



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 14, 2018 – 12:06 am GMT

PDB ID : 3VQ2
Title : Crystal structure of mouse TLR4/MD-2/LPS complex
Authors : Ohto, U.; Shimizu, T.
Deposited on : 2012-03-17
Resolution : 2.48 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 : 1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix) : 1.13
EDS : trunk31020
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) : trunk31020

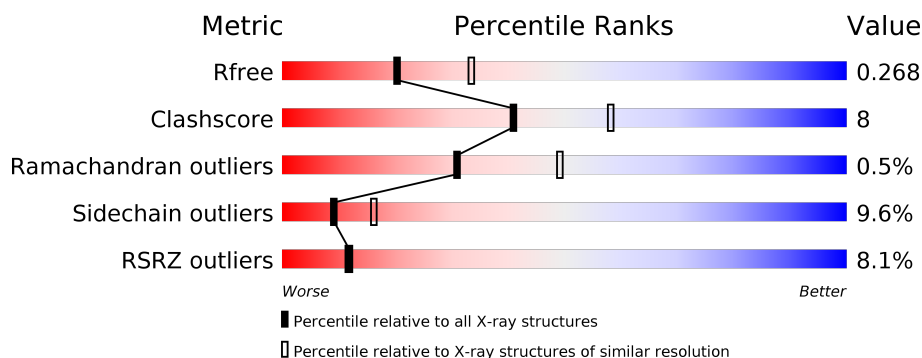
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.48 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	5140 (2.50-2.46)
Clashscore	122126	5860 (2.50-2.46)
Ramachandran outliers	120053	5763 (2.50-2.46)
Sidechain outliers	120020	5765 (2.50-2.46)
RSRZ outliers	108989	5026 (2.50-2.46)

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	606	<div> <div>7%</div> <div> <div></div> <div>74%</div> <div>18%</div> <div>• •</div> </div> </div>
1	B	606	<div> <div>11%</div> <div> <div></div> <div>73%</div> <div>20%</div> <div>• •</div> </div> </div>
2	C	144	<div> <div>3%</div> <div> <div></div> <div>66%</div> <div>24%</div> <div>• • 6%</div> </div> </div>
2	D	144	<div> <div>2%</div> <div> <div></div> <div>64%</div> <div>26%</div> <div>• • 6%</div> </div> </div>

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 11815 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.

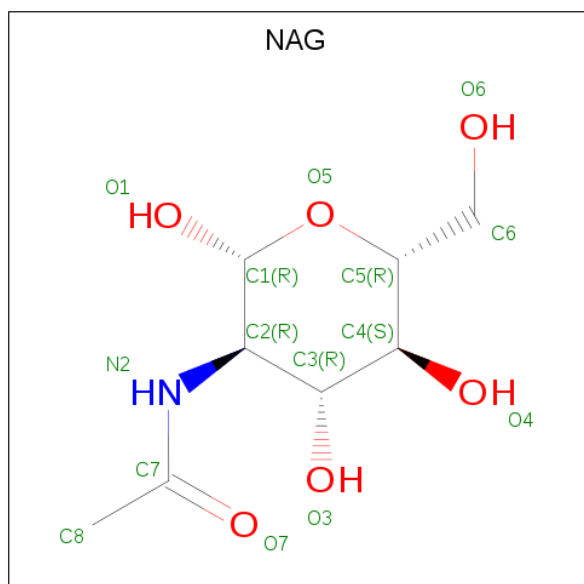
- Molecule 1 is a protein called Toll-like receptor 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	581	Total	C	N	O	S	0	0	0
			4637	2972	764	875	26			
1	B	581	Total	C	N	O	S	0	0	0
			4637	2972	764	875	26			

- Molecule 2 is a protein called Lymphocyte antigen 96.

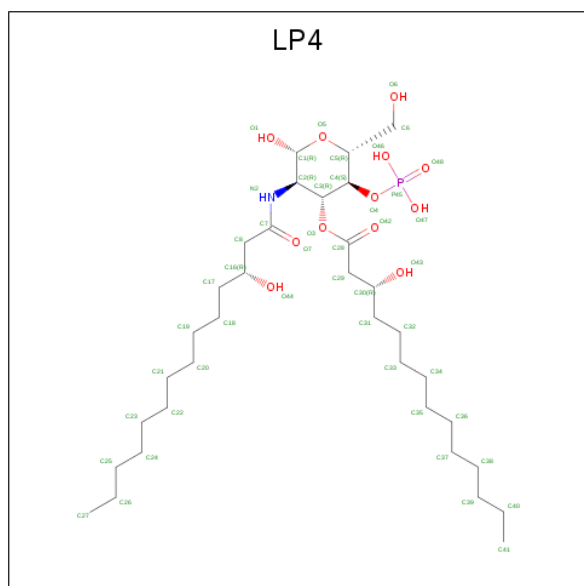
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	135	Total	C	N	O	S	0	0	0
			1092	706	182	197	7			
2	D	135	Total	C	N	O	S	0	0	0
			1092	706	182	197	7			

- Molecule 3 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

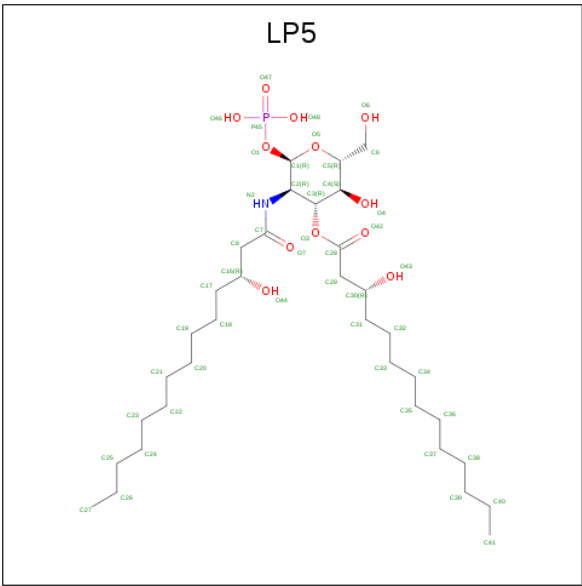
- Molecule 4 is 2-deoxy-3-O-[(3R)-3-hydroxytetradecanoyl]-2-[[[(3R)-3-hydroxytetradecanoyl]amino]-4-O-phosphono-beta-D-glucopyranose (three-letter code: LP4) (formula: $C_{34}H_{66}NO_{12}P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	C	1	Total	C	N	O	P	0	0
			45	32	1	11	1		
4	D	1	Total	C	N	O	P	0	0
			45	32	1	11	1		

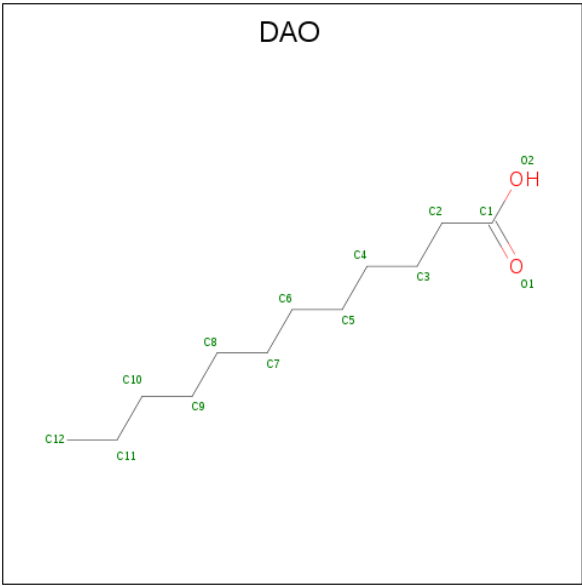
- Molecule 5 is (R)-((2R,3S,4R,5R,6R)-3-HYDROXY-2-(HYDROXYMETHYL)-5-((R)-3-HYDROXYTETRADECANAMIDO)-6-(PHOSPHONOOXY)TETRAHYDRO-2H-PYRAN-4-YL) 3-HYDROXYTETRADECANOATE (three-letter code: LP5) (formula:

C₃₄H₆₆NO₁₂P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	C	1	Total 48	C 34	N 1	O 12	P 1	0	0
5	D	1	Total 48	C 34	N 1	O 12	P 1	0	0

- Molecule 6 is LAURIC ACID (three-letter code: DAO) (formula: C₁₂H₂₄O₂).



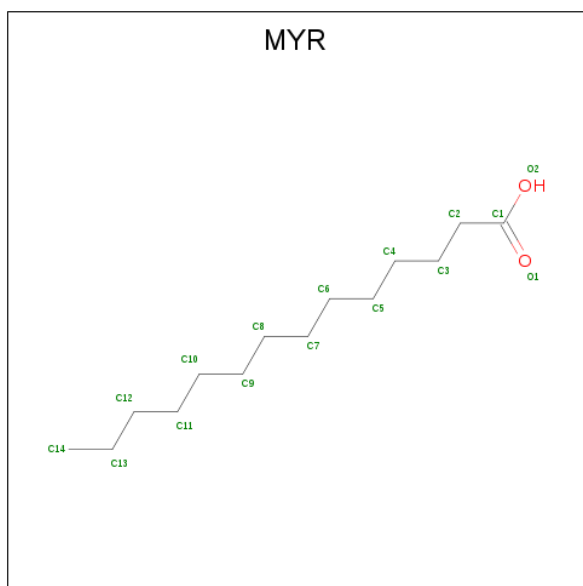
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	C	1	Total	C	O	0	0
			13	12	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	D	1	Total	C	O	0	0
			13	12	1		

- Molecule 7 is MYRISTIC ACID (three-letter code: MYR) (formula: $C_{14}H_{28}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	C	1	Total	C	O	0	0
			15	14	1		
7	D	1	Total	C	O	0	0
			15	14	1		

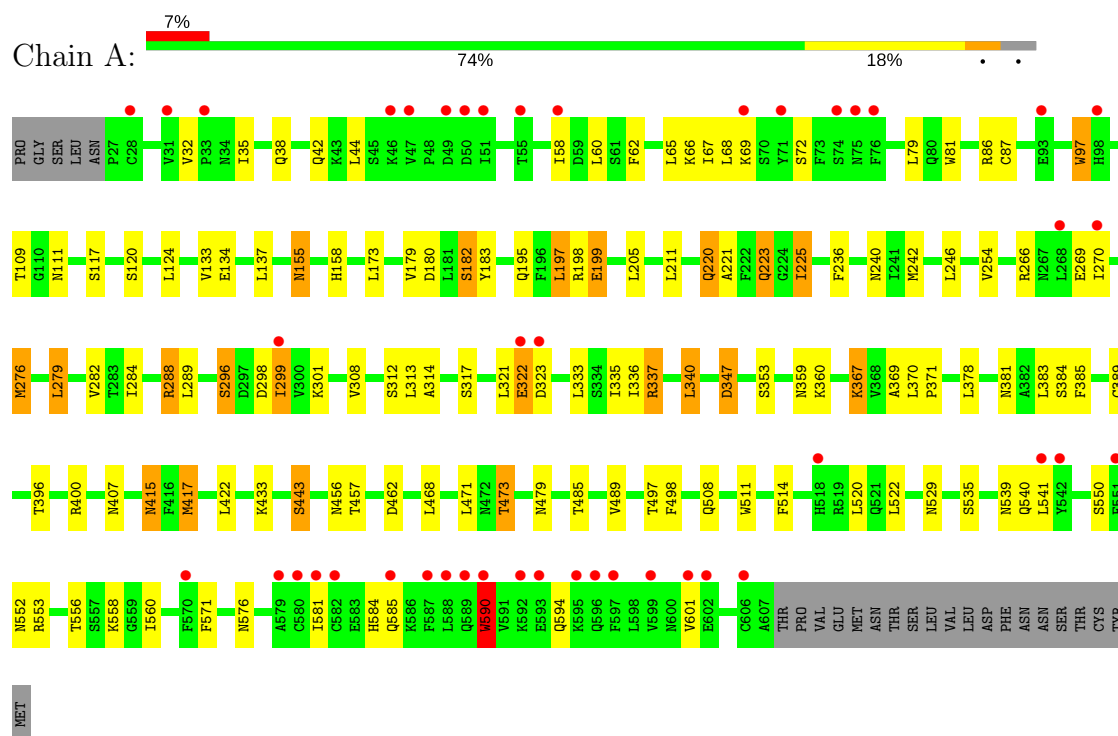
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	8	Total	O	0	0
			8	8		
8	B	9	Total	O	0	0
			9	9		

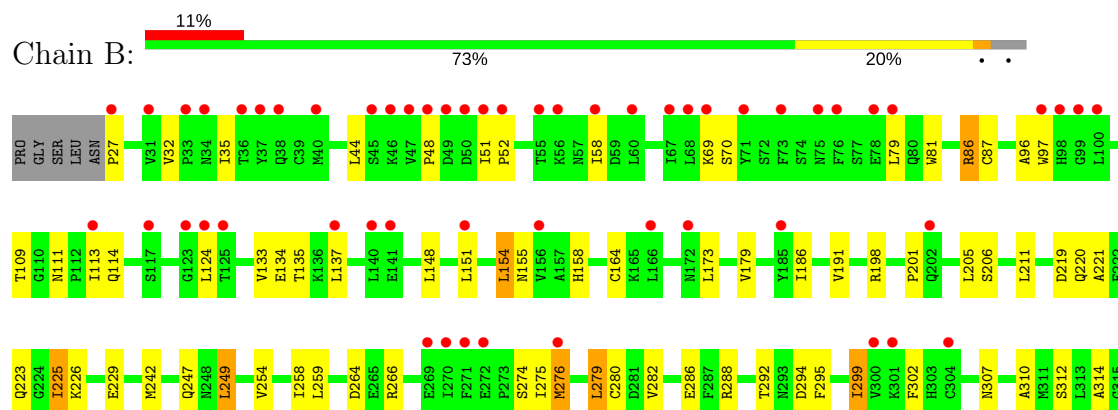
3 Residue-property plots [i](#)

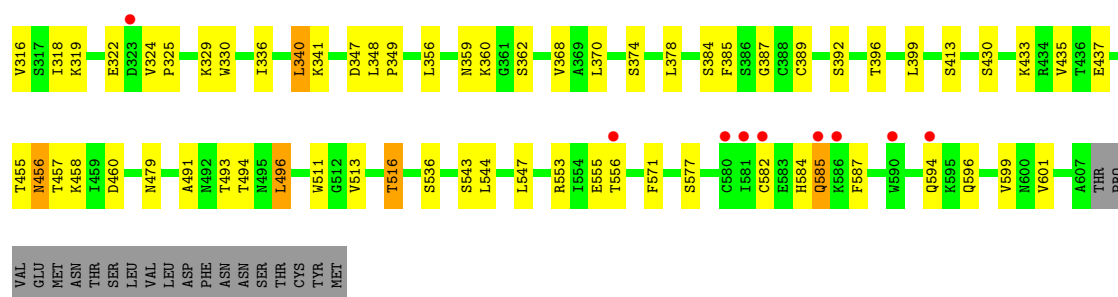
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: Toll-like receptor 4

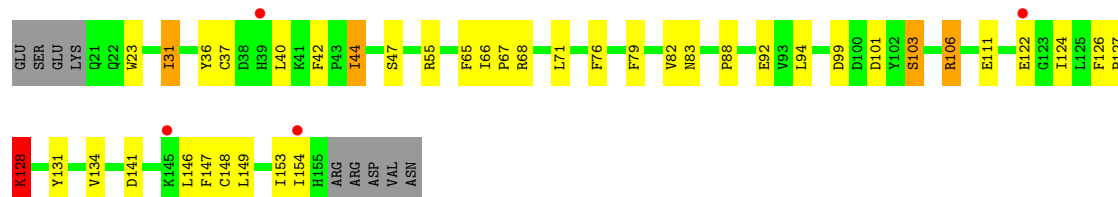


• Molecule 1: Toll-like receptor 4

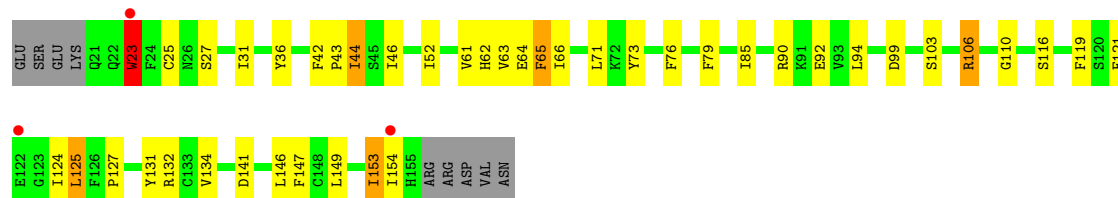




• Molecule 2: Lymphocyte antigen 96



• Molecule 2: Lymphocyte antigen 96



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	85.81Å 144.32Å 86.94Å 90.00° 95.16° 90.00°	Depositor
Resolution (Å)	86.59 – 2.48 72.16 – 2.48	Depositor EDS
% Data completeness (in resolution range)	98.4 (86.59-2.48) 98.4 (72.16-2.48)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.93 (at 2.48Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.221 , 0.267 0.226 , 0.268	Depositor DCC
R_{free} test set	3710 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	56.5	Xtriage
Anisotropy	0.034	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 49.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.024 for l,-k,h	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11815	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.47% 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: LP4, LP5, MYR, NAG, DAO

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	0.50	4/4735 (0.1%)	0.66	2/6414 (0.0%)
1	B	0.50	4/4735 (0.1%)	0.62	0/6414
2	C	0.52	1/1123 (0.1%)	0.68	1/1519 (0.1%)
2	D	0.50	1/1123 (0.1%)	0.60	0/1519
All	All	0.50	10/11716 (0.1%)	0.64	3/15866 (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	1

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	23	TRP	CD2-CE2	5.82	1.48	1.41
1	B	511	TRP	CD2-CE2	5.56	1.48	1.41
1	A	97	TRP	CD2-CE2	5.46	1.47	1.41
1	A	81	TRP	CD2-CE2	5.40	1.47	1.41
1	B	97	TRP	CD2-CE2	5.24	1.47	1.41

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	383	LEU	CA-CB-CG	5.98	129.06	115.30
2	C	128	LYS	N-CA-C	-5.56	95.99	111.00
1	A	337	ARG	NE-CZ-NH1	-5.47	117.56	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	323	ASP	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	4637	0	4611	74	0
1	B	4637	0	4613	62	0
2	C	1092	0	1051	26	0
2	D	1092	0	1051	34	0
3	A	70	0	64	2	0
3	B	28	0	25	0	0
4	C	45	0	53	0	0
4	D	45	0	53	0	0
5	C	48	0	63	1	0
5	D	48	0	63	2	0
6	C	13	0	23	0	0
6	D	13	0	23	2	0
7	C	15	0	27	0	0
7	D	15	0	27	0	0
8	A	8	0	0	0	0
8	B	9	0	0	0	0
All	All	11815	0	11747	181	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 8.

The worst 5 of 181 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:556:THR:HG21	1:B:584:HIS:CG	2.12	0.84
1:A:87:CYS:H	1:A:111:ASN:HD21	1.25	0.84
2:C:44:ILE:HD13	2:C:149:LEU:HD21	1.58	0.83
1:B:295:PHE:CE1	1:B:299:ILE:HG21	2.22	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:387:GLY:HA2	1:B:413:SER:HB3	1.70	0.73

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	579/606 (96%)	533 (92%)	43 (7%)	3 (0%)	31	49
1	B	579/606 (96%)	529 (91%)	47 (8%)	3 (0%)	31	49
2	C	133/144 (92%)	127 (96%)	5 (4%)	1 (1%)	21	35
2	D	133/144 (92%)	129 (97%)	4 (3%)	0	100	100
All	All	1424/1500 (95%)	1318 (93%)	99 (7%)	7 (0%)	31	49

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	581	ILE
2	C	128	LYS
1	B	52	PRO
1	A	317	SER
1	A	560	ILE

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	540/564 (96%)	487 (90%)	53 (10%)	9	15
1	B	540/564 (96%)	485 (90%)	55 (10%)	8	14
2	C	122/131 (93%)	112 (92%)	10 (8%)	12	23
2	D	122/131 (93%)	113 (93%)	9 (7%)	15	27
All	All	1324/1390 (95%)	1197 (90%)	127 (10%)	9	16

5 of 127 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	65	PHE
1	B	173	LEU
1	B	601	VAL
2	C	103	SER
1	B	86	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	540	GLN
1	B	98	HIS
2	D	21	GLN
2	C	155	HIS
1	B	102	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

15 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	NAG	A	800	1	14,14,15	1.83	1 (7%)	17,19,21	2.46	4 (23%)
3	NAG	A	801	1	14,14,15	0.70	1 (7%)	17,19,21	1.98	4 (23%)
3	NAG	A	802	1,3	14,14,15	1.54	1 (7%)	17,19,21	2.31	3 (17%)
3	NAG	A	803	3	14,14,15	0.66	0	17,19,21	1.40	1 (5%)
3	NAG	A	804	-	14,14,15	0.51	0	17,19,21	0.88	0
3	NAG	B	701	1,3	14,14,15	0.55	0	17,19,21	1.41	3 (17%)
3	NAG	B	702	3	14,14,15	0.59	0	17,19,21	1.32	1 (5%)
4	LP4	C	300	5,7,6	45,45,48	0.76	1 (2%)	51,56,60	1.00	3 (5%)
5	LP5	C	301	4	47,48,48	0.88	3 (6%)	56,60,60	1.28	5 (8%)
6	DAO	C	302	4	12,12,13	0.94	1 (8%)	11,11,13	0.58	0
7	MYR	C	303	4	14,14,15	0.87	1 (7%)	13,13,15	0.65	0
4	LP4	D	300	5,7,6	45,45,48	0.67	0	51,56,60	1.15	4 (7%)
5	LP5	D	301	4	47,48,48	0.83	1 (2%)	56,60,60	1.08	6 (10%)
6	DAO	D	302	4	12,12,13	0.96	1 (8%)	11,11,13	0.58	0
7	MYR	D	303	4	14,14,15	0.87	1 (7%)	13,13,15	0.68	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
3	NAG	A	800	1	-	0/6/23/26	0/1/1/1
3	NAG	A	801	1	-	0/6/23/26	0/1/1/1
3	NAG	A	802	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	803	3	-	0/6/23/26	0/1/1/1
3	NAG	A	804	-	-	0/6/23/26	0/1/1/1
3	NAG	B	701	1,3	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	B	702	3	-	0/6/23/26	0/1/1/1
4	LP4	C	300	5,7,6	-	0/43/60/65	0/1/1/1
5	LP5	C	301	4	-	0/44/65/65	0/1/1/1
6	DAO	C	302	4	-	0/10/10/11	0/0/0/0
7	MYR	C	303	4	-	0/12/12/13	0/0/0/0
4	LP4	D	300	5,7,6	-	0/43/60/65	0/1/1/1
5	LP5	D	301	4	-	0/44/65/65	0/1/1/1
6	DAO	D	302	4	-	0/10/10/11	0/0/0/0
7	MYR	D	303	4	-	0/12/12/13	0/0/0/0

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	800	NAG	O5-C1	-6.60	1.33	1.43
3	A	802	NAG	O5-C1	-5.43	1.34	1.43
6	D	302	DAO	O2-C1	-3.24	1.25	1.42
6	C	302	DAO	O2-C1	-3.17	1.25	1.42
7	D	303	MYR	O2-C1	-3.16	1.25	1.42

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	802	NAG	O5-C1-C2	-8.00	100.47	111.52
3	A	800	NAG	C1-O5-C5	-7.77	101.49	112.19
3	A	800	NAG	O5-C1-C2	-3.71	106.40	111.52
5	C	301	LP5	C8-C7-N2	-3.69	111.47	116.32
3	A	801	NAG	C2-N2-C7	-3.27	118.17	122.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	802	NAG	1	0
3	A	804	NAG	2	0
5	C	301	LP5	1	0
5	D	301	LP5	2	0
6	D	302	DAO	2	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	581/606 (95%)	0.59	45 (7%) 13 13	42, 65, 119, 169	0
1	B	581/606 (95%)	0.72	64 (11%) 5 5	38, 68, 128, 184	0
2	C	135/144 (93%)	0.34	4 (2%) 50 52	46, 64, 92, 112	2 (1%)
2	D	135/144 (93%)	0.39	3 (2%) 62 63	57, 72, 97, 142	2 (1%)
All	All	1432/1500 (95%)	0.60	116 (8%) 12 12	38, 68, 121, 184	4 (0%)

The worst 5 of 116 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	582	CYS	10.3
1	B	50	ASP	7.0
1	B	31	VAL	6.2
1	B	55	THR	5.1
1	A	579	ALA	5.0

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
3	NAG	A	804	14/15	0.83	0.20	81,105,125,136	0
3	NAG	A	801	14/15	0.85	0.20	71,82,105,111	0
7	MYR	D	303	15/16	0.89	0.33	66,91,101,116	0
7	MYR	C	303	15/16	0.90	0.38	68,79,99,122	0
4	LP4	C	300	45/48	0.91	0.21	45,64,81,99	0
3	NAG	A	802	14/15	0.91	0.19	65,75,85,96	0
3	NAG	A	800	14/15	0.91	0.17	59,73,84,85	0
3	NAG	A	803	14/15	0.91	0.14	79,94,120,130	0
6	DAO	C	302	13/14	0.92	0.28	68,75,88,90	0
4	LP4	D	300	45/48	0.93	0.20	60,72,90,96	0
3	NAG	B	702	14/15	0.93	0.19	63,78,94,120	0
5	LP5	D	301	48/48	0.94	0.19	52,78,102,119	0
5	LP5	C	301	48/48	0.94	0.22	48,68,102,109	0
6	DAO	D	302	13/14	0.94	0.26	72,82,97,103	0
3	NAG	B	701	14/15	0.98	0.18	47,54,70,80	0

6.5 Other polymers [i](#)

There are no such residues in this entry.