



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 06:12 AM GMT

PDB ID : 2W8B  
Title : CRYSTAL STRUCTURE OF PROCESSED TOLB IN COMPLEX WITH PAL  
Authors : Sharma, A.; Bonsor, D.A.; Kleanthous, C.  
Deposited on : 2009-01-15  
Resolution : 1.86 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 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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) : trunk26865

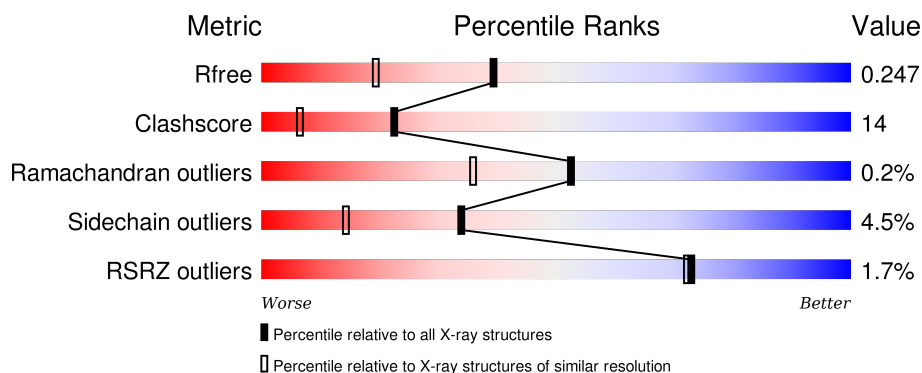
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.86 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))
$R_{free}$	91344	1745 (1.86-1.86)
Clashscore	102246	1898 (1.86-1.86)
Ramachandran outliers	100387	1875 (1.86-1.86)
Sidechain outliers	100360	1875 (1.86-1.86)
RSRZ outliers	91569	1747 (1.86-1.86)

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	409	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="display: flex; justify-content: space-between;"> <span>%</span> <span>88%</span> <span>10%</span> <span>•</span> </div> </div>
2	B	409	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="display: flex; justify-content: space-between;"> <span>%</span> <span>85%</span> <span>12%</span> <span>•</span> </div> </div>
2	D	409	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="display: flex; justify-content: space-between;"> <span>%</span> <span>84%</span> <span>14%</span> <span>•</span> </div> </div>
2	F	409	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="display: flex; justify-content: space-between;"> <span>%</span> <span>81%</span> <span>16%</span> <span>•</span> </div> </div>
3	C	118	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="display: flex; justify-content: space-between;"> <span>7%</span> <span>52%</span> <span>27%</span> <span>8%</span> <span>•</span> <span>12%</span> </div> </div>

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Mol	Chain	Length	Quality of chain
3	E	118	
3	G	118	
3	H	118	

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
4	SO4	A	1431	-	-	-	X
4	SO4	A	1432	-	-	-	X
4	SO4	D	1431	-	-	-	X
4	SO4	F	1431	-	-	-	X
5	GOL	A	1434	-	-	X	-
5	GOL	B	1433	-	-	-	X
5	GOL	C	1174	-	-	X	-
5	GOL	D	1433	-	-	X	-
6	ACT	A	1435	-	-	X	X
6	ACT	B	1435	-	-	X	-
6	ACT	D	1434	-	-	X	-

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 17488 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 TOLB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	409	Total	C	N	O	S	0	6	0
			3110	1956	546	601	7			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	390	LEU	ILE	CONFLICT	UNP P0A855

- Molecule 2 is a protein called PROTEIN TOLB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	409	Total	C	N	O	S	0	5	0
			3100	1947	544	603	6			
2	D	409	Total	C	N	O	S	0	3	0
			3091	1942	544	599	6			
2	F	409	Total	C	N	O	S	0	13	0
			3147	1978	553	609	7			

- Molecule 3 is a protein called PEPTIDOGLYCAN-ASSOCIATED LIPOPROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	104	Total	C	N	O	S	0	2	0
			833	524	147	160	2			
3	E	107	Total	C	N	O	S	0	1	0
			857	539	152	164	2			
3	G	108	Total	C	N	O	S	0	3	0
			869	546	153	167	3			
3	H	108	Total	C	N	O	S	0	2	0
			864	542	153	167	2			

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



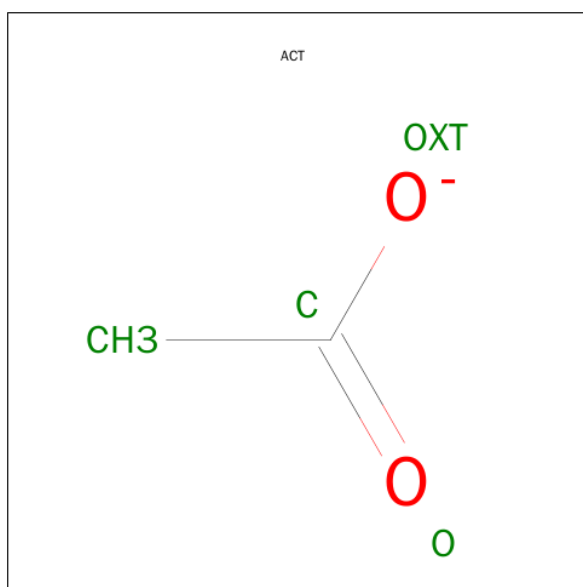
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	D	1	Total	O	S	0	0
			5	4	1		
4	F	1	Total	O	S	0	0
			5	4	1		
4	G	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		
5	C	1	Total	C	O	0	0
			6	3	3		
5	D	1	Total	C	O	0	0
			6	3	3		
5	D	1	Total	C	O	0	0
			6	3	3		
5	F	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is ACETATE ION (three-letter code: ACT) (formula: C<sub>2</sub>H<sub>3</sub>O<sub>2</sub>).



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

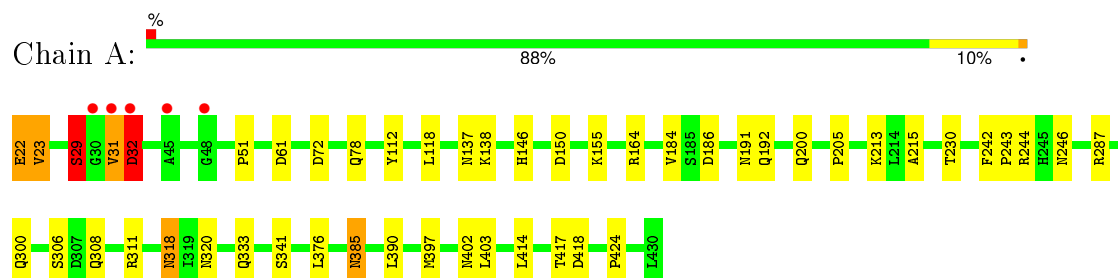
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	354	Total	O	0	0
			354	354		
7	B	314	Total	O	0	0
			314	314		
7	C	35	Total	O	0	0
			35	35		
7	D	316	Total	O	0	0
			316	316		
7	E	55	Total	O	0	0
			55	55		
7	F	329	Total	O	0	0
			329	329		
7	G	60	Total	O	0	0
			60	60		
7	H	56	Total	O	0	0
			56	56		

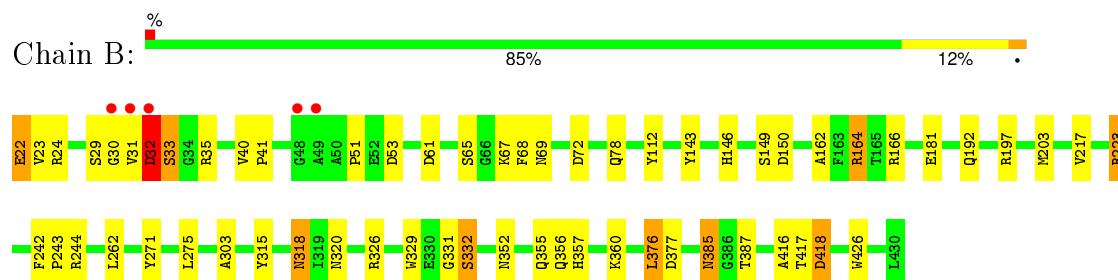
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

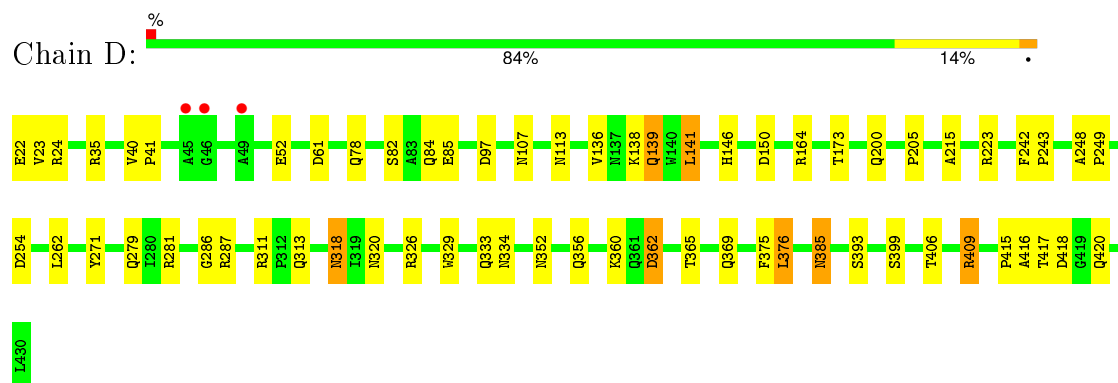
#### • Molecule 1: PROTEIN TOLB



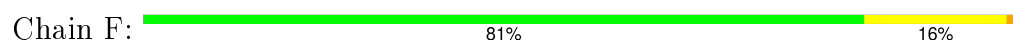
#### • Molecule 2: PROTEIN TOLB



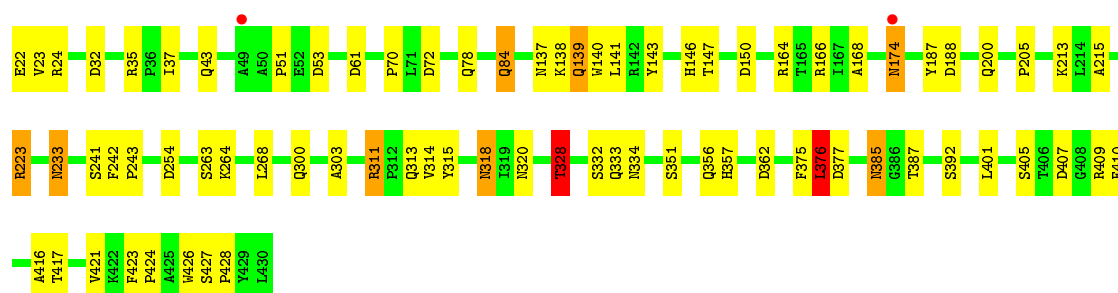
#### • Molecule 2: PROTEIN TOLB



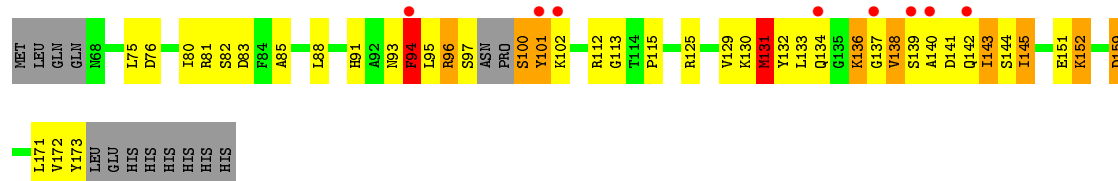
#### • Molecule 2: PROTEIN TOLB







• Molecule 3: PEPTIDOGLYCAN-ASSOCIATED LIPOPROTEIN



• Molecule 3: PEPTIDOGLYCAN-ASSOCIATED LIPOPROTEIN



• Molecule 3: PEPTIDOGLYCAN-ASSOCIATED LIPOPROTEIN



• Molecule 3: PEPTIDOGLYCAN-ASSOCIATED LIPOPROTEIN



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	74.74Å 89.24Å 90.90Å 86.81° 89.81° 68.62°	Depositor
Resolution (Å)	45.36 – 1.86 45.37 – 1.86	Depositor EDS
% Data completeness (in resolution range)	96.2 (45.36-1.86) 84.6 (45.37-1.86)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.51 (at 1.86Å)	Xtriage
Refinement program	REFMAC 5.4.0077	Depositor
R, $R_{free}$	0.191 , 0.247 0.192 , 0.247	Depositor DCC
$R_{free}$ test set	7981 reflections (5.30%)	DCC
Wilson B-factor (Å <sup>2</sup> )	17.3	Xtriage
Anisotropy	0.121	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 50.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 158490 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	17488	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	19.0	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 43.20 % 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 1.8264e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, SO4, ACT

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	1.02	1/3196 (0.0%)	0.92	2/4354 (0.0%)
2	B	0.95	0/3189	0.94	7/4345 (0.2%)
2	D	0.95	0/3174	0.92	2/4326 (0.0%)
2	F	1.00	1/3251 (0.0%)	0.96	9/4427 (0.2%)
3	C	0.85	0/853	0.93	4/1148 (0.3%)
3	E	0.85	0/873	0.94	3/1178 (0.3%)
3	G	0.88	0/894	0.89	0/1205
3	H	0.86	0/886	0.92	1/1195 (0.1%)
All	All	0.96	2/16316 (0.0%)	0.93	28/22178 (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	1
2	B	0	1
2	F	1	0
3	E	0	1
All	All	1	3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	187	TYR	CD2-CE2	6.79	1.49	1.39
1	A	184	VAL	CB-CG2	5.81	1.65	1.52

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	75	LEU	CB-CA-C	-10.40	90.44	110.20
3	E	75	LEU	N-CA-C	8.42	133.74	111.00
2	F	166	ARG	NE-CZ-NH2	-8.12	116.24	120.30
2	B	32	ASP	N-CA-C	-7.10	91.82	111.00
1	A	31	VAL	CB-CA-C	-6.75	98.56	111.40

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	F	328	THR	CB

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	29	SER	Peptide
2	B	32	ASP	Peptide
3	E	75	LEU	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	3110	0	3034	62	0
2	B	3100	0	3020	85	0
2	D	3091	0	3008	61	0
2	F	3147	0	3086	73	0
3	C	833	0	817	84	0
3	E	857	0	838	29	0
3	G	869	0	855	23	0
3	H	864	0	846	27	0
4	A	15	0	0	0	0
4	B	10	0	0	0	0
4	D	5	0	0	0	0
4	F	5	0	0	0	0
4	G	5	0	0	0	0
5	A	6	0	8	4	0
5	B	12	0	16	5	0
5	C	6	0	8	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	12	0	16	5	0
5	F	6	0	8	3	0
6	A	4	0	3	8	0
6	B	4	0	3	9	0
6	D	4	0	3	6	0
6	H	4	0	3	0	0
7	A	354	0	0	8	0
7	B	314	0	0	17	0
7	C	35	0	0	5	0
7	D	316	0	0	7	0
7	E	55	0	0	6	0
7	F	329	0	0	2	0
7	G	60	0	0	6	0
7	H	56	0	0	2	0
All	All	17488	0	15572	433	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 14.

The worst 5 of 433 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)
3:C:95:LEU:O	3:C:96:ARG:HD3	1.26	1.29
3:C:101:TYR:HD1	3:C:102:LYS:N	1.31	1.26
3:C:75:LEU:HD12	3:C:76:ASP:N	1.46	1.26
3:C:95:LEU:C	3:C:96:ARG:HD3	1.55	1.25
3:E:75:LEU:HD11	3:E:112:ARG:NH2	1.55	1.19

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	413/409 (101%)	402 (97%)	9 (2%)	2 (0%)	34	17
2	B	412/409 (101%)	399 (97%)	13 (3%)	0	100	100
2	D	410/409 (100%)	402 (98%)	8 (2%)	0	100	100
2	F	420/409 (103%)	414 (99%)	6 (1%)	0	100	100
3	C	102/118 (86%)	91 (89%)	9 (9%)	2 (2%)	9	2
3	E	106/118 (90%)	104 (98%)	2 (2%)	0	100	100
3	G	109/118 (92%)	107 (98%)	2 (2%)	0	100	100
3	H	108/118 (92%)	106 (98%)	2 (2%)	0	100	100
All	All	2080/2108 (99%)	2025 (97%)	51 (2%)	4 (0%)	52	36

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	94	PHE
1	A	32	ASP
1	A	23	VAL
3	C	143	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	332/327 (102%)	321 (97%)	11 (3%)	45	25
2	B	332/327 (102%)	320 (96%)	12 (4%)	42	21
2	D	329/327 (101%)	317 (96%)	12 (4%)	42	21
2	F	340/327 (104%)	322 (95%)	18 (5%)	28	10
3	C	88/100 (88%)	78 (89%)	10 (11%)	7	1
3	E	90/100 (90%)	87 (97%)	3 (3%)	45	25
3	G	93/100 (93%)	86 (92%)	7 (8%)	17	4
3	H	92/100 (92%)	86 (94%)	6 (6%)	21	6
All	All	1696/1708 (99%)	1617 (95%)	79 (5%)	34	13

5 of 79 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	84	GLN
2	D	409	ARG
3	H	75	LEU
2	D	139	GLN
2	D	318	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 70 such sidechains are listed below:

Mol	Chain	Res	Type
2	D	333	GLN
2	D	420	GLN
3	G	142	GLN
2	D	352	ASN
2	D	369	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

19 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
4	SO4	A	1431	-	4,4,4	0.75	0	6,6,6	0.80	0
4	SO4	A	1432	-	4,4,4	0.21	0	6,6,6	0.33	0
4	SO4	A	1433	-	4,4,4	0.24	0	6,6,6	0.52	0
5	GOL	A	1434	-	5,5,5	0.65	0	5,5,5	1.34	1 (20%)
6	ACT	A	1435	-	1,3,3	3.94	1 (100%)	0,3,3	0.00	-
4	SO4	B	1431	-	4,4,4	0.22	0	6,6,6	0.28	0
4	SO4	B	1432	-	4,4,4	0.20	0	6,6,6	0.58	0
5	GOL	B	1433	-	5,5,5	0.94	0	5,5,5	2.32	1 (20%)
5	GOL	B	1434	-	5,5,5	0.72	0	5,5,5	1.01	0
6	ACT	B	1435	-	1,3,3	0.69	0	0,3,3	0.00	-
5	GOL	C	1174	-	5,5,5	0.39	0	5,5,5	0.68	0
4	SO4	D	1431	-	4,4,4	0.26	0	6,6,6	0.43	0
5	GOL	D	1432	-	5,5,5	0.88	0	5,5,5	0.71	0
5	GOL	D	1433	-	5,5,5	0.90	0	5,5,5	1.16	1 (20%)
6	ACT	D	1434	-	1,3,3	1.63	0	0,3,3	0.00	-
4	SO4	F	1431	-	4,4,4	0.14	0	6,6,6	0.46	0
5	GOL	F	1432	-	5,5,5	0.19	0	5,5,5	1.40	1 (20%)
4	SO4	G	1175	-	4,4,4	0.16	0	6,6,6	0.41	0
6	ACT	H	1175	-	1,3,3	1.85	0	0,3,3	0.00	-

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
4	SO4	A	1431	-	-	0/0/0/0	0/0/0/0
4	SO4	A	1432	-	-	0/0/0/0	0/0/0/0
4	SO4	A	1433	-	-	0/0/0/0	0/0/0/0
5	GOL	A	1434	-	-	0/4/4/4	0/0/0/0
6	ACT	A	1435	-	-	0/0/0/0	0/0/0/0
4	SO4	B	1431	-	-	0/0/0/0	0/0/0/0
4	SO4	B	1432	-	-	0/0/0/0	0/0/0/0
5	GOL	B	1433	-	-	0/4/4/4	0/0/0/0
5	GOL	B	1434	-	-	0/4/4/4	0/0/0/0
6	ACT	B	1435	-	-	0/0/0/0	0/0/0/0
5	GOL	C	1174	-	-	0/4/4/4	0/0/0/0
4	SO4	D	1431	-	-	0/0/0/0	0/0/0/0
5	GOL	D	1432	-	-	0/4/4/4	0/0/0/0
5	GOL	D	1433	-	-	0/4/4/4	0/0/0/0
6	ACT	D	1434	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	SO4	F	1431	-	-	0/0/0/0	0/0/0/0
5	GOL	F	1432	-	-	0/4/4/4	0/0/0/0
4	SO4	G	1175	-	-	0/0/0/0	0/0/0/0
6	ACT	H	1175	-	-	0/0/0/0	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	1435	ACT	CH3-C	-3.94	1.43	1.48

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1434	GOL	O2-C2-C1	-2.47	97.30	108.65
5	F	1432	GOL	C3-C2-C1	-2.37	101.81	111.12
5	D	1433	GOL	C3-C2-C1	2.04	119.13	111.12
5	B	1433	GOL	O2-C2-C3	4.35	128.58	108.65

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 48 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1434	GOL	4	0
6	A	1435	ACT	8	0
5	B	1433	GOL	2	0
5	B	1434	GOL	3	0
6	B	1435	ACT	9	0
5	C	1174	GOL	8	0
5	D	1433	GOL	5	0
6	D	1434	ACT	6	0
5	F	1432	GOL	3	0

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

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<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	409/409 (100%)	-0.42	5 (1%) 81 81	7, 14, 30, 48	0
2	B	409/409 (100%)	-0.38	5 (1%) 81 81	7, 16, 31, 54	0
2	D	409/409 (100%)	-0.45	3 (0%) 89 88	8, 15, 30, 39	0
2	F	409/409 (100%)	-0.51	2 (0%) 91 91	8, 15, 29, 40	0
3	C	104/118 (88%)	0.22	8 (7%) 16 15	11, 29, 55, 61	0
3	E	107/118 (90%)	-0.10	4 (3%) 45 43	10, 23, 42, 49	0
3	G	108/118 (91%)	0.06	4 (3%) 45 43	10, 24, 46, 55	0
3	H	108/118 (91%)	-0.08	4 (3%) 45 43	7, 22, 43, 50	0
All	All	2063/2108 (97%)	-0.34	35 (1%) 73 72	7, 16, 37, 61	0

The worst 5 of 35 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	31	VAL	7.4
1	A	30	GLY	6.2
3	C	101	TYR	5.8
2	B	32	ASP	4.7
2	B	30	GLY	4.6

### 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 carbohydrates in this entry.

## 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(Å <sup>2</sup> )	Q<0.9
4	SO4	F	1431	5/5	0.74	0.26	32.96	79,81,82,82	0
4	SO4	A	1431	5/5	0.86	0.22	20.70	21,28,40,43	0
5	GOL	B	1433	6/6	0.92	0.16	9.90	16,22,25,30	0
6	ACT	A	1435	4/4	0.84	0.15	5.60	10,16,16,20	0
4	SO4	D	1431	5/5	0.95	0.21	4.84	48,48,49,50	0
4	SO4	A	1432	5/5	0.92	0.18	2.09	69,70,71,71	0
5	GOL	D	1433	6/6	0.80	0.14	1.62	35,36,37,41	0
4	SO4	A	1433	5/5	0.90	0.12	1.39	57,58,60,61	0
5	GOL	F	1432	6/6	0.91	0.12	1.17	28,31,34,38	0
6	ACT	B	1435	4/4	0.88	0.10	1.14	12,17,17,19	0
5	GOL	B	1434	6/6	0.89	0.15	0.77	31,34,35,40	0
5	GOL	A	1434	6/6	0.85	0.12	0.42	33,34,36,39	0
5	GOL	D	1432	6/6	0.91	0.11	0.38	27,32,35,38	0
5	GOL	C	1174	6/6	0.92	0.11	-0.49	35,37,39,42	0
6	ACT	H	1175	4/4	0.96	0.08	-0.62	16,18,18,18	0
6	ACT	D	1434	4/4	0.97	0.07	-0.72	10,13,14,16	0
4	SO4	G	1175	5/5	0.88	0.17	-	60,61,62,65	0
4	SO4	B	1431	5/5	0.93	0.13	-	50,52,54,54	0
4	SO4	B	1432	5/5	0.96	0.10	-	54,56,57,58	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.