wwPDB X-ray Structure Validation Summary Report (i)

Jan 21, 2024 – 10:04 PM EST

PDB ID	:	4M3C
Title	:	Structure of a binary complex between homologous tetrameric legume lectins from Butea monosperma and Spatholobus parviflorus seeds
Authors	:	Surya, S.; Abhilash, J.; Geethanandan, K.; Sadasivan, C.; Haridas, M.
Deposited on	:	2013-08-06
Resolution	:	2.50 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

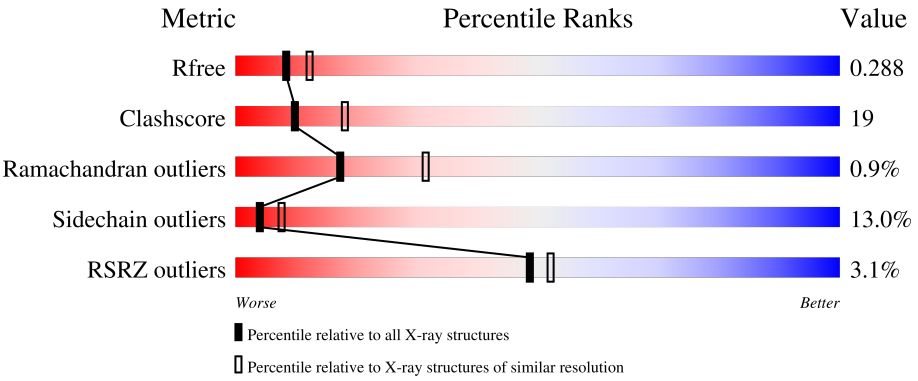
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.50 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}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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 <=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	255	5% 59% 30% 9%
1	C	255	5% 60% 32% 5%
2	B	239	2% 64% 28% 8%
2	D	239	3% 63% 30% 7%
3	E	251	4% 58% 35% 6%

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Mol	Chain	Length	Quality of chain
3	G	251	4% 71% 20% 8%
4	F	239	% 62% 33% 5%
4	H	239	% 64% 31% 5%

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
7	ABU	B	303	-	-	X	-
7	ABU	C	303	-	-	X	-
7	ABU	D	303	-	-	X	-
7	ABU	H	303	-	-	X	-

2 Entry composition (i)

There are 9 unique types of molecules in this entry. The entry contains 15035 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 Lectin Alpha chain.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	249	Total 1880	C 1220	N 294	O 366	0	0	0
1	C	249	Total 1880	C 1220	N 294	O 366	0	0	0

- Molecule 2 is a protein called Lectin Beta Chain.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	239	Total 1811	C 1174	N 284	O 353	0	0	0
2	D	239	Total 1811	C 1174	N 284	O 353	0	0	0

- Molecule 3 is a protein called Seed lectin alpha chain.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	249	Total 1850	C 1198	N 289	O 363	0	0	0
3	G	249	Total 1850	C 1198	N 289	O 363	0	0	0

- Molecule 4 is a protein called Seed lectin beta chain.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	F	239	Total 1790	C 1162	N 277	O 351	0	0	0
4	H	239	Total 1790	C 1162	N 277	O 351	0	0	0

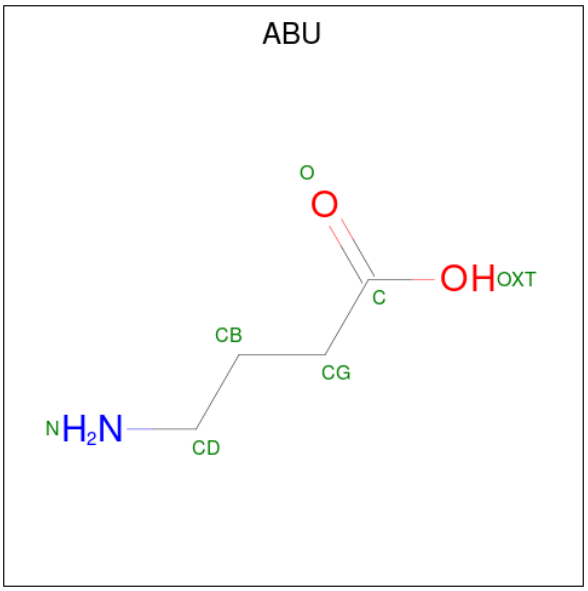
- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Ca 1 1	0	0
5	B	1	Total Ca 1 1	0	0
5	C	1	Total Ca 1 1	0	0
5	D	1	Total Ca 1 1	0	0
5	E	1	Total Ca 1 1	0	0
5	F	1	Total Ca 1 1	0	0
5	G	1	Total Ca 1 1	0	0
5	H	1	Total Ca 1 1	0	0

- Molecule 6 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

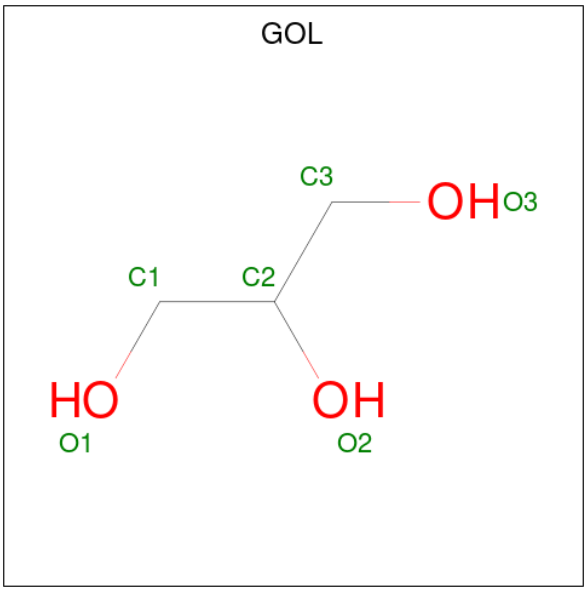
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total Mn 1 1	0	0
6	B	1	Total Mn 1 1	0	0
6	C	1	Total Mn 1 1	0	0
6	D	1	Total Mn 1 1	0	0
6	E	1	Total Mn 1 1	0	0
6	F	1	Total Mn 1 1	0	0
6	G	1	Total Mn 1 1	0	0
6	H	1	Total Mn 1 1	0	0

- Molecule 7 is GAMMA-AMINO-BUTANOIC ACID (three-letter code: ABU) (formula: $C_4H_9NO_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total C N O 7 4 1 2	0	0
7	B	1	Total C N O 7 4 1 2	0	0
7	C	1	Total C N O 7 4 1 2	0	0
7	D	1	Total C N O 7 4 1 2	0	0
7	E	1	Total C N O 7 4 1 2	0	0
7	H	1	Total C N O 7 4 1 2	0	0

- Molecule 8 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	C	1	Total C O 6 3 3	0	0
8	D	1	Total C O 6 3 3	0	0
8	F	1	Total C O 6 3 3	0	0

- Molecule 9 is water.

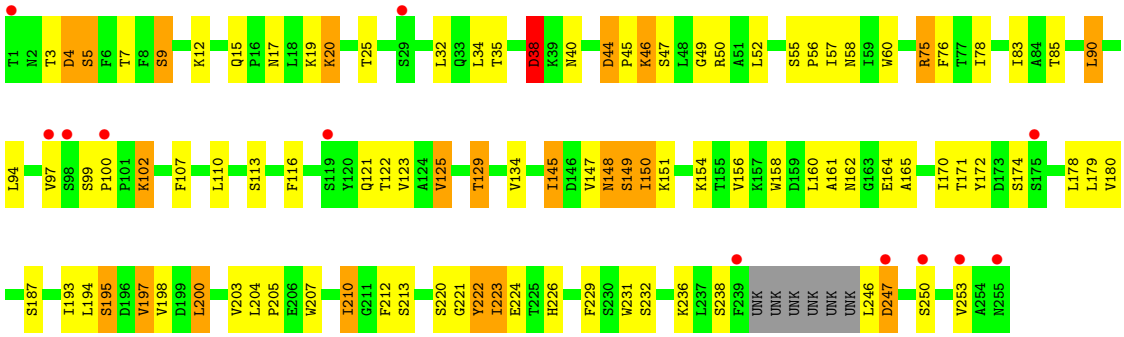
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	33	Total O 33 33	0	0
9	B	39	Total O 39 39	0	0
9	C	36	Total O 36 36	0	0
9	D	34	Total O 34 34	0	0
9	E	40	Total O 40 40	0	0
9	F	35	Total O 35 35	0	0
9	G	42	Total O 42 42	0	0
9	H	38	Total O 38 38	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

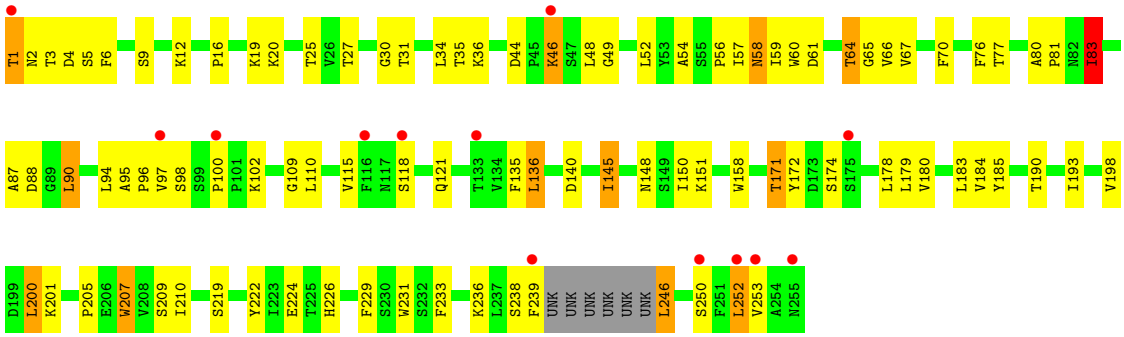
• Molecule 1: Lectin Alpha chain

Chain A:



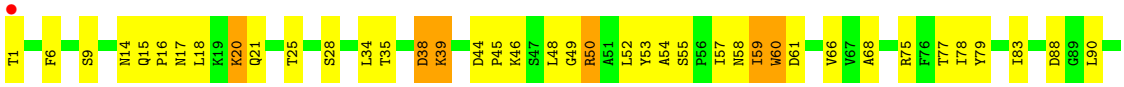
• Molecule 1: Lectin Alpha chain

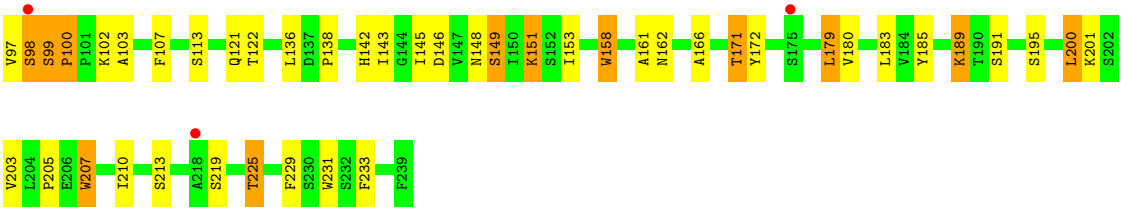
Chain C:



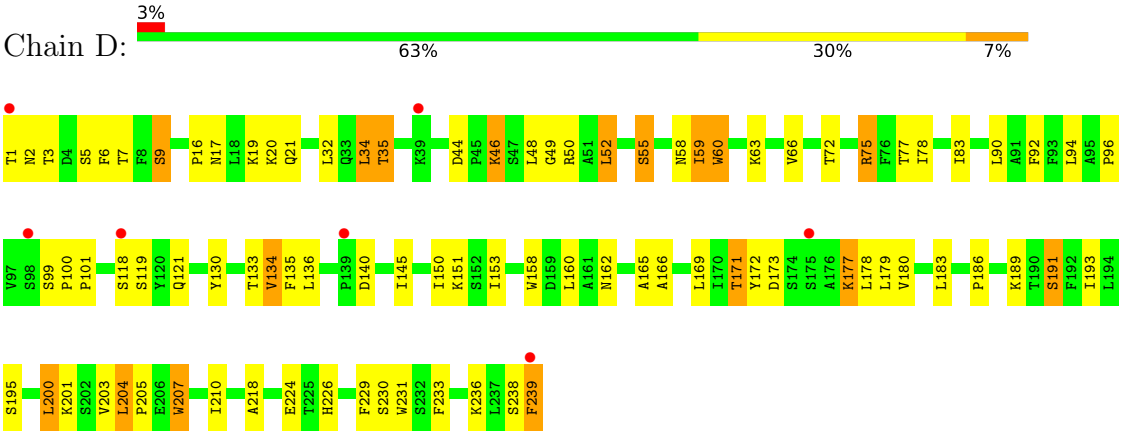
• Molecule 2: Lectin Beta Chain

Chain B:

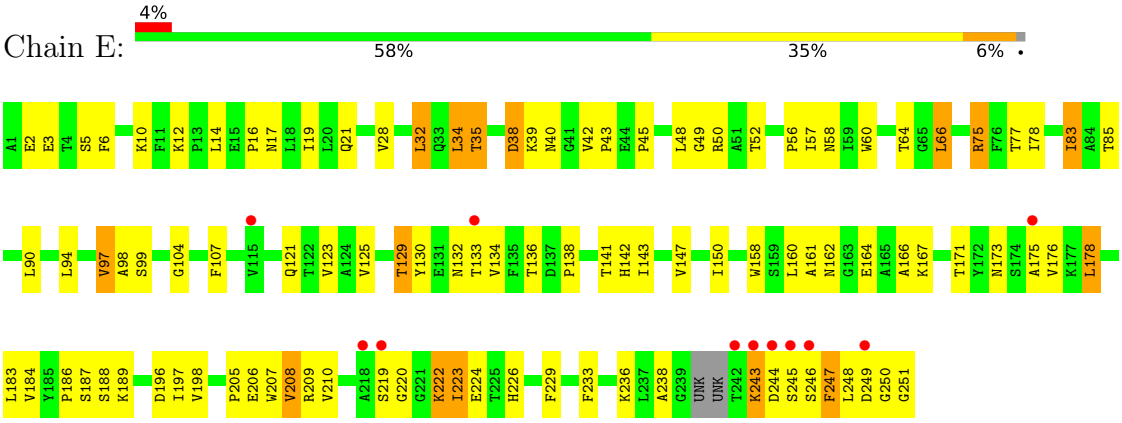




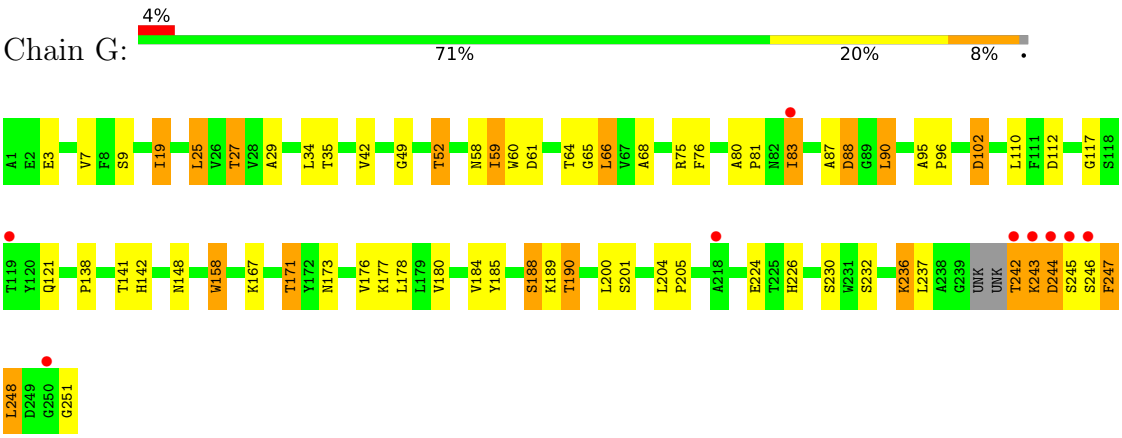
• Molecule 2: Lectin Beta Chain



• Molecule 3: Seed lectin alpha chain

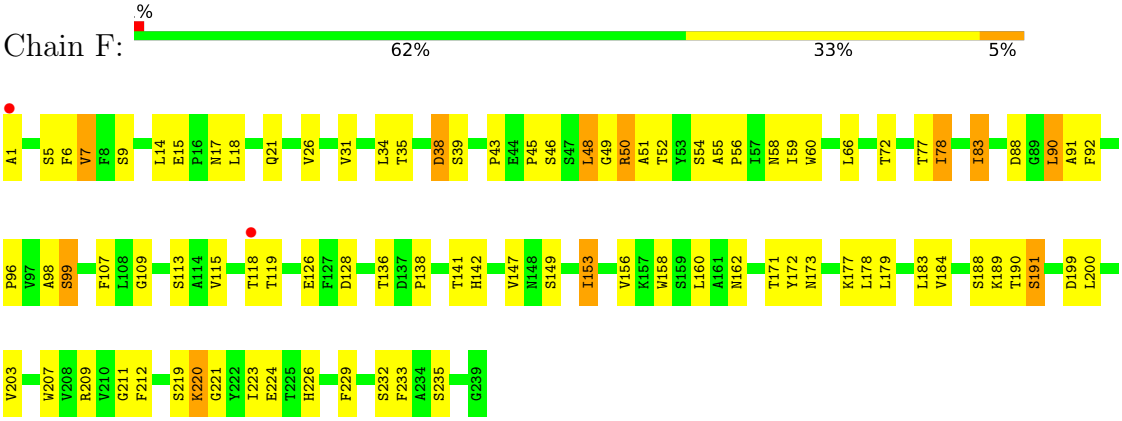


• Molecule 3: Seed lectin alpha chain



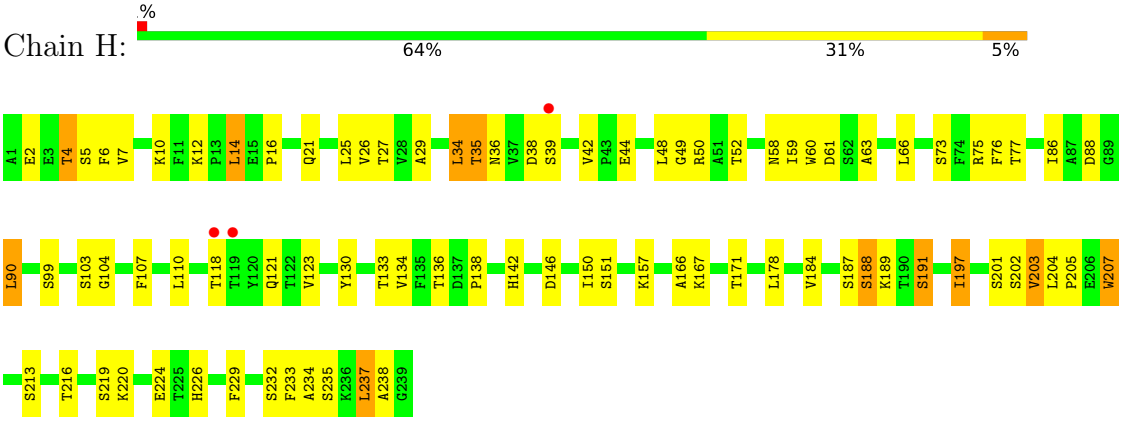
• Molecule 4: Seed lectin beta chain

Chain F:



• Molecule 4: Seed lectin beta chain

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	77.11Å 78.63Å 96.19Å 96.00° 89.99° 100.37°	Depositor
Resolution (Å)	15.84 – 2.50 15.84 – 2.50	Depositor EDS
% Data completeness (in resolution range)	95.2 (15.84-2.50) 95.6 (15.84-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.97 (at 2.48Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.211 , 0.289 0.211 , 0.288	Depositor DCC
R_{free} test set	3641 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	29.4	Xtriage
Anisotropy	0.293	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 38.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	15035	wwPDB-VP
Average B, all atoms (Å^2)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 72.07 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.3496e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: ABU, GOL, MN, CA

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	0.83	4/1927 (0.2%)	0.93	3/2628 (0.1%)
1	C	0.77	3/1927 (0.2%)	0.84	2/2628 (0.1%)
2	B	0.81	3/1858 (0.2%)	0.94	1/2536 (0.0%)
2	D	0.81	4/1858 (0.2%)	0.90	1/2536 (0.0%)
3	E	0.80	2/1895 (0.1%)	0.88	0/2589
3	G	0.79	2/1895 (0.1%)	0.90	2/2589 (0.1%)
4	F	0.78	1/1836 (0.1%)	0.88	0/2515
4	H	0.82	2/1836 (0.1%)	0.90	2/2515 (0.1%)
All	All	0.80	21/15032 (0.1%)	0.90	11/20536 (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	2
1	C	0	1
3	E	0	2
3	G	0	1
4	F	0	1
All	All	0	7

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	4	ASP	CB-CG	-6.95	1.37	1.51
2	B	60	TRP	CD2-CE2	6.86	1.49	1.41
4	H	60	TRP	CD2-CE2	6.37	1.49	1.41
1	A	60	TRP	CD2-CE2	6.25	1.48	1.41
3	G	158	TRP	CD2-CE2	6.21	1.48	1.41

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	H	90	LEU	CA-CB-CG	6.67	130.64	115.30
2	B	66	VAL	CB-CA-C	6.34	123.45	111.40
4	H	237	LEU	CA-CB-CG	6.34	129.88	115.30
1	A	38	ASP	CB-CG-OD2	6.06	123.76	118.30
3	G	25	LEU	CA-CB-CG	6.05	129.22	115.30

There are no chirality outliers.

5 of 7 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	148	ASN	Peptide
1	A	222	TYR	Peptide
1	C	246	LEU	Peptide
3	E	222	LYS	Peptide
3	E	97	VAL	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	1880	0	1859	88	0
1	C	1880	0	1860	96	0
2	B	1811	0	1794	81	0
2	D	1811	0	1794	75	0
3	E	1850	0	1819	81	0
3	G	1850	0	1819	64	0
4	F	1790	0	1756	65	0
4	H	1790	0	1757	60	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
5	E	1	0	0	0	0
5	F	1	0	0	0	0
5	G	1	0	0	0	0
5	H	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
6	E	1	0	0	0	0
6	F	1	0	0	0	0
6	G	1	0	0	0	0
6	H	1	0	0	0	0
7	A	7	0	0	3	0
7	B	7	0	0	4	0
7	C	7	0	0	4	0
7	D	7	0	0	4	0
7	E	7	0	0	3	0
7	H	7	0	0	6	0
8	C	6	0	8	1	0
8	D	6	0	8	3	0
8	F	6	0	8	1	0
9	A	33	0	0	10	0
9	B	39	0	0	7	0
9	C	36	0	0	12	0
9	D	34	0	0	7	0
9	E	40	0	0	7	0
9	F	35	0	0	4	0
9	G	42	0	0	6	0
9	H	38	0	0	6	0
All	All	15035	0	14482	562	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 19.

The worst 5 of 562 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:35:THR:HG21	1:A:226:HIS:HD2	1.05	1.11
3:G:61:ASP:OD2	3:G:64:THR:HG22	1.53	1.04
1:A:20:LYS:HZ1	1:A:20:LYS:HA	1.21	1.03
1:C:145:ILE:HG21	9:C:436:HOH:O	1.58	1.01
2:D:239:PHE:HD1	2:D:239:PHE:H	1.03	1.00

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	245/255 (96%)	227 (93%)	15 (6%)	3 (1%)	13 24
1	C	245/255 (96%)	232 (95%)	11 (4%)	2 (1%)	19 35
2	B	237/239 (99%)	222 (94%)	12 (5%)	3 (1%)	12 21
2	D	237/239 (99%)	226 (95%)	10 (4%)	1 (0%)	34 54
3	E	245/251 (98%)	223 (91%)	17 (7%)	5 (2%)	7 12
3	G	245/251 (98%)	223 (91%)	19 (8%)	3 (1%)	13 24
4	F	237/239 (99%)	221 (93%)	16 (7%)	0	100 100
4	H	237/239 (99%)	219 (92%)	17 (7%)	1 (0%)	34 54
All	All	1928/1968 (98%)	1793 (93%)	117 (6%)	18 (1%)	17 31

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	150	ILE
3	E	243	LYS
3	E	249	ASP
4	H	38	ASP
1	C	83	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	208/209 (100%)	176 (85%)	32 (15%)	2 5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	C	208/209 (100%)	182 (88%)	26 (12%)	4 8
2	B	201/201 (100%)	180 (90%)	21 (10%)	7 13
2	D	201/201 (100%)	174 (87%)	27 (13%)	4 7
3	E	200/201 (100%)	172 (86%)	28 (14%)	3 6
3	G	200/201 (100%)	178 (89%)	22 (11%)	6 12
4	F	194/194 (100%)	168 (87%)	26 (13%)	4 7
4	H	194/194 (100%)	167 (86%)	27 (14%)	3 6
All	All	1606/1610 (100%)	1397 (87%)	209 (13%)	4 7

5 of 209 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	E	66	LEU
4	F	66	LEU
4	H	171	THR
3	E	123	VAL
3	E	198	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	33	GLN
3	G	226	HIS
3	E	21	GLN
4	H	58	ASN
4	F	148	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 25 ligands modelled in this entry, 16 are monoatomic - leaving 9 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	$\#\|Z\| > 2$
8	GOL	C	304	-	5,5,5	0.17	0	5,5,5	0.69	0
8	GOL	F	303	-	5,5,5	0.51	0	5,5,5	0.26	0
7	ABU	C	303	-	6,6,6	1.15	1 (16%)	6,6,6	1.25	0
7	ABU	H	303	-	6,6,6	0.98	0	6,6,6	0.93	0
8	GOL	D	304	-	5,5,5	0.36	0	5,5,5	0.40	0
7	ABU	B	303	-	6,6,6	0.61	0	6,6,6	1.92	2 (33%)
7	ABU	A	303	-	6,6,6	0.56	0	6,6,6	2.03	2 (33%)
7	ABU	D	303	-	6,6,6	0.80	0	6,6,6	0.98	0
7	ABU	E	303	-	6,6,6	0.69	0	6,6,6	1.14	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
8	GOL	C	304	-	-	0/4/4/4	-
8	GOL	F	303	-	-	3/4/4/4	-
7	ABU	C	303	-	-	3/4/4/4	-
7	ABU	H	303	-	-	1/4/4/4	-
8	GOL	D	304	-	-	2/4/4/4	-
7	ABU	B	303	-	-	1/4/4/4	-
7	ABU	A	303	-	-	1/4/4/4	-
7	ABU	D	303	-	-	4/4/4/4	-
7	ABU	E	303	-	-	1/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	C	303	ABU	OXT-C	-2.47	1.22	1.30

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	A	303	ABU	O-C-CG	-3.75	111.02	123.08
7	B	303	ABU	OXT-C-CG	3.27	124.52	114.03
7	A	303	ABU	OXT-C-CG	3.06	123.86	114.03
7	B	303	ABU	O-C-CG	-3.02	113.38	123.08

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	D	303	ABU	CD-CB-CG-C
7	E	303	ABU	CD-CB-CG-C
8	D	304	GOL	O1-C1-C2-C3
8	F	303	GOL	C1-C2-C3-O3
8	F	303	GOL	O1-C1-C2-C3

There are no ring outliers.

9 monomers are involved in 29 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	C	304	GOL	1	0
8	F	303	GOL	1	0
7	C	303	ABU	4	0
7	H	303	ABU	6	0
8	D	304	GOL	3	0
7	B	303	ABU	4	0
7	A	303	ABU	3	0
7	D	303	ABU	4	0
7	E	303	ABU	3	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

6.1 Protein, DNA and RNA chains

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^{th} 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	249/255 (97%)	-0.09	12 (4%)	30	32	12, 24, 45, 65	1 (0%)
1	C	249/255 (97%)	0.05	13 (5%)	27	29	11, 26, 49, 77	0
2	B	239/239 (100%)	-0.21	4 (1%)	70	72	12, 24, 39, 62	1 (0%)
2	D	239/239 (100%)	-0.16	7 (2%)	51	55	10, 23, 40, 62	0
3	E	249/251 (99%)	0.03	11 (4%)	34	37	11, 24, 47, 114	0
3	G	249/251 (99%)	-0.11	9 (3%)	42	46	11, 24, 44, 100	0
4	F	239/239 (100%)	-0.18	2 (0%)	86	87	12, 24, 38, 54	0
4	H	239/239 (100%)	-0.25	3 (1%)	77	79	11, 22, 35, 49	0
All	All	1952/1968 (99%)	-0.11	61 (3%)	49	52	10, 24, 44, 114	2 (0%)

The worst 5 of 61 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	E	242	THR	8.6
3	E	245	SER	6.8
3	G	244	ASP	6.7
3	G	245	SER	6.7
1	A	1	THR	5.3

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no monosaccharides 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, 95^{th} 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(Å^2)	Q<0.9
7	ABU	A	303	7/7	0.85	0.29	14,16,17,18	7
7	ABU	D	303	7/7	0.86	0.29	25,29,36,42	7
7	ABU	B	303	7/7	0.87	0.27	15,16,17,19	7
8	GOL	C	304	6/6	0.87	0.22	30,32,34,35	6
7	ABU	H	303	7/7	0.88	0.26	15,17,19,20	7
7	ABU	E	303	7/7	0.90	0.29	23,25,27,27	7
8	GOL	D	304	6/6	0.91	0.16	25,26,26,27	6
8	GOL	F	303	6/6	0.91	0.17	23,27,28,28	6
7	ABU	C	303	7/7	0.94	0.20	19,21,21,23	7
5	CA	F	301	1/1	0.98	0.04	28,28,28,28	0
5	CA	G	301	1/1	0.98	0.03	22,22,22,22	0
5	CA	H	301	1/1	0.98	0.05	23,23,23,23	0
6	MN	A	302	1/1	0.98	0.04	39,39,39,39	0
6	MN	D	302	1/1	0.98	0.03	33,33,33,33	0
6	MN	E	302	1/1	0.98	0.06	35,35,35,35	0
6	MN	H	302	1/1	0.98	0.04	41,41,41,41	0
5	CA	C	301	1/1	0.98	0.04	38,38,38,38	0
5	CA	D	301	1/1	0.99	0.04	25,25,25,25	0
6	MN	G	302	1/1	0.99	0.02	30,30,30,30	0
6	MN	B	302	1/1	0.99	0.04	27,27,27,27	0
5	CA	B	301	1/1	0.99	0.07	23,23,23,23	0
6	MN	F	302	1/1	1.00	0.01	31,31,31,31	0
6	MN	C	302	1/1	1.00	0.04	36,36,36,36	0
5	CA	E	301	1/1	1.00	0.08	31,31,31,31	0
5	CA	A	301	1/1	1.00	0.04	18,18,18,18	0

6.5 Other polymers (i)

There are no such residues in this entry.