



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 03:13 am GMT

PDB ID : 2HQS
Title : Crystal structure of TolB/Pal complex
Authors : Grishkovskaya, I.; Bonsor, D.A.; Kleanthous, C.; Dodson, E.J.
Deposited on : 2006-07-19
Resolution : 1.50 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

<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

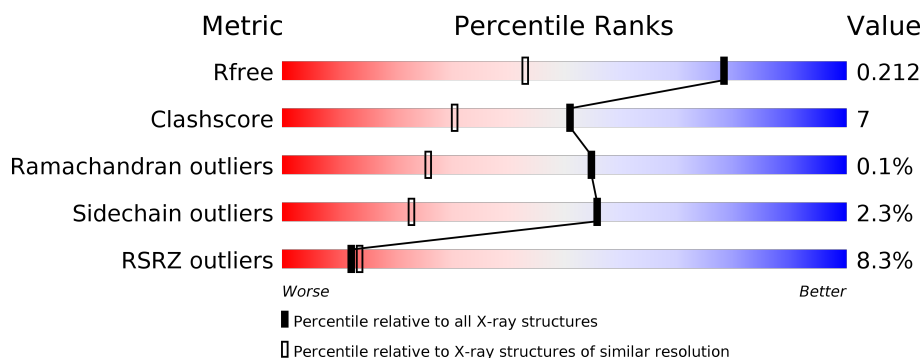
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.50 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.



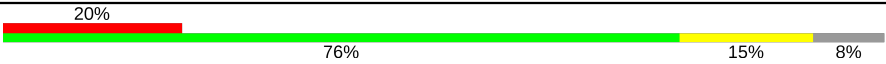

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	2279 (1.50-1.50)
Clashscore	112137	2503 (1.50-1.50)
Ramachandran outliers	110173	2445 (1.50-1.50)
Sidechain outliers	110143	2443 (1.50-1.50)
RSRZ outliers	101464	2305 (1.50-1.50)

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 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	415	<div> <div>6%</div> <div> <div></div> <div>88%</div> <div>10%</div> <div>..</div> </div> </div>
1	B	415	<div> <div>7%</div> <div> <div></div> <div>88%</div> <div>10%</div> <div>..</div> </div> </div>
1	D	415	<div> <div>5%</div> <div> <div></div> <div>89%</div> <div>9%</div> <div>.</div> </div> </div>
1	F	415	<div> <div>4%</div> <div> <div></div> <div>89%</div> <div>9%</div> <div>..</div> </div> </div>
2	C	118	<div> <div>19%</div> <div> <div></div> <div>77%</div> <div>13%</div> <div>.</div> <div>9%</div> </div> </div>
2	E	118	<div> <div>10%</div> <div> <div></div> <div>78%</div> <div>12%</div> <div>.</div> <div>9%</div> </div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	G	118	
2	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
3	ACT	C	5015	-	-	X	-
3	ACT	E	5016	-	-	X	-
3	ACT	G	5017	-	-	X	-
3	ACT	H	5011	-	-	X	-
4	SO4	D	6007	-	-	-	X
4	SO4	F	6005	-	-	-	X
5	GOL	A	4663	-	-	X	X
5	GOL	B	4665	-	-	-	X
5	GOL	F	4666	-	-	-	X
5	GOL	F	4667	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 18839 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	412	Total	C	N	O	S	0	5	0
			3127	1965	554	601	7			
1	B	410	Total	C	N	O	S	0	5	0
			3111	1954	549	602	6			
1	D	410	Total	C	N	O	S	0	4	0
			3108	1955	549	598	6			
1	F	410	Total	C	N	O	S	0	11	0
			3135	1972	551	605	7			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	23	MET	-	INITIATING MET	UNP P0A855
A	432	HIS	-	EXPRESSION TAG	UNP P0A855
A	433	HIS	-	EXPRESSION TAG	UNP P0A855
A	434	HIS	-	EXPRESSION TAG	UNP P0A855
A	436	HIS	-	EXPRESSION TAG	UNP P0A855
A	437	HIS	-	EXPRESSION TAG	UNP P0A855
A	438	HIS	-	EXPRESSION TAG	UNP P0A855
B	23	MET	-	INITIATING MET	UNP P0A855
B	432	HIS	-	EXPRESSION TAG	UNP P0A855
B	433	HIS	-	EXPRESSION TAG	UNP P0A855
B	434	HIS	-	EXPRESSION TAG	UNP P0A855
B	436	HIS	-	EXPRESSION TAG	UNP P0A855
B	437	HIS	-	EXPRESSION TAG	UNP P0A855
B	438	HIS	-	EXPRESSION TAG	UNP P0A855
D	23	MET	-	INITIATING MET	UNP P0A855
D	432	HIS	-	EXPRESSION TAG	UNP P0A855
D	433	HIS	-	EXPRESSION TAG	UNP P0A855
D	434	HIS	-	EXPRESSION TAG	UNP P0A855
D	436	HIS	-	EXPRESSION TAG	UNP P0A855
D	437	HIS	-	EXPRESSION TAG	UNP P0A855
D	438	HIS	-	EXPRESSION TAG	UNP P0A855

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
F	23	MET	-	INITIATING MET	UNP P0A855
F	432	HIS	-	EXPRESSION TAG	UNP P0A855
F	433	HIS	-	EXPRESSION TAG	UNP P0A855
F	434	HIS	-	EXPRESSION TAG	UNP P0A855
F	436	HIS	-	EXPRESSION TAG	UNP P0A855
F	437	HIS	-	EXPRESSION TAG	UNP P0A855
F	438	HIS	-	EXPRESSION TAG	UNP P0A855

- Molecule 2 is a protein called Peptidoglycan-associated lipoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	108	Total	C	N	O	S	0	3	0
			868	546	153	167	2			
2	C	107	Total	C	N	O	S	0	2	0
			856	539	151	164	2			
2	E	107	Total	C	N	O	S	0	0	0
			849	533	151	163	2			
2	G	108	Total	C	N	O	S	0	4	0
			873	550	153	167	3			

There are 36 discrepancies between the modelled and reference sequences:

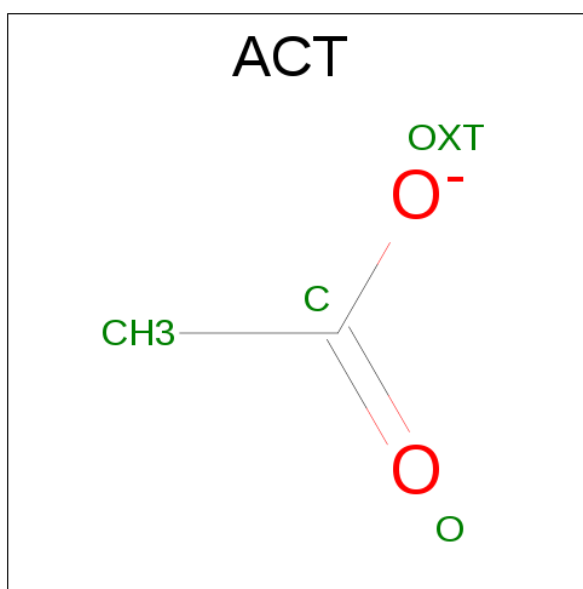
Chain	Residue	Modelled	Actual	Comment	Reference
H	64	MET	-	INITIATING MET	UNP P0A912
H	174	LEU	-	CLONING ARTIFACT	UNP P0A912
H	175	GLU	-	CLONING ARTIFACT	UNP P0A912
H	176	HIS	-	EXPRESSION TAG	UNP P0A912
H	177	HIS	-	EXPRESSION TAG	UNP P0A912
H	178	HIS	-	EXPRESSION TAG	UNP P0A912
H	179	HIS	-	EXPRESSION TAG	UNP P0A912
H	180	HIS	-	EXPRESSION TAG	UNP P0A912
H	181	HIS	-	EXPRESSION TAG	UNP P0A912
E	64	MET	-	INITIATING MET	UNP P0A912
E	174	LEU	-	CLONING ARTIFACT	UNP P0A912
E	175	GLU	-	CLONING ARTIFACT	UNP P0A912
E	176	HIS	-	EXPRESSION TAG	UNP P0A912
E	177	HIS	-	EXPRESSION TAG	UNP P0A912
E	178	HIS	-	EXPRESSION TAG	UNP P0A912
E	179	HIS	-	EXPRESSION TAG	UNP P0A912
E	180	HIS	-	EXPRESSION TAG	UNP P0A912
E	181	HIS	-	EXPRESSION TAG	UNP P0A912
C	64	MET	-	INITIATING MET	UNP P0A912

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	174	LEU	-	CLONING ARTIFACT	UNP P0A912
C	175	GLU	-	CLONING ARTIFACT	UNP P0A912
C	176	HIS	-	EXPRESSION TAG	UNP P0A912
C	177	HIS	-	EXPRESSION TAG	UNP P0A912
C	178	HIS	-	EXPRESSION TAG	UNP P0A912
C	179	HIS	-	EXPRESSION TAG	UNP P0A912
C	180	HIS	-	EXPRESSION TAG	UNP P0A912
C	181	HIS	-	EXPRESSION TAG	UNP P0A912
G	64	MET	-	INITIATING MET	UNP P0A912
G	174	LEU	-	CLONING ARTIFACT	UNP P0A912
G	175	GLU	-	CLONING ARTIFACT	UNP P0A912
G	176	HIS	-	EXPRESSION TAG	UNP P0A912
G	177	HIS	-	EXPRESSION TAG	UNP P0A912
G	178	HIS	-	EXPRESSION TAG	UNP P0A912
G	179	HIS	-	EXPRESSION TAG	UNP P0A912
G	180	HIS	-	EXPRESSION TAG	UNP P0A912
G	181	HIS	-	EXPRESSION TAG	UNP P0A912

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



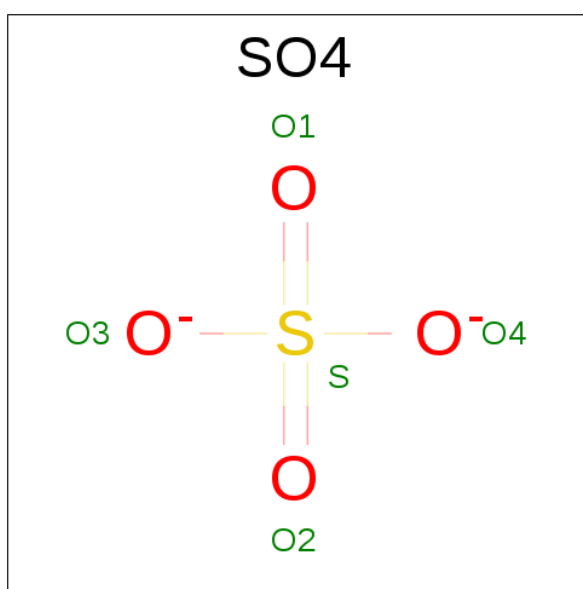
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	H	1	Total C O 4 2 2	0	0
3	B	1	Total C O 4 2 2	0	0
3	F	1	Total C O 4 2 2	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		
3	E	1	Total	C	O	0	0
			4	2	2		
3	G	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	605	Total	O	0	0
			605	605		
6	B	564	Total	O	0	0
			564	564		
6	C	109	Total	O	0	0
			109	109		
6	D	604	Total	O	0	0
			604	604		
6	E	142	Total	O	0	0
			142	142		

Continued on next page...

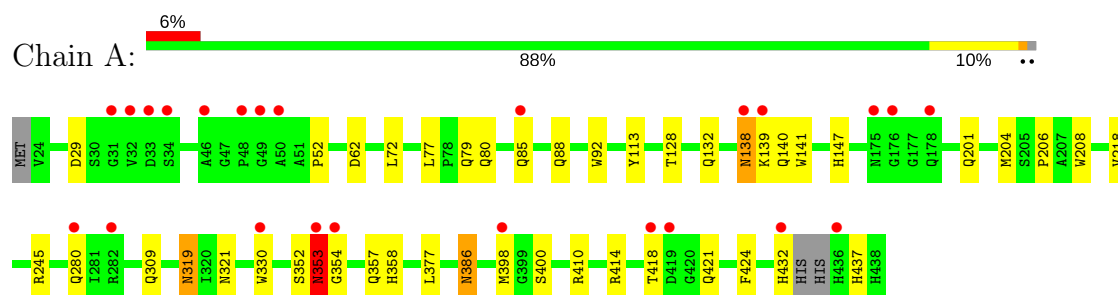
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	F	582	Total 582	O 582	0	0
6	G	98	Total 98	O 98	0	0
6	H	108	Total 108	O 108	0	0

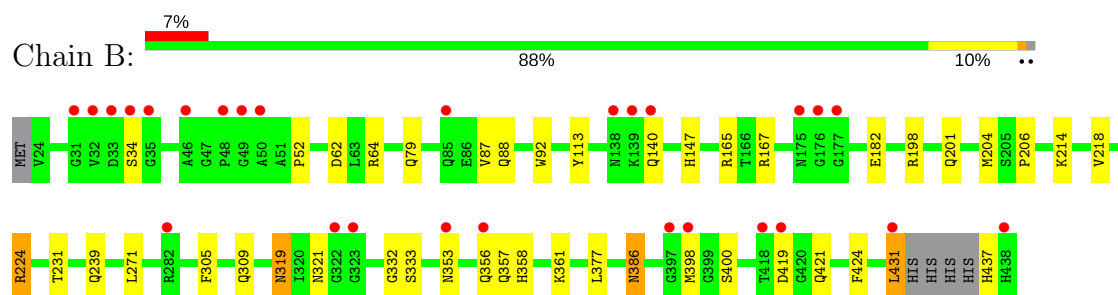
3 Residue-property plots [i](#)

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.

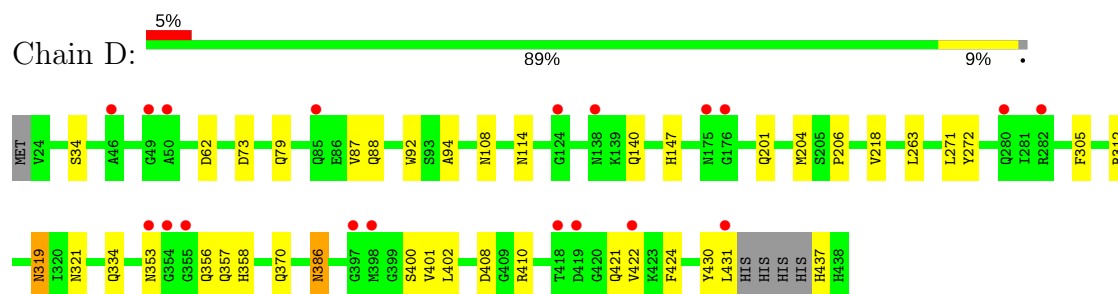
• Molecule 1: Protein tolB



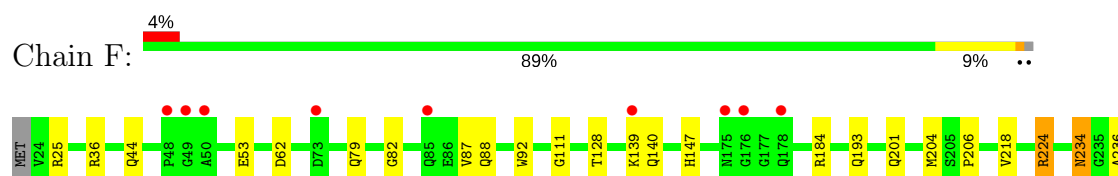
• Molecule 1: Protein tolB



• Molecule 1: Protein tolB

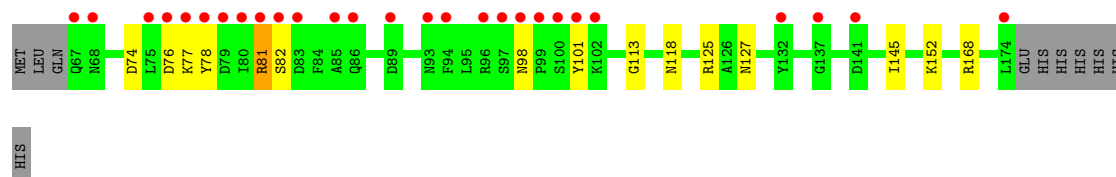
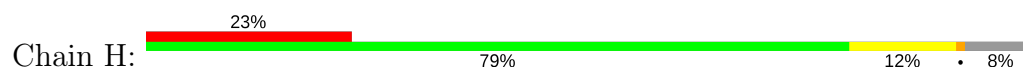


• Molecule 1: Protein tolB

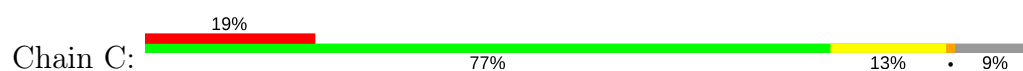




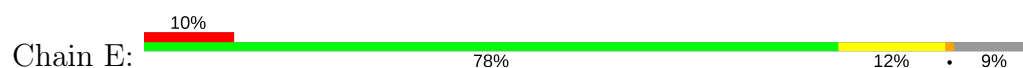
• Molecule 2: Peptidoglycan-associated lipoprotein



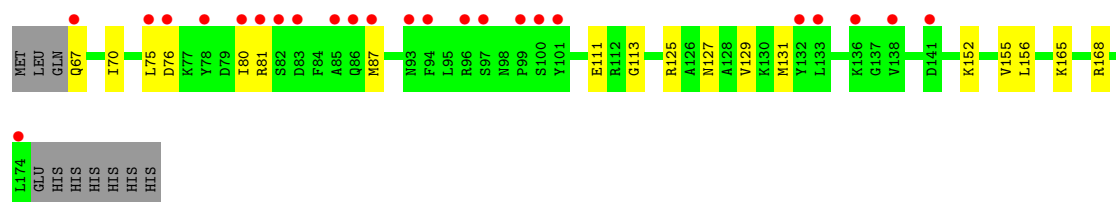
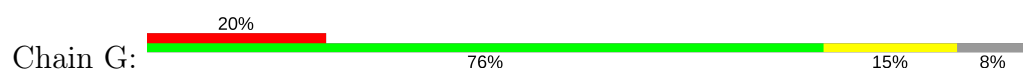
• Molecule 2: Peptidoglycan-associated lipoprotein



• Molecule 2: Peptidoglycan-associated lipoprotein



• Molecule 2: Peptidoglycan-associated lipoprotein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	74.85Å 89.05Å 91.05Å 87.15° 89.62° 68.81°	Depositor
Resolution (Å)	38.32 – 1.50 38.32 – 1.50	Depositor EDS
% Data completeness (in resolution range)	95.4 (38.32-1.50) 93.9 (38.32-1.50)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.68 (at 1.50Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.180 , 0.213 0.179 , 0.212	Depositor DCC
R_{free} test set	16823 reflections (5.30%)	DCC
Wilson B-factor (Å ²)	13.0	Xtriage
Anisotropy	0.051	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 59.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.000 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	18839	wwPDB-VP
Average B, all atoms (Å ²)	17.0	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 42.71 % 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 1.9595e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

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	0.47	0/3219	0.64	1/4385 (0.0%)
1	B	0.45	0/3201	0.61	0/4360
1	D	0.45	0/3195	0.63	1/4354 (0.0%)
1	F	0.47	0/3243	0.63	0/4417
2	C	0.40	0/878	0.55	0/1185
2	E	0.43	0/865	0.56	0/1167
2	G	0.42	0/901	0.55	0/1215
2	H	0.42	0/893	0.58	0/1205
All	All	0.45	0/16395	0.62	2/22288 (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

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	354	GLY	N-CA-C	-5.48	99.39	113.10
1	D	73	ASP	CB-CG-OD1	5.15	122.94	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	353	ASN	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	3127	0	3038	41	0
1	B	3111	0	3027	47	0
1	D	3108	0	3031	41	0
1	F	3135	0	3070	38	0
2	C	856	0	842	14	0
2	E	849	0	828	14	0
2	G	873	0	864	15	0
2	H	868	0	855	13	0
3	A	4	0	3	1	0
3	B	4	0	3	1	0
3	C	4	0	3	4	0
3	E	4	0	3	4	0
3	F	4	0	3	1	0
3	G	4	0	3	6	0
3	H	4	0	3	4	0
4	A	5	0	0	0	0
4	B	5	0	0	0	0
4	D	5	0	0	0	0
4	F	15	0	0	0	0
5	A	12	0	16	4	0
5	B	12	0	16	0	0
5	D	6	0	8	0	0
5	F	12	0	16	2	0
6	A	605	0	0	8	0
6	B	564	0	0	11	0
6	C	109	0	0	1	0
6	D	604	0	0	6	0
6	E	142	0	0	2	0
6	F	582	0	0	8	0
6	G	98	0	0	0	0
6	H	108	0	0	0	0
All	All	18839	0	15632	206	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 7.

The worst 5 of 206 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)
2:G:125:ARG:HH22	3:G:5017:ACT:H1	1.07	1.14
5:F:4667:GOL:H12	6:F:6587:HOH:O	1.50	1.09
2:E:125:ARG:HH22	3:E:5016:ACT:H1	1.11	1.08
2:H:125:ARG:HH22	3:H:5011:ACT:H1	1.03	1.07
1:A:113:TYR:HE1	1:A:139:LYS:HG2	1.17	1.03

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	413/415 (100%)	408 (99%)	4 (1%)	1 (0%)	51	24
1	B	411/415 (99%)	401 (98%)	9 (2%)	1 (0%)	51	24
1	D	410/415 (99%)	406 (99%)	4 (1%)	0	100	100
1	F	417/415 (100%)	413 (99%)	4 (1%)	0	100	100
2	C	107/118 (91%)	106 (99%)	1 (1%)	0	100	100
2	E	105/118 (89%)	104 (99%)	1 (1%)	0	100	100
2	G	110/118 (93%)	109 (99%)	1 (1%)	0	100	100
2	H	109/118 (92%)	107 (98%)	2 (2%)	0	100	100
All	All	2082/2132 (98%)	2054 (99%)	26 (1%)	2 (0%)	55	26

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	34	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	353	ASN

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	334/333 (100%)	326 (98%)	8 (2%)	54	21
1	B	333/333 (100%)	327 (98%)	6 (2%)	64	33
1	D	332/333 (100%)	330 (99%)	2 (1%)	89	76
1	F	339/333 (102%)	333 (98%)	6 (2%)	64	33
2	C	91/100 (91%)	87 (96%)	4 (4%)	33	6
2	E	89/100 (89%)	85 (96%)	4 (4%)	32	6
2	G	94/100 (94%)	90 (96%)	4 (4%)	33	6
2	H	93/100 (93%)	88 (95%)	5 (5%)	26	4
All	All	1705/1732 (98%)	1666 (98%)	39 (2%)	56	23

5 of 39 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	398	MET
2	C	145	ILE
2	G	87[A]	MET
1	B	431	LEU
2	C	78	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 78 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	421	GLN
1	D	201	GLN
1	F	386	ASN
1	B	437	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	79	GLN

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 ⓘ

20 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	$\# Z > 2$
5	GOL	A	4662	-	5,5,5	0.36	0	5,5,5	0.36	0
5	GOL	A	4663	-	5,5,5	0.22	0	5,5,5	0.56	0
3	ACT	A	5014	-	1,3,3	0.94	0	0,3,3	0.00	-
4	SO4	A	6002	-	4,4,4	0.10	0	6,6,6	0.28	0
5	GOL	B	4664	-	5,5,5	0.37	0	5,5,5	0.24	0
5	GOL	B	4665	-	5,5,5	0.46	0	5,5,5	0.67	0
3	ACT	B	5012	-	1,3,3	1.14	0	0,3,3	0.00	-
4	SO4	B	6004	-	4,4,4	0.10	0	6,6,6	0.24	0
3	ACT	C	5015	-	1,3,3	0.66	0	0,3,3	0.00	-
5	GOL	D	4668	-	5,5,5	0.32	0	5,5,5	0.27	0
4	SO4	D	6007	-	4,4,4	0.09	0	6,6,6	0.39	0
3	ACT	E	5016	-	1,3,3	0.06	0	0,3,3	0.00	-
5	GOL	F	4666	-	5,5,5	0.32	0	5,5,5	0.41	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	GOL	F	4667	-	5,5,5	0.26	0	5,5,5	0.63	0
3	ACT	F	5013	-	1,3,3	1.10	0	0,3,3	0.00	-
4	SO4	F	6005	-	4,4,4	0.11	0	6,6,6	0.33	0
4	SO4	F	6006	-	4,4,4	0.12	0	6,6,6	0.16	0
4	SO4	F	6008	-	4,4,4	0.15	0	6,6,6	0.10	0
3	ACT	G	5017	-	1,3,3	0.17	0	0,3,3	0.00	-
3	ACT	H	5011	-	1,3,3	0.53	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
5	GOL	A	4662	-	-	0/4/4/4	0/0/0/0
5	GOL	A	4663	-	-	0/4/4/4	0/0/0/0
3	ACT	A	5014	-	-	0/0/0/0	0/0/0/0
4	SO4	A	6002	-	-	0/0/0/0	0/0/0/0
5	GOL	B	4664	-	-	0/4/4/4	0/0/0/0
5	GOL	B	4665	-	-	0/4/4/4	0/0/0/0
3	ACT	B	5012	-	-	0/0/0/0	0/0/0/0
4	SO4	B	6004	-	-	0/0/0/0	0/0/0/0
3	ACT	C	5015	-	-	0/0/0/0	0/0/0/0
5	GOL	D	4668	-	-	0/4/4/4	0/0/0/0
4	SO4	D	6007	-	-	0/0/0/0	0/0/0/0
3	ACT	E	5016	-	-	0/0/0/0	0/0/0/0
5	GOL	F	4666	-	-	0/4/4/4	0/0/0/0
5	GOL	F	4667	-	-	0/4/4/4	0/0/0/0
3	ACT	F	5013	-	-	0/0/0/0	0/0/0/0
4	SO4	F	6005	-	-	0/0/0/0	0/0/0/0
4	SO4	F	6006	-	-	0/0/0/0	0/0/0/0
4	SO4	F	6008	-	-	0/0/0/0	0/0/0/0
3	ACT	G	5017	-	-	0/0/0/0	0/0/0/0
3	ACT	H	5011	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	4663	GOL	4	0
3	A	5014	ACT	1	0
3	B	5012	ACT	1	0
3	C	5015	ACT	4	0
3	E	5016	ACT	4	0
5	F	4667	GOL	2	0
3	F	5013	ACT	1	0
3	G	5017	ACT	6	0
3	H	5011	ACT	4	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	412/415 (99%)	0.14	24 (5%) 24 27	7, 11, 23, 32	0
1	B	410/415 (98%)	0.27	27 (6%) 19 22	7, 13, 25, 34	0
1	D	410/415 (98%)	0.14	19 (4%) 33 37	6, 12, 24, 29	0
1	F	410/415 (98%)	0.16	17 (4%) 38 42	7, 12, 23, 28	0
2	C	107/118 (90%)	1.00	23 (21%) 1 1	7, 21, 40, 41	0
2	E	107/118 (90%)	0.58	12 (11%) 6 7	7, 17, 32, 38	0
2	G	108/118 (91%)	1.02	24 (22%) 1 1	7, 19, 38, 42	0
2	H	108/118 (91%)	0.93	27 (25%) 1 1	6, 18, 35, 38	0
All	All	2072/2132 (97%)	0.33	173 (8%) 12 14	6, 13, 29, 42	0

The worst 5 of 173 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	G	78	TYR	8.6
2	E	75	LEU	8.4
1	B	398	MET	7.5
1	B	34	SER	7.2
2	E	76	ASP	7.2

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(Å ²)	Q<0.9
5	GOL	B	4665	6/6	0.90	0.37	15.37	2,10,11,13	6
5	GOL	F	4667	6/6	0.90	0.33	9.90	2,5,7,11	6
5	GOL	A	4663	6/6	0.79	0.28	9.52	3,6,10,14	6
4	SO4	F	6005	5/5	0.94	0.22	2.88	10,11,13,13	5
4	SO4	D	6007	5/5	0.94	0.20	2.75	11,12,15,16	5
5	GOL	F	4666	6/6	0.96	0.13	2.22	11,12,13,13	0
4	SO4	B	6004	5/5	0.96	0.18	1.67	13,15,17,18	5
4	SO4	A	6002	5/5	0.95	0.21	1.57	13,14,16,17	5
4	SO4	F	6008	5/5	0.94	0.14	1.37	20,21,22,23	5
3	ACT	H	5011	4/4	0.87	0.17	0.67	14,17,18,19	0
3	ACT	E	5016	4/4	0.88	0.17	0.60	15,16,17,19	0
3	ACT	G	5017	4/4	0.90	0.16	0.57	16,18,18,19	0
3	ACT	C	5015	4/4	0.84	0.15	0.25	22,23,24,24	0
4	SO4	F	6006	5/5	0.93	0.13	0.03	26,26,27,27	5
3	ACT	A	5014	4/4	0.91	0.11	-0.27	28,29,29,29	0
3	ACT	B	5012	4/4	0.93	0.10	-0.43	38,38,38,38	0
5	GOL	A	4662	6/6	0.98	0.09	-0.58	10,13,14,14	0
5	GOL	B	4664	6/6	0.96	0.08	-1.45	14,14,14,15	0
5	GOL	D	4668	6/6	0.97	0.08	-1.51	11,11,13,13	0
3	ACT	F	5013	4/4	0.86	0.12	-	30,30,30,30	0

6.5 Other polymers [i](#)

There are no such residues in this entry.