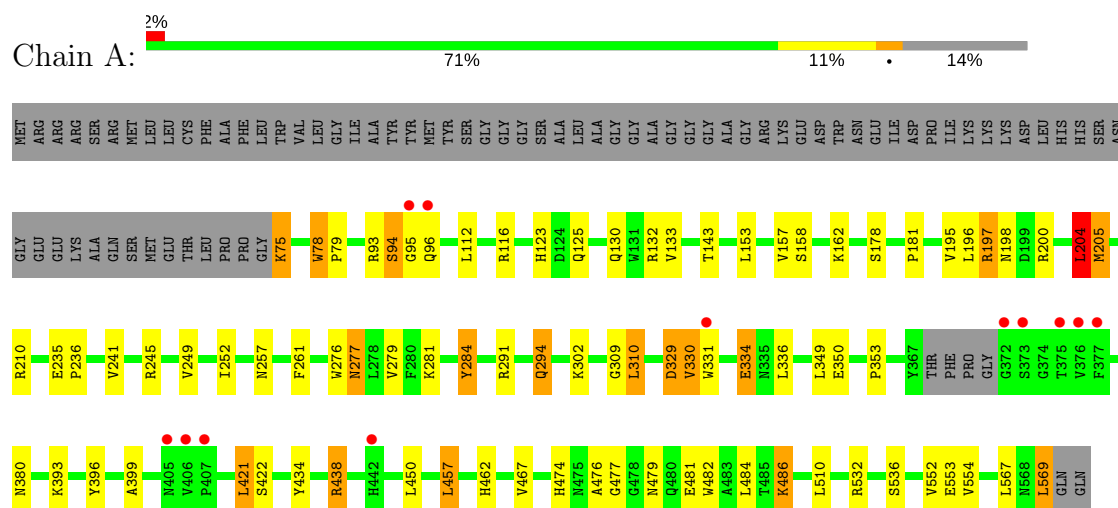


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total 25	C 9	N 2	O 12	P 2	0	0
6	B	1	Total 25	C 9	N 2	O 12	P 2	0	0
6	C	1	Total 25	C 9	N 2	O 12	P 2	0	0
6	D	1	Total 25	C 9	N 2	O 12	P 2	0	0
6	E	1	Total 25	C 9	N 2	O 12	P 2	0	0
6	F	1	Total 25	C 9	N 2	O 12	P 2	0	0

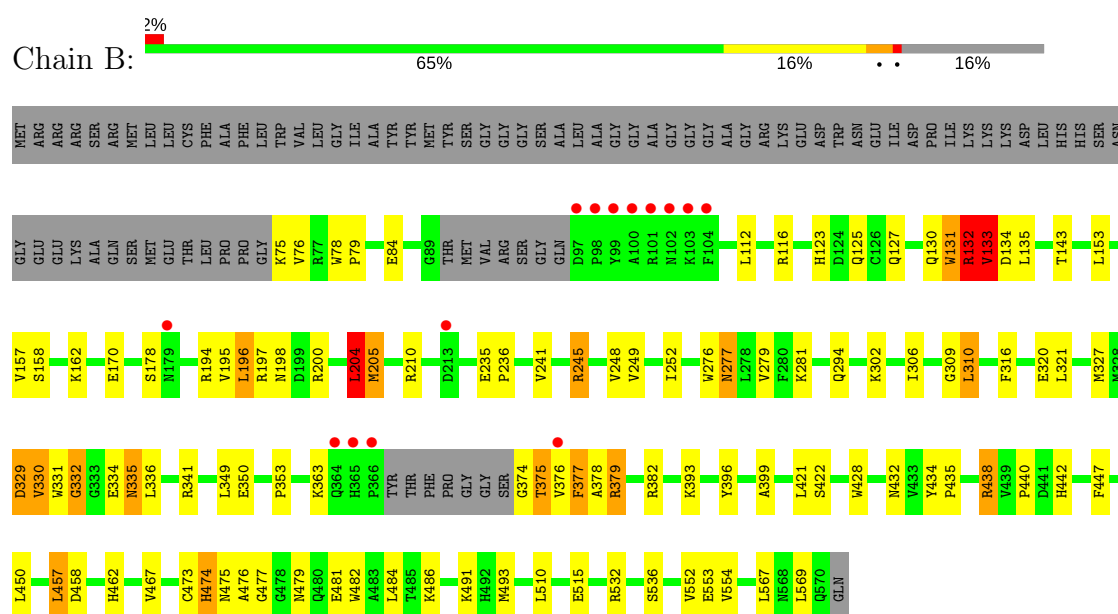
3 Residue-property plots

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: POLYPEPTIDE GALNAC-TRANSFERASE T2

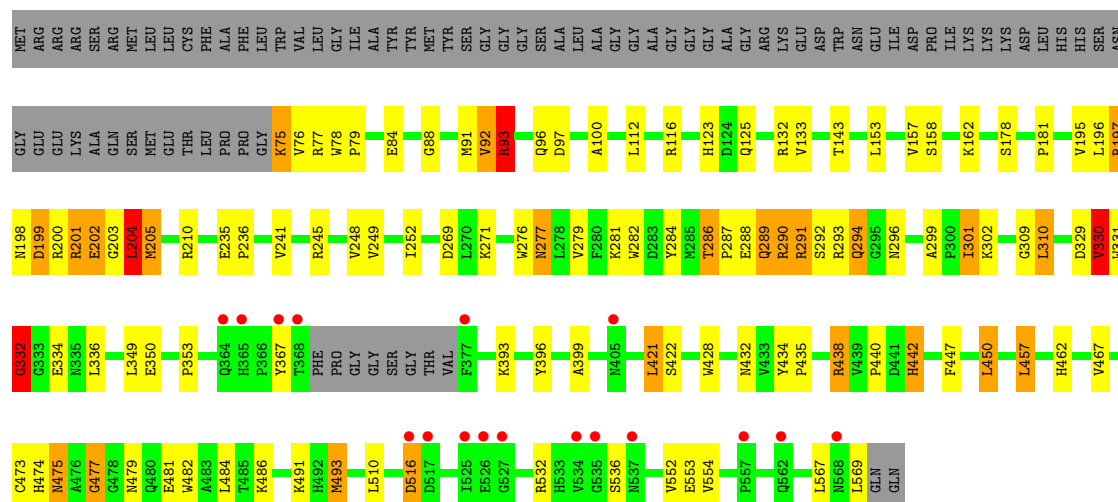


• Molecule 1: POLYPEPTIDE GALNAC-TRANSFERASE T2

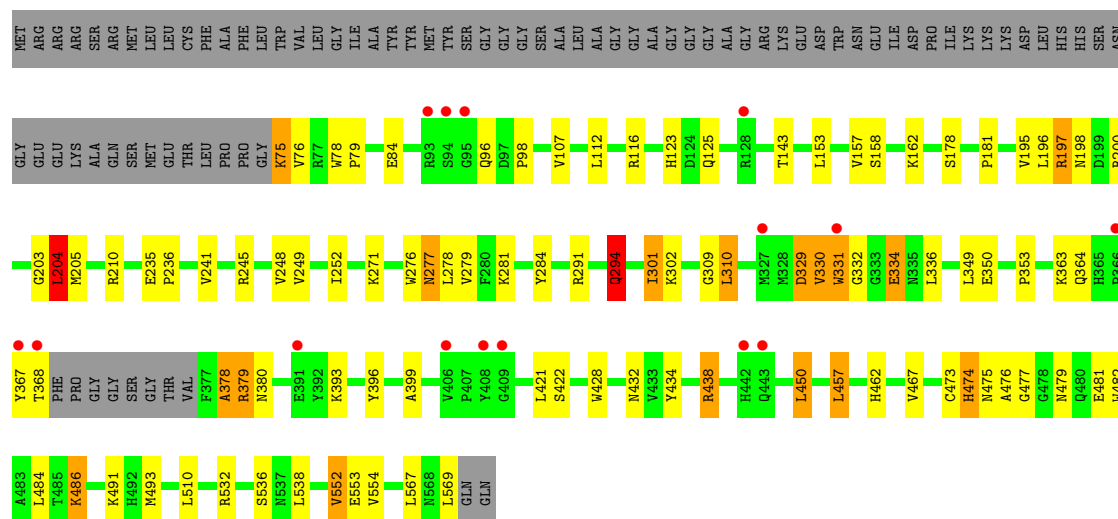


• Molecule 1: POLYPEPTIDE GALNAC-TRANSFERASE T2

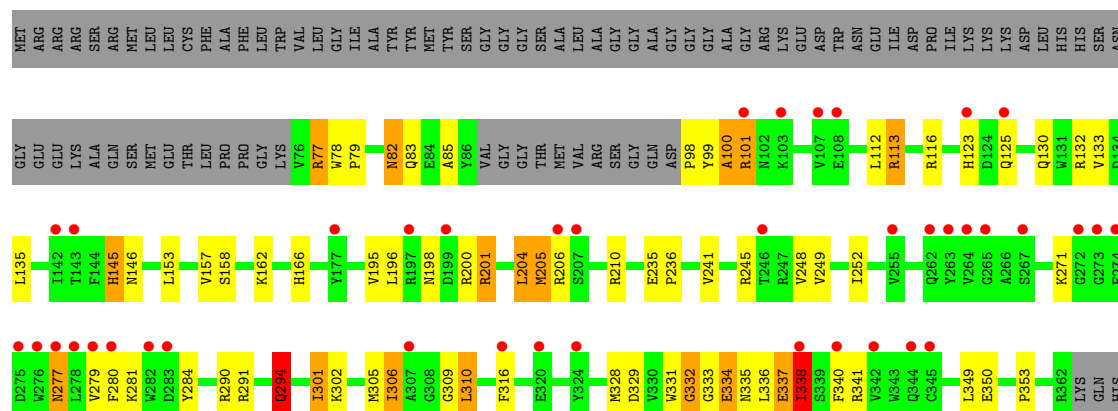
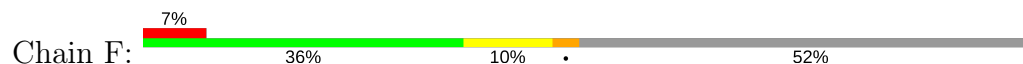




• Molecule 1: POLYPEPTIDE GALNAC-TRANSFERASE T2



• Molecule 1: POLYPEPTIDE GALNAC-TRANSFERASE T2

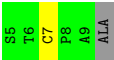




● Molecule 3: PEPTIDE



● Molecule 3: PEPTIDE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	116.77Å 120.90Å 249.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	249.61 – 2.85 46.14 – 2.85	Depositor EDS
% Data completeness (in resolution range)	100.0 (249.61-2.85) 100.0 (46.14-2.85)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.98 (at 2.86Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.216 , 0.235 0.219 , 0.236	Depositor DCC
R_{free} test set	2285 reflections (2.83%)	DCC
Wilson B-factor (Å ²)	64.9	Xtriage
Anisotropy	0.339	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 49.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.018 for k,h,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	21829	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.04% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: UDP, MN, BBK

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	0.95	4/4027 (0.1%)	1.03	4/5443 (0.1%)
1	B	1.19	5/3967 (0.1%)	1.05	6/5361 (0.1%)
1	D	1.18	4/4005 (0.1%)	1.05	8/5413 (0.1%)
1	E	1.12	3/4006 (0.1%)	1.05	7/5415 (0.1%)
1	F	0.84	1/2297 (0.0%)	1.03	2/3104 (0.1%)
2	C	0.90	2/3639 (0.1%)	1.03	3/4909 (0.1%)
3	L	0.64	0/32	0.65	0/44
3	O	0.87	0/32	1.25	0/44
3	P	0.94	0/32	1.33	0/44
3	X	0.68	0/32	0.89	0/44
3	Z	0.90	0/31	0.93	0/42
All	All	1.05	19/22100 (0.1%)	1.04	30/29863 (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	D	0	1
2	C	0	1
All	All	0	2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	75	LYS	CB-CG	-34.06	0.60	1.52
1	D	202	GLU	C-N	-33.06	0.73	1.33
1	B	84	GLU	CB-CG	-32.47	0.90	1.52
1	E	84	GLU	CB-CG	-30.61	0.94	1.52
1	D	486	LYS	CB-CG	-25.67	0.83	1.52

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	75	LYS	CB-CG-CD	18.38	159.39	111.60
1	B	84	GLU	CA-CB-CG	13.47	143.04	113.40
1	A	294	GLN	CA-CB-CG	11.16	137.95	113.40
1	B	75	LYS	CA-CB-CG	11.01	137.63	113.40
2	C	75	LYS	CB-CG-CD	10.64	139.28	111.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	127	GLN	Peptide
1	D	332	GLY	Peptide

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	3938	0	3863	41	0
1	B	3877	0	3804	99	0
1	D	3916	0	3842	83	0
1	E	3917	0	3843	76	0
1	F	2246	0	2214	88	0
2	C	3560	0	3495	106	0
3	L	32	0	28	3	0
3	O	32	0	28	1	0
3	P	32	0	28	0	0
3	X	32	0	28	7	0
3	Z	31	0	28	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
5	A	15	0	14	4	0
5	B	15	0	15	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	15	0	15	1	0
5	E	15	0	15	1	0
6	A	25	0	11	0	0
6	B	25	0	11	0	0
6	C	25	0	11	0	0
6	D	25	0	11	0	0
6	E	25	0	11	1	0
6	F	25	0	11	0	0
All	All	21829	0	21326	492	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 11.

The worst 5 of 492 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:F:328:MET:SD	1:F:334:GLU:CB	2.07	1.42
1:D:202:GLU:C	1:D:203:GLY:CA	1.92	1.36
1:D:202:GLU:CA	1:D:203:GLY:N	1.92	1.30
1:F:328:MET:SD	1:F:334:GLU:HB2	1.68	1.29
1:B:329:ASP:HB2	1:B:379:ARG:NH2	1.47	1.28

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	487/571 (85%)	461 (95%)	24 (5%)	2 (0%)	38 68
1	B	477/571 (84%)	445 (93%)	26 (6%)	6 (1%)	14 39
1	D	483/571 (85%)	449 (93%)	28 (6%)	6 (1%)	15 42

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	483/571 (85%)	457 (95%)	21 (4%)	5 (1%)	18	46
1	F	272/571 (48%)	252 (93%)	15 (6%)	5 (2%)	10	31
2	C	422/571 (74%)	387 (92%)	27 (6%)	8 (2%)	9	29
3	L	4/6 (67%)	1 (25%)	1 (25%)	2 (50%)	0	0
3	O	4/6 (67%)	2 (50%)	2 (50%)	0	100	100
3	P	4/6 (67%)	3 (75%)	0	1 (25%)	0	0
3	X	4/6 (67%)	1 (25%)	2 (50%)	1 (25%)	0	0
3	Z	3/6 (50%)	3 (100%)	0	0	100	100
All	All	2643/3456 (76%)	2461 (93%)	146 (6%)	36 (1%)	13	37

5 of 36 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	330	VAL
1	A	477	GLY
1	B	132	ARG
1	B	477	GLY
2	C	365	HIS

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	425/485 (88%)	386 (91%)	39 (9%)	11	28
1	B	418/485 (86%)	379 (91%)	39 (9%)	10	28
1	D	423/485 (87%)	379 (90%)	44 (10%)	8	22
1	E	423/485 (87%)	384 (91%)	39 (9%)	11	28
1	F	244/485 (50%)	215 (88%)	29 (12%)	6	16
2	C	385/486 (79%)	340 (88%)	45 (12%)	6	16
3	L	4/4 (100%)	4 (100%)	0	100	100
3	O	4/4 (100%)	2 (50%)	2 (50%)	0	0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	P	4/4 (100%)	3 (75%)	1 (25%)	1	1
3	X	4/4 (100%)	4 (100%)	0	100	100
3	Z	4/4 (100%)	3 (75%)	1 (25%)	1	1
All	All	2338/2931 (80%)	2099 (90%)	239 (10%)	8	23

5 of 239 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	434	TYR
1	D	199	ASP
1	F	204	LEU
2	C	457	LEU
2	C	528	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 61 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	380	ASN
1	D	277	ASN
1	F	145	HIS
2	C	405	ASN
2	C	462	HIS

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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 16 ligands modelled in this entry, 6 are monoatomic - leaving 10 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	BBK	A	1571	-	13,15,15	9.04	2 (15%)	15,21,21	1.41	4 (26%)
6	UDP	A	1572	4	21,26,26	1.19	3 (14%)	22,40,40	1.70	3 (13%)
5	BBK	B	1572	-	13,15,15	8.91	4 (30%)	15,21,21	1.63	2 (13%)
6	UDP	B	1573	4	21,26,26	1.13	2 (9%)	22,40,40	1.96	3 (13%)
6	UDP	C	1571	4	21,26,26	1.27	2 (9%)	22,40,40	1.73	2 (9%)
6	UDP	D	1571	4	21,26,26	1.34	3 (14%)	22,40,40	1.61	2 (9%)
5	BBK	D	1572	-	13,15,15	9.07	4 (30%)	15,21,21	1.64	4 (26%)
5	BBK	E	1571	-	13,15,15	9.33	4 (30%)	15,21,21	1.49	1 (6%)
6	UDP	E	1572	4	21,26,26	1.25	2 (9%)	22,40,40	1.62	2 (9%)
6	UDP	F	1364	4	21,26,26	1.08	2 (9%)	22,40,40	2.05	2 (9%)

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	BBK	A	1571	-	-	0/6/26/26	0/1/1/1
6	UDP	A	1572	4	-	0/12/32/32	0/2/2/2
5	BBK	B	1572	-	-	0/6/26/26	0/1/1/1
6	UDP	B	1573	4	-	0/12/32/32	0/2/2/2
6	UDP	C	1571	4	-	0/12/32/32	0/2/2/2
6	UDP	D	1571	4	-	0/12/32/32	0/2/2/2
5	BBK	D	1572	-	-	0/6/26/26	0/1/1/1
5	BBK	E	1571	-	-	0/6/26/26	0/1/1/1
6	UDP	E	1572	4	-	0/12/32/32	0/2/2/2
6	UDP	F	1364	4	-	0/12/32/32	0/2/2/2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	1571	BBK	C5-S5	-26.28	1.43	1.82
5	A	1571	BBK	C5-S5	-25.58	1.44	1.82
5	D	1572	BBK	C5-S5	-25.45	1.44	1.82
5	B	1572	BBK	C5-S5	-24.98	1.45	1.82
5	E	1571	BBK	C1-S5	-20.58	1.43	1.83

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	1572	BBK	C3-C2-N2	-2.83	105.19	110.61
5	A	1571	BBK	O1-C1-C2	-2.78	103.57	109.25
5	A	1571	BBK	C3-C2-N2	-2.17	106.46	110.61
5	A	1571	BBK	C1-C2-N2	-2.04	107.55	111.36
6	A	1572	UDP	O3A-PB-O1B	-2.03	98.93	111.44

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1571	BBK	4	0
5	B	1572	BBK	5	0
5	D	1572	BBK	1	0
5	E	1571	BBK	1	0
6	E	1572	UDP	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	A	491/571 (85%)	-0.02	12 (2%)	59	55	28, 56, 96, 129	5 (1%)
1	B	482/571 (84%)	0.10	14 (2%)	52	46	32, 65, 115, 151	5 (1%)
1	D	487/571 (85%)	0.12	17 (3%)	44	38	29, 64, 110, 144	5 (1%)
1	E	487/571 (85%)	0.11	15 (3%)	49	43	31, 58, 105, 159	5 (1%)
1	F	276/571 (48%)	0.88	40 (14%)	3	2	59, 112, 167, 187	2 (0%)
2	C	436/571 (76%)	0.54	53 (12%)	5	3	35, 89, 149, 182	5 (1%)
3	L	6/6 (100%)	1.40	1 (16%)	2	1	86, 109, 116, 126	0
3	O	6/6 (100%)	0.77	0	100	100	72, 94, 105, 110	0
3	P	6/6 (100%)	0.36	0	100	100	44, 72, 78, 90	0
3	X	6/6 (100%)	2.76	4 (66%)	0	0	91, 106, 118, 123	0
3	Z	5/6 (83%)	0.49	0	100	100	72, 73, 88, 92	0
All	All	2688/3456 (77%)	0.25	156 (5%)	24	19	28, 67, 136, 187	27 (1%)

The worst 5 of 156 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	X	10	ALA	7.2
1	F	264	VAL	7.0
2	C	500	VAL	6.3
1	F	276	TRP	6.0
2	C	511	GLN	5.8

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
5	BBK	E	1571	15/15	0.82	0.30	5.21	67,86,120,144	0
5	BBK	B	1572	15/15	0.83	0.26	4.00	66,81,110,110	0
5	BBK	D	1572	15/15	0.80	0.27	2.06	97,106,117,122	0
5	BBK	A	1571	15/15	0.87	0.22	1.24	52,76,82,88	0
6	UDP	D	1571	25/25	0.92	0.21	-0.22	64,98,118,128	0
6	UDP	C	1571	25/25	0.92	0.19	-0.29	83,96,111,114	0
6	UDP	A	1572	25/25	0.97	0.16	-0.57	54,74,89,97	0
6	UDP	B	1573	25/25	0.94	0.17	-0.84	77,89,97,106	0
6	UDP	E	1572	25/25	0.96	0.17	-0.91	69,78,89,97	0
6	UDP	F	1364	25/25	0.93	0.17	-1.20	107,134,151,177	0
4	MN	A	1570	1/1	0.99	0.10	-	46,46,46,46	0
4	MN	C	1570	1/1	0.99	0.13	-	67,67,67,67	0
4	MN	E	1570	1/1	0.97	0.12	-	46,46,46,46	0
4	MN	D	1570	1/1	0.98	0.13	-	58,58,58,58	0
4	MN	B	1571	1/1	0.99	0.15	-	63,63,63,63	0
4	MN	F	1363	1/1	0.98	0.10	-	93,93,93,93	0

6.5 Other polymers [i](#)

There are no such residues in this entry.