Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:18 AM GMT

PDB ID	:	3OEI
Title	:	Crystal structure of Mycobacterium tuberculosis RelJK (Rv3357-Rv3358-RelBE3)
Authors	:	Miallau, L.; Cascio, D.; Eisenberg, D.; TB Structural Genomics Consortium (TBSGC)
Deposited on	:	2010-08-12
Resolution	:	2.15 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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 ①) were used in the production of this report:

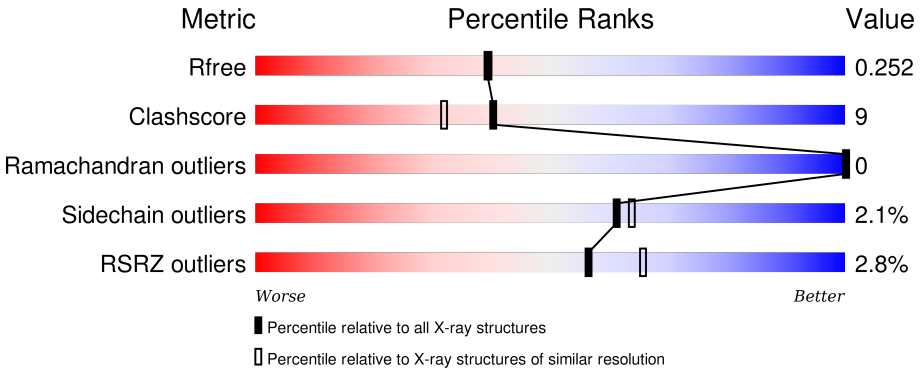
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.15 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	1693 (2.16-2.12)
Clashscore	102246	1824 (2.16-2.12)
Ramachandran outliers	100387	1798 (2.16-2.12)
Sidechain outliers	100360	1798 (2.16-2.12)
RSRZ outliers	91569	1699 (2.16-2.12)

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 <=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	98	65% 23% 11%
1	B	98	% 83% 10% 7%
1	I	98	2% 77% 8% 15%
1	J	98	% 74% 13% 12%
1	M	98	6% 70% 16% 13%

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Mol	Chain	Length	Quality of chain
1	N	98	4% 69% 15% 15%
2	C	96	% 74% 15% 11%
2	D	96	% 77% 10% • 11%
2	G	96	% 69% 17% • 14%
2	H	96	2% 68% 20% • 11%
2	K	96	2% 69% 18% • 13%
2	L	96	% 67% 20% • 13%
2	O	96	8% 63% 22% • 14%
2	P	96	4% 61% 25% • 13%
3	E	98	4% 71% 12% 16%
3	F	98	76% 12% 12%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 11529 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 RelJ (Antitoxin Rv3357).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	87	Total	C	N	O	S	0	1	0
			691	423	130	135	3			
1	B	91	Total	C	N	O	S	0	0	0
			713	435	131	143	4			
1	I	83	Total	C	N	O	S	0	0	0
			658	404	121	130	3			
1	J	86	Total	C	N	O	S	0	1	0
			684	419	126	136	3			
1	M	85	Total	C	N	O	S	0	0	0
			673	413	125	132	3			
1	N	83	Total	C	N	O	S	0	0	0
			657	404	121	129	3			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	92	MET	-	expression tag	UNP P65067
A	93	GLN	-	expression tag	UNP P65067
A	94	ALA	-	expression tag	UNP P65067
A	95	GLY	-	expression tag	UNP P65067
A	96	PRO	-	expression tag	UNP P65067
A	97	ALA	-	expression tag	UNP P65067
A	98	LEU	-	expression tag	UNP P65067
B	92	MET	-	expression tag	UNP P65067
B	93	GLN	-	expression tag	UNP P65067
B	94	ALA	-	expression tag	UNP P65067
B	95	GLY	-	expression tag	UNP P65067
B	96	PRO	-	expression tag	UNP P65067
B	97	ALA	-	expression tag	UNP P65067
B	98	LEU	-	expression tag	UNP P65067
I	92	MET	-	expression tag	UNP P65067
I	93	GLN	-	expression tag	UNP P65067
I	94	ALA	-	expression tag	UNP P65067

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Chain	Residue	Modelled	Actual	Comment	Reference
I	95	GLY	-	expression tag	UNP P65067
I	96	PRO	-	expression tag	UNP P65067
I	97	ALA	-	expression tag	UNP P65067
I	98	LEU	-	expression tag	UNP P65067
J	92	MET	-	expression tag	UNP P65067
J	93	GLN	-	expression tag	UNP P65067
J	94	ALA	-	expression tag	UNP P65067
J	95	GLY	-	expression tag	UNP P65067
J	96	PRO	-	expression tag	UNP P65067
J	97	ALA	-	expression tag	UNP P65067
J	98	LEU	-	expression tag	UNP P65067
M	92	MET	-	expression tag	UNP P65067
M	93	GLN	-	expression tag	UNP P65067
M	94	ALA	-	expression tag	UNP P65067
M	95	GLY	-	expression tag	UNP P65067
M	96	PRO	-	expression tag	UNP P65067
M	97	ALA	-	expression tag	UNP P65067
M	98	LEU	-	expression tag	UNP P65067
N	92	MET	-	expression tag	UNP P65067
N	93	GLN	-	expression tag	UNP P65067
N	94	ALA	-	expression tag	UNP P65067
N	95	GLY	-	expression tag	UNP P65067
N	96	PRO	-	expression tag	UNP P65067
N	97	ALA	-	expression tag	UNP P65067
N	98	LEU	-	expression tag	UNP P65067

- Molecule 2 is a protein called RelK (Toxin Rv3358).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	85	Total	C	N	O	S	0	1	0
			721	457	134	129	1			
2	D	85	Total	C	N	O	S	0	1	0
			721	457	134	129	1			
2	G	83	Total	C	N	O	S	0	0	0
			695	441	126	127	1			
2	H	85	Total	C	N	O	S	0	0	0
			713	452	131	129	1			
2	K	84	Total	C	N	O	S	0	2	0
			719	455	133	130	1			
2	L	84	Total	C	N	O	S	0	1	0
			714	452	133	128	1			
2	O	83	Total	C	N	O	S	0	0	0
			696	441	126	128	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	84	Total	C	N	O	S	0	0	0
			706	447	130	128	1			

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-10	HIS	-	expression tag	UNP P64528
C	-9	HIS	-	expression tag	UNP P64528
C	-8	HIS	-	expression tag	UNP P64528
C	-7	HIS	-	expression tag	UNP P64528
C	-6	HIS	-	expression tag	UNP P64528
C	-5	HIS	-	expression tag	UNP P64528
C	-4	ASP	-	expression tag	UNP P64528
C	-3	ASP	-	expression tag	UNP P64528
C	-2	ASP	-	expression tag	UNP P64528
C	-1	ASP	-	expression tag	UNP P64528
C	0	LYS	-	expression tag	UNP P64528
C	1	VAL	-	expression tag	UNP P64528
D	-10	HIS	-	expression tag	UNP P64528
D	-9	HIS	-	expression tag	UNP P64528
D	-8	HIS	-	expression tag	UNP P64528
D	-7	HIS	-	expression tag	UNP P64528
D	-6	HIS	-	expression tag	UNP P64528
D	-5	HIS	-	expression tag	UNP P64528
D	-4	ASP	-	expression tag	UNP P64528
D	-3	ASP	-	expression tag	UNP P64528
D	-2	ASP	-	expression tag	UNP P64528
D	-1	ASP	-	expression tag	UNP P64528
D	0	LYS	-	expression tag	UNP P64528
D	1	VAL	-	expression tag	UNP P64528
G	-10	HIS	-	expression tag	UNP P64528
G	-9	HIS	-	expression tag	UNP P64528
G	-8	HIS	-	expression tag	UNP P64528
G	-7	HIS	-	expression tag	UNP P64528
G	-6	HIS	-	expression tag	UNP P64528
G	-5	HIS	-	expression tag	UNP P64528
G	-4	ASP	-	expression tag	UNP P64528
G	-3	ASP	-	expression tag	UNP P64528
G	-2	ASP	-	expression tag	UNP P64528
G	-1	ASP	-	expression tag	UNP P64528
G	0	LYS	-	expression tag	UNP P64528
G	1	VAL	-	expression tag	UNP P64528

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Chain	Residue	Modelled	Actual	Comment	Reference
H	-10	HIS	-	expression tag	UNP P64528
H	-9	HIS	-	expression tag	UNP P64528
H	-8	HIS	-	expression tag	UNP P64528
H	-7	HIS	-	expression tag	UNP P64528
H	-6	HIS	-	expression tag	UNP P64528
H	-5	HIS	-	expression tag	UNP P64528
H	-4	ASP	-	expression tag	UNP P64528
H	-3	ASP	-	expression tag	UNP P64528
H	-2	ASP	-	expression tag	UNP P64528
H	-1	ASP	-	expression tag	UNP P64528
H	0	LYS	-	expression tag	UNP P64528
H	1	VAL	-	expression tag	UNP P64528
K	-10	HIS	-	expression tag	UNP P64528
K	-9	HIS	-	expression tag	UNP P64528
K	-8	HIS	-	expression tag	UNP P64528
K	-7	HIS	-	expression tag	UNP P64528
K	-6	HIS	-	expression tag	UNP P64528
K	-5	HIS	-	expression tag	UNP P64528
K	-4	ASP	-	expression tag	UNP P64528
K	-3	ASP	-	expression tag	UNP P64528
K	-2	ASP	-	expression tag	UNP P64528
K	-1	ASP	-	expression tag	UNP P64528
K	0	LYS	-	expression tag	UNP P64528
K	1	VAL	-	expression tag	UNP P64528
L	-10	HIS	-	expression tag	UNP P64528
L	-9	HIS	-	expression tag	UNP P64528
L	-8	HIS	-	expression tag	UNP P64528
L	-7	HIS	-	expression tag	UNP P64528
L	-6	HIS	-	expression tag	UNP P64528
L	-5	HIS	-	expression tag	UNP P64528
L	-4	ASP	-	expression tag	UNP P64528
L	-3	ASP	-	expression tag	UNP P64528
L	-2	ASP	-	expression tag	UNP P64528
L	-1	ASP	-	expression tag	UNP P64528
L	0	LYS	-	expression tag	UNP P64528
L	1	VAL	-	expression tag	UNP P64528
O	-10	HIS	-	expression tag	UNP P64528
O	-9	HIS	-	expression tag	UNP P64528
O	-8	HIS	-	expression tag	UNP P64528
O	-7	HIS	-	expression tag	UNP P64528
O	-6	HIS	-	expression tag	UNP P64528
O	-5	HIS	-	expression tag	UNP P64528

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Chain	Residue	Modelled	Actual	Comment	Reference
O	-4	ASP	-	expression tag	UNP P64528
O	-3	ASP	-	expression tag	UNP P64528
O	-2	ASP	-	expression tag	UNP P64528
O	-1	ASP	-	expression tag	UNP P64528
O	0	LYS	-	expression tag	UNP P64528
O	1	VAL	-	expression tag	UNP P64528
P	-10	HIS	-	expression tag	UNP P64528
P	-9	HIS	-	expression tag	UNP P64528
P	-8	HIS	-	expression tag	UNP P64528
P	-7	HIS	-	expression tag	UNP P64528
P	-6	HIS	-	expression tag	UNP P64528
P	-5	HIS	-	expression tag	UNP P64528
P	-4	ASP	-	expression tag	UNP P64528
P	-3	ASP	-	expression tag	UNP P64528
P	-2	ASP	-	expression tag	UNP P64528
P	-1	ASP	-	expression tag	UNP P64528
P	0	LYS	-	expression tag	UNP P64528
P	1	VAL	-	expression tag	UNP P64528

- Molecule 3 is a protein called RelJ (Antitoxin Rv3357).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	82	Total	C	N	O	S	0	0	0
			655	403	120	129	3			
3	F	86	Total	C	N	O	S	0	0	0
			680	417	126	134	3			

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	92	MET	-	expression tag	UNP P65067
E	93	GLN	-	expression tag	UNP P65067
E	94	ALA	-	expression tag	UNP P65067
E	95	GLY	-	expression tag	UNP P65067
E	96	PRO	-	expression tag	UNP P65067
E	97	ALA	-	expression tag	UNP P65067
E	98	LEU	-	expression tag	UNP P65067
F	92	MET	-	expression tag	UNP P65067
F	93	GLN	-	expression tag	UNP P65067
F	94	ALA	-	expression tag	UNP P65067
F	95	GLY	-	expression tag	UNP P65067
F	96	PRO	-	expression tag	UNP P65067

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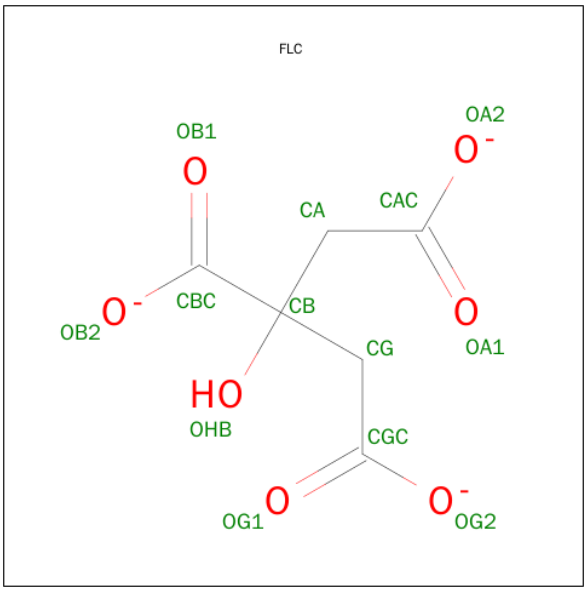
Chain	Residue	Modelled	Actual	Comment	Reference
F	97	ALA	-	expression tag	UNP P65067
F	98	LEU	-	expression tag	UNP P65067

- Molecule 4 is CITRATE ANION (three-letter code: FLC) (formula: $C_6H_5O_7$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	1	Total C O 13 6 7	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	41	Total O 41 41	0	0
5	B	38	Total O 38 38	0	0
5	C	43	Total O 43 43	0	0
5	D	31	Total O 31 31	0	0
5	E	32	Total O 32 32	0	0
5	F	37	Total O 37 37	0	0
5	G	22	Total O 22 22	0	0

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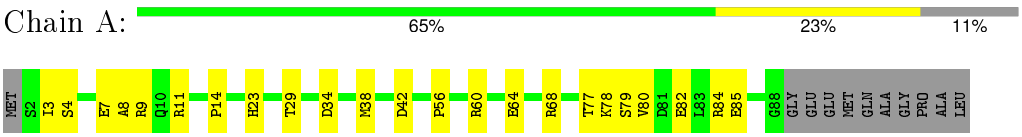
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	H	20	Total O 20 20	0	0
5	I	24	Total O 24 24	0	0
5	J	28	Total O 28 28	0	0
5	K	30	Total O 30 30	0	0
5	L	29	Total O 29 29	0	0
5	M	13	Total O 13 13	0	0
5	N	17	Total O 17 17	0	0
5	O	8	Total O 8 8	0	0
5	P	7	Total O 7 7	0	0

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 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.

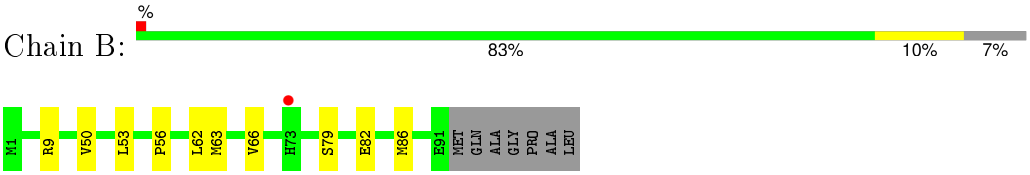
- Molecule 1: RelJ (Antitoxin Rv3357)

Chain A:



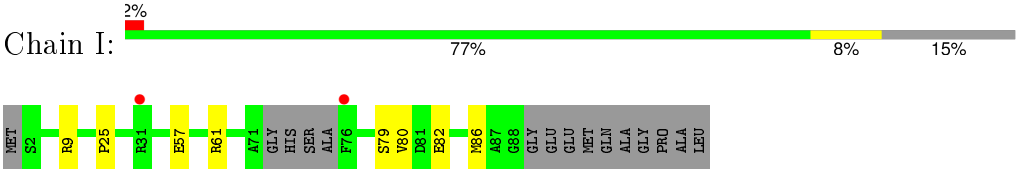
- Molecule 1: RelJ (Antitoxin Rv3357)

Chain B:



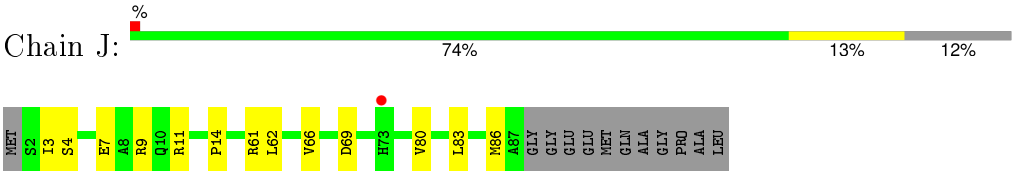
- Molecule 1: RelJ (Antitoxin Rv3357)

Chain I:



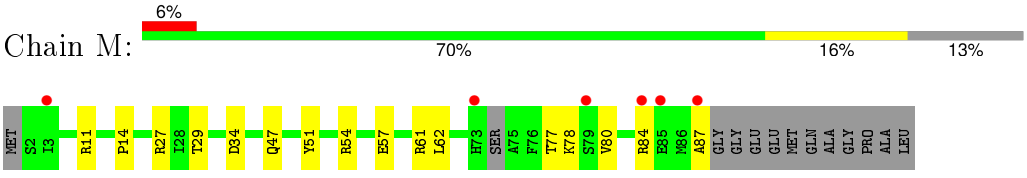
- Molecule 1: RelJ (Antitoxin Rv3357)

Chain J:



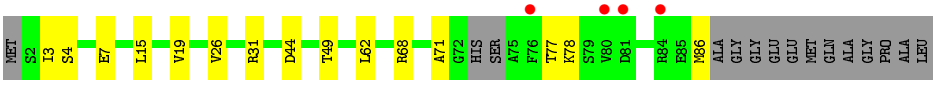
- Molecule 1: RelJ (Antitoxin Rv3357)

Chain M:

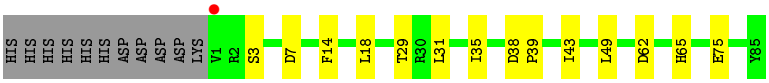


- Molecule 1: RelJ (Antitoxin Rv3357)

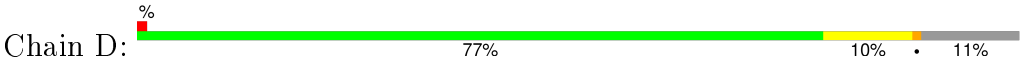
Chain N:

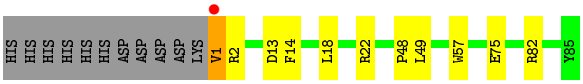


• Molecule 2: RelK (Toxin Rv3358)

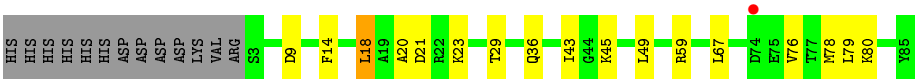


• Molecule 2: RelK (Toxin Rv3358)

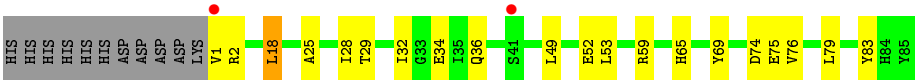




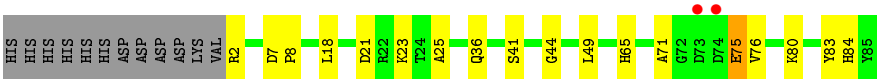
• Molecule 2: RelK (Toxin Rv3358)



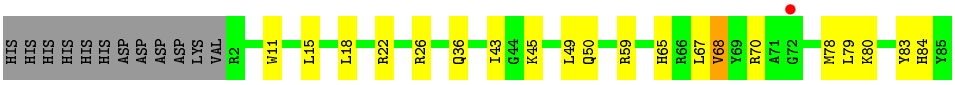
• Molecule 2: RelK (Toxin Rv3358)



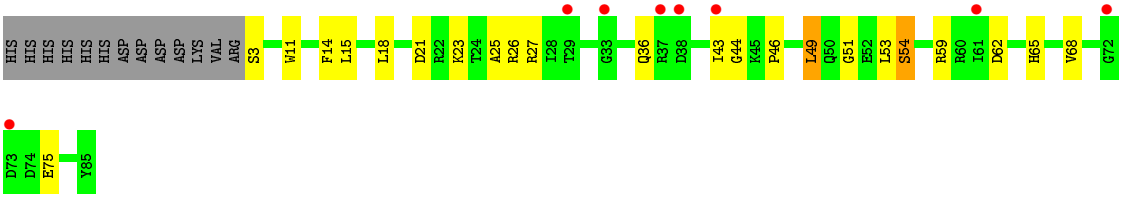
• Molecule 2: RelK (Toxin Rv3358)



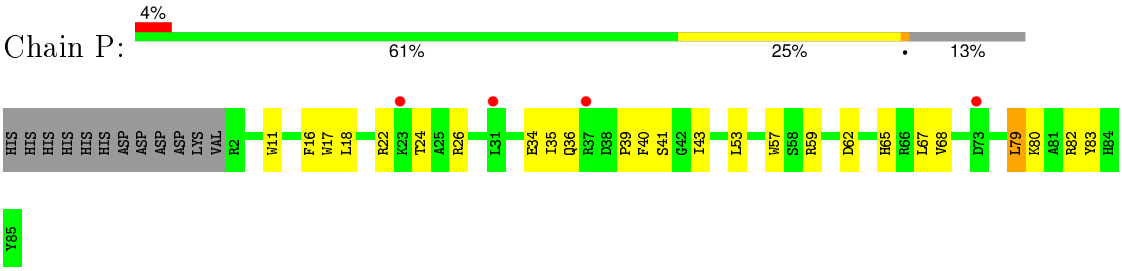
• Molecule 2: RelK (Toxin Rv3358)



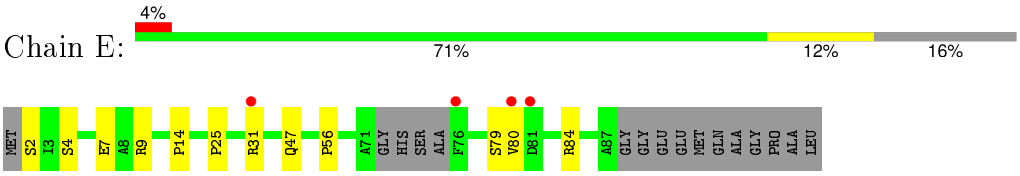
• Molecule 2: RelK (Toxin Rv3358)



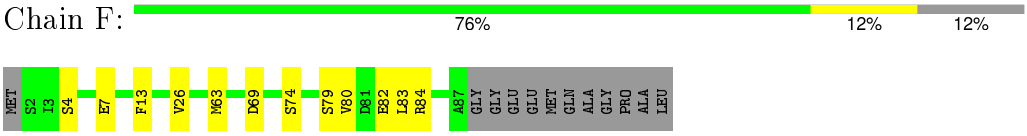
• Molecule 2: RelK (Toxin Rv3358)



• Molecule 3: RelJ (Antitoxin Rv3357)



• Molecule 3: RelJ (Antitoxin Rv3357)



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	42.22Å 187.51Å 113.88Å 90.00° 94.46° 90.00°	Depositor
Resolution (Å)	40.51 – 2.15 40.51 – 2.15	Depositor EDS
% Data completeness (in resolution range)	85.6 (40.51-2.15) 89.6 (40.51-2.15)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.35 (at 2.14Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_403)	Depositor
R, R_{free}	0.203 , 0.256 0.206 , 0.252	Depositor DCC
R_{free} test set	4303 reflections (5.25%)	DCC
Wilson B-factor (Å^2)	33.5	Xtriage
Anisotropy	0.353	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 46.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Outliers	0 of 86230 reflections	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	11529	wwPDB-VP
Average B, all atoms (Å^2)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.69% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: MLZ, FLC

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	0.45	0/704	0.58	0/950
1	B	0.45	0/723	0.55	0/975
1	I	0.40	0/666	0.55	0/898
1	J	0.40	0/697	0.50	0/942
1	M	0.36	0/682	0.53	0/920
1	N	0.36	0/665	0.50	0/897
2	C	0.42	0/743	0.56	0/1003
2	D	0.48	1/743 (0.1%)	0.61	1/1003 (0.1%)
2	G	0.39	0/714	0.53	0/965
2	H	0.36	0/732	0.51	0/989
2	K	0.40	0/744	0.53	0/1005
2	L	0.39	0/736	0.54	0/993
2	O	0.31	0/715	0.47	0/965
2	P	0.49	1/725 (0.1%)	0.49	0/979
3	E	0.42	0/652	0.55	0/879
3	F	0.41	0/679	0.54	0/917
All	All	0.41	2/11320 (0.0%)	0.54	1/15280 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	P	36	GLN	C-N	9.57	1.56	1.34
2	D	1	VAL	C-N	-5.70	1.21	1.34

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	1	VAL	O-C-N	-5.40	114.07	122.70

There are no chirality outliers.

There are no planarity outliers.

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	691	0	678	23	0
1	B	713	0	692	8	0
1	I	658	0	644	8	0
1	J	684	0	666	12	0
1	M	673	0	656	15	0
1	N	657	0	644	17	0
2	C	721	0	701	12	0
2	D	721	0	700	7	0
2	G	695	0	663	14	0
2	H	713	0	688	22	0
2	K	719	0	693	13	0
2	L	714	0	689	16	0
2	O	696	0	663	21	0
2	P	706	0	676	20	0
3	E	655	0	642	12	0
3	F	680	0	663	11	0
4	C	13	0	5	3	0
5	A	41	0	0	1	0
5	B	38	0	0	0	0
5	C	43	0	0	3	0
5	D	31	0	0	1	0
5	E	32	0	0	4	0
5	F	37	0	0	0	0
5	G	22	0	0	2	0
5	H	20	0	0	1	0
5	I	24	0	0	1	0
5	J	28	0	0	0	0
5	K	30	0	0	0	0
5	L	29	0	0	1	0
5	M	13	0	0	0	0
5	N	17	0	0	0	0
5	O	8	0	0	0	0
5	P	7	0	0	0	0
All	All	11529	0	10763	190	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 9.

All (190) 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:I:79:SER:HB3	1:I:82:GLU:HG3	1.40	1.02
2:H:65:HIS:HD2	2:H:83:TYR:H	1.10	0.99
1:A:85:GLU:HG3	1:N:31:ARG:HH11	1.29	0.94
2:P:65:HIS:HD2	2:P:83:TYR:H	1.06	0.92
2:K:65:HIS:HD2	2:K:83:TYR:H	1.17	0.92
3:E:4:SER:OG	3:E:7:GLU:HG3	1.72	0.88
2:P:65:HIS:CD2	2:P:83:TYR:H	1.93	0.84
1:B:63:MET:SD	5:D:241:HOH:O	2.39	0.80
1:J:80:VAL:HA	1:J:83:LEU:HD12	1.64	0.79
2:L:65:HIS:HD2	2:L:83:TYR:H	1.30	0.78
3:E:9:ARG:HD2	5:E:433:HOH:O	1.83	0.78
2:P:34:GLU:HG3	2:P:43:ILE:HD12	1.67	0.77
1:B:79:SER:OG	1:B:82:GLU:HG3	1.83	0.77
3:F:63:MET:HE3	2:H:53:LEU:HD21	1.68	0.75
1:N:86:MET:HB3	2:P:18:LEU:HD21	1.70	0.74
1:A:68:ARG:HD2	2:C:7:ASP:OD2	1.90	0.71
3:F:63:MET:CE	2:H:53:LEU:HD21	2.21	0.70
2:C:14:PHE:O	2:C:18:LEU:HD13	1.91	0.70
2:O:21:ASP:OD1	2:O:23:LYS:HG2	1.92	0.69
1:A:38:MET:CE	5:C:437:HOH:O	2.40	0.68
2:H:65:HIS:CD2	2:H:83:TYR:H	2.02	0.68
2:G:9:ASP:OD2	2:G:80:LYS:HE2	1.93	0.68
2:D:14:PHE:O	2:D:18:LEU:HD13	1.94	0.67
2:C:62:ASP:HB2	2:C:65:HIS:H	1.59	0.66
1:M:27:ARG:HH22	1:N:44:ASP:CG	1.98	0.65
2:C:14:PHE:CE2	2:C:18:LEU:HD11	2.32	0.65
1:J:69:ASP:OD2	2:L:70:ARG:NH1	2.31	0.64
1:M:27:ARG:NH2	1:N:44:ASP:OD2	2.30	0.64
2:D:1:VAL:HG12	2:D:2:ARG:N	2.12	0.63
2:K:18:LEU:HD12	2:K:25:ALA:CB	2.29	0.62
1:A:38:MET:HE1	5:C:437:HOH:O	1.98	0.62
2:O:43:ILE:HG12	2:O:44:GLY:N	2.15	0.62
1:I:25:PRO:HD3	5:I:257:HOH:O	2.01	0.61
1:B:86:MET:O	2:D:22:ARG:NH2	2.33	0.61
1:M:80:VAL:HG21	2:O:36:GLN:NE2	2.16	0.61
1:M:80:VAL:HG21	2:O:36:GLN:HE22	1.65	0.61
1:N:77:THR:HG22	1:N:78:LYS:N	2.15	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:3:SER:OG	2:C:75:GLU:HG2	2.01	0.61
2:O:14:PHE:O	2:O:18:LEU:HD13	1.99	0.61
1:M:57:GLU:O	1:M:61:ARG:HG2	2.00	0.60
1:A:84:ARG:HG2	2:C:29:THR:CG2	2.31	0.60
1:A:84:ARG:HG2	2:C:29:THR:HG21	1.84	0.60
1:M:80:VAL:O	1:M:84:ARG:HG3	2.02	0.60
1:M:78:LYS:HE2	2:O:11:TRP:CH2	2.37	0.60
4:C:86:FLC:HG1	2:K:44:GLY:H	1.66	0.60
2:O:51:GLY:O	2:O:54:SER:HB3	2.02	0.59
2:C:43:ILE:HG22	4:C:86:FLC:HA1	1.85	0.58
1:I:80:VAL:HG21	2:K:36:GLN:OE1	2.03	0.58
1:I:79:SER:HB3	1:I:82:GLU:CG	2.26	0.58
1:A:79:SER:OG	1:A:82:GLU:HG2	2.02	0.58
1:N:3:ILE:HD11	1:N:15:LEU:HD11	1.86	0.57
1:A:85:GLU:CG	1:N:31:ARG:HH11	2.10	0.57
1:J:4:SER:OG	1:J:7:GLU:HG2	2.04	0.57
1:A:38:MET:HE3	5:C:437:HOH:O	2.03	0.56
1:J:11:ARG:O	1:J:14:PRO:HG2	2.05	0.56
1:B:53:LEU:HD21	1:B:63:MET:CE	2.36	0.56
2:P:40:PHE:CD1	2:P:57:TRP:CE2	2.94	0.56
1:A:29:THR:HA	1:A:34:ASP:OD2	2.06	0.56
1:M:77:THR:O	1:M:78:LYS:HG3	2.06	0.55
2:G:67:LEU:HD11	2:G:78:MET:HE2	1.88	0.55
3:E:56:PRO:HD2	2:H:52:GLU:OE1	2.06	0.55
2:G:20:ALA:HB2	5:G:171:HOH:O	2.06	0.55
2:H:1:VAL:HG12	2:H:2:ARG:N	2.21	0.55
2:P:22:ARG:O	2:P:26:ARG:HG3	2.07	0.55
2:G:79:LEU:O	2:G:80:LYS:HD2	2.06	0.55
2:L:43:ILE:O	2:L:59:ARG:HD3	2.07	0.54
2:D:14:PHE:CE2	2:D:18:LEU:HD11	2.42	0.54
1:A:85:GLU:HG3	1:N:31:ARG:HD2	1.89	0.54
2:L:22:ARG:HD2	2:L:26[B]:ARG:NH2	2.22	0.54
2:K:65:HIS:CD2	2:K:83:TYR:H	2.09	0.54
3:F:69:ASP:HB2	2:H:79:LEU:HD11	1.88	0.54
2:H:59:ARG:HG3	2:H:69:TYR:HE1	1.72	0.54
3:F:80:VAL:HG21	2:H:36:GLN:OE1	2.08	0.54
2:D:48:PRO:HD3	2:D:57:TRP:CZ3	2.43	0.53
2:G:67:LEU:HG	2:G:78:MET:HE1	1.91	0.52
3:F:80:VAL:O	3:F:84:ARG:HG3	2.09	0.52
2:H:75:GLU:OE1	2:H:75:GLU:N	2.41	0.52
3:E:84:ARG:HG2	2:G:29:THR:HG21	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:1:VAL:HG12	2:H:2:ARG:H	1.75	0.51
2:H:18:LEU:HD12	2:H:25:ALA:CB	2.40	0.51
1:A:56:PRO:HB3	1:B:63:MET:HE2	1.92	0.51
1:J:86:MET:HE2	2:L:18:LEU:HD11	1.93	0.51
3:E:25:PRO:HD3	5:E:185:HOH:O	2.10	0.51
2:K:7:ASP:CG	2:K:8:PRO:HD2	2.31	0.50
1:J:80:VAL:HG21	2:L:36:GLN:OE1	2.11	0.50
2:P:39:PRO:O	2:P:59:ARG:NH2	2.44	0.50
3:E:80:VAL:HG21	2:G:36:GLN:OE1	2.12	0.50
2:K:71:ALA:CB	2:K:76:VAL:HG12	2.42	0.50
2:L:11:TRP:NE1	2:L:15:LEU:HD11	2.27	0.49
2:O:62:ASP:HB2	2:O:65:HIS:H	1.77	0.49
3:F:4:SER:OG	3:F:7:GLU:HG3	2.13	0.49
1:M:11:ARG:O	1:M:14:PRO:HG2	2.11	0.49
1:A:23:HIS:CE1	5:A:159:HOH:O	2.64	0.49
2:H:18:LEU:HD12	2:H:25:ALA:HB1	1.95	0.49
1:I:82:GLU:O	1:I:86:MET:HG3	2.13	0.49
2:H:34:GLU:HA	2:H:34:GLU:OE2	2.13	0.49
1:A:77:THR:HG22	1:A:78:LYS:N	2.28	0.49
1:A:3:ILE:HD12	1:A:8:ALA:HB2	1.94	0.48
1:N:4:SER:OG	1:N:7:GLU:HG2	2.13	0.48
1:I:9:ARG:HG3	1:J:9:ARG:O	2.12	0.48
2:C:38:ASP:HA	2:C:39:PRO:HD3	1.65	0.48
1:N:77:THR:HG22	1:N:78:LYS:H	1.78	0.48
1:A:9:ARG:O	1:B:9:ARG:HG3	2.14	0.48
1:A:60:ARG:HG2	1:B:56:PRO:HB3	1.95	0.48
2:O:21:ASP:OD2	2:O:23:LYS:HE2	2.13	0.47
1:A:60:ARG:HD2	1:A:64:GLU:OE2	2.13	0.47
2:G:14:PHE:CZ	2:G:18:LEU:HD11	2.49	0.47
2:P:62:ASP:HB3	2:P:65:HIS:H	1.79	0.47
2:G:67:LEU:HG	2:G:78:MET:CE	2.44	0.47
1:M:29:THR:HA	1:M:34:ASP:OD2	2.15	0.47
2:K:2:ARG:HG2	2:K:75:GLU:N	2.30	0.47
2:H:2:ARG:HD3	2:H:76:VAL:HG13	1.97	0.47
2:H:79:LEU:N	2:H:79:LEU:HD22	2.30	0.47
1:N:62:LEU:HA	2:P:80:LYS:HD2	1.97	0.47
1:M:77:THR:O	1:M:78:LYS:CG	2.63	0.46
2:O:18:LEU:HD12	2:O:25:ALA:CB	2.45	0.46
2:L:67:LEU:HD11	2:L:78:MET:HE2	1.97	0.46
1:M:77:THR:HG22	1:M:78:LYS:N	2.30	0.46
3:E:31:ARG:HB2	3:E:31:ARG:NH1	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:62:LEU:HD11	2:O:68:VAL:HG11	1.96	0.46
2:K:18:LEU:CD1	2:K:25:ALA:HB1	2.46	0.46
2:H:52:GLU:HG3	5:H:224:HOH:O	2.14	0.46
1:A:11[B]:ARG:HG3	1:A:14:PRO:HG2	1.98	0.46
1:A:23:HIS:HA	1:A:42:ASP:OD2	2.16	0.46
2:P:17:TRP:CE2	2:P:24:THR:HG21	2.51	0.46
3:F:84:ARG:HG2	2:H:29:THR:HG21	1.98	0.45
2:P:65:HIS:HD2	2:P:83:TYR:N	1.90	0.45
2:K:21:ASP:OD1	2:K:23:LYS:HE3	2.17	0.45
2:P:17:TRP:CD2	2:P:24:THR:HG21	2.52	0.45
1:J:69:ASP:HB2	2:L:79:LEU:HD11	1.98	0.44
2:G:45:LYS:HD2	5:G:368:HOH:O	2.16	0.44
1:B:62:LEU:O	1:B:66:VAL:HG23	2.17	0.44
1:J:62:LEU:O	1:J:66:VAL:HG23	2.17	0.44
2:L:68:VAL:HG13	2:L:80:LYS:HB2	1.99	0.44
2:D:13:ASP:CG	2:D:82[B]:ARG:HB2	2.38	0.44
2:K:18:LEU:HD12	2:K:25:ALA:HB1	1.99	0.44
2:O:11:TRP:NE1	2:O:15:LEU:HD11	2.32	0.44
2:O:49:LEU:HB3	2:O:53:LEU:HB3	2.00	0.43
1:M:87:ALA:HB1	2:O:26:ARG:HG2	1.98	0.43
3:E:31:ARG:HH11	3:E:31:ARG:HB2	1.83	0.43
1:J:3:ILE:HB	1:J:7:GLU:HG3	2.00	0.43
2:O:43:ILE:HG12	2:O:44:GLY:H	1.82	0.43
2:C:14:PHE:CZ	2:C:18:LEU:HD11	2.54	0.43
1:A:11[B]:ARG:HG3	1:A:14:PRO:CG	2.49	0.43
2:G:43:ILE:O	2:G:59:ARG:HD3	2.19	0.43
2:G:23:LYS:HB3	2:G:23:LYS:HE2	1.78	0.43
1:N:3:ILE:HB	1:N:7:GLU:HG3	2.01	0.43
2:O:53:LEU:HD23	2:O:53:LEU:HA	1.89	0.43
1:N:3:ILE:HB	1:N:7:GLU:CD	2.39	0.43
1:I:57:GLU:HG3	1:I:61:ARG:HE	1.84	0.43
2:O:3:SER:O	2:O:75:GLU:HA	2.18	0.43
1:J:69:ASP:CG	2:L:70:ARG:HH12	2.22	0.42
2:H:28:ILE:O	2:H:32:ILE:HG13	2.19	0.42
3:E:14:PRO:HB2	5:E:371:HOH:O	2.18	0.42
1:M:51:TYR:O	1:M:54:ARG:HG2	2.19	0.42
2:L:79:LEU:O	2:L:80:LYS:HG2	2.19	0.42
2:O:18:LEU:HD12	2:O:25:ALA:HB1	2.02	0.42
3:F:79:SER:O	3:F:82:GLU:HG2	2.18	0.42
3:E:2:SER:N	5:E:104:HOH:O	2.51	0.42
2:P:18:LEU:HA	2:P:18:LEU:HD12	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:43:ILE:CG2	4:C:86:FLC:HA1	2.49	0.42
3:E:84:ARG:HG2	2:G:29:THR:CG2	2.49	0.42
1:J:61:ARG:NH1	2:L:84:HIS:CE1	2.87	0.42
2:G:21:ASP:OD1	2:G:23:LYS:HE2	2.20	0.42
2:C:31:LEU:O	2:C:35:ILE:HG13	2.20	0.42
1:A:4:SER:OG	1:A:7:GLU:HG2	2.20	0.42
3:F:63:MET:HE1	2:H:53:LEU:HD21	1.98	0.42
2:O:46:PRO:HA	2:O:59:ARG:HG2	2.01	0.42
2:L:50:GLN:NE2	5:L:155:HOH:O	2.52	0.42
2:P:22:ARG:HG2	2:P:26:ARG:NH1	2.35	0.41
2:L:65:HIS:CD2	2:L:83:TYR:H	2.20	0.41
1:N:49:THR:HG23	2:P:53:LEU:HD12	2.02	0.41
2:P:67:LEU:HD12	2:P:80:LYS:O	2.20	0.41
1:I:61:ARG:HD2	2:K:84:HIS:CD2	2.55	0.41
1:N:19:VAL:HG12	1:N:26:VAL:HG13	2.02	0.41
3:E:9:ARG:NH2	3:F:13:PHE:CE1	2.88	0.41
1:A:80:VAL:O	1:A:84:ARG:HG3	2.21	0.41
2:H:2:ARG:HA	2:H:74:ASP:O	2.20	0.41
2:O:27:ARG:HH12	2:O:43:ILE:HD11	1.85	0.41
2:H:59:ARG:HG3	2:H:69:TYR:CE1	2.53	0.41
2:O:15:LEU:HA	2:O:18:LEU:HD22	2.02	0.41
2:P:35:ILE:HG12	2:P:59:ARG:HE	1.86	0.41
2:P:16:PHE:CD2	2:P:82:ARG:HD2	2.55	0.41
1:N:78:LYS:HE3	2:P:11:TRP:CH2	2.56	0.40
2:P:79:LEU:O	2:P:80:LYS:HG3	2.21	0.40
2:D:75:GLU:OE1	2:D:75:GLU:N	2.54	0.40
2:K:80:LYS:HE3	2:K:80:LYS:HB3	1.88	0.40
1:N:68:ARG:O	1:N:71:ALA:HB3	2.22	0.40
2:L:11:TRP:CD1	2:L:15:LEU:HD11	2.56	0.40
3:F:79:SER:O	3:F:83:LEU:HD13	2.21	0.40

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	86/98 (88%)	86 (100%)	0	0	100	100
1	B	89/98 (91%)	89 (100%)	0	0	100	100
1	I	79/98 (81%)	79 (100%)	0	0	100	100
1	J	85/98 (87%)	82 (96%)	3 (4%)	0	100	100
1	M	81/98 (83%)	79 (98%)	2 (2%)	0	100	100
1	N	79/98 (81%)	79 (100%)	0	0	100	100
2	C	84/96 (88%)	82 (98%)	2 (2%)	0	100	100
2	D	84/96 (88%)	82 (98%)	2 (2%)	0	100	100
2	G	81/96 (84%)	79 (98%)	2 (2%)	0	100	100
2	H	83/96 (86%)	82 (99%)	1 (1%)	0	100	100
2	K	84/96 (88%)	81 (96%)	3 (4%)	0	100	100
2	L	83/96 (86%)	81 (98%)	2 (2%)	0	100	100
2	O	81/96 (84%)	81 (100%)	0	0	100	100
2	P	82/96 (85%)	79 (96%)	3 (4%)	0	100	100
3	E	77/98 (79%)	77 (100%)	0	0	100	100
3	F	83/98 (85%)	79 (95%)	4 (5%)	0	100	100
All	All	1321/1552 (85%)	1297 (98%)	24 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	73/79 (92%)	73 (100%)	0	100	100
1	B	75/79 (95%)	74 (99%)	1 (1%)	76	80
1	I	70/79 (89%)	70 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	J	73/79 (92%)	73 (100%)	0	100 100
1	M	71/79 (90%)	70 (99%)	1 (1%)	74 78
1	N	70/79 (89%)	70 (100%)	0	100 100
2	C	74/84 (88%)	73 (99%)	1 (1%)	74 78
2	D	74/84 (88%)	73 (99%)	1 (1%)	74 78
2	G	71/84 (84%)	68 (96%)	3 (4%)	36 32
2	H	73/84 (87%)	71 (97%)	2 (3%)	52 52
2	K	74/84 (88%)	71 (96%)	3 (4%)	37 34
2	L	73/84 (87%)	70 (96%)	3 (4%)	37 34
2	O	71/84 (84%)	69 (97%)	2 (3%)	51 50
2	P	72/84 (86%)	69 (96%)	3 (4%)	36 32
3	E	69/78 (88%)	67 (97%)	2 (3%)	50 48
3	F	71/78 (91%)	69 (97%)	2 (3%)	51 50
All	All	1154/1302 (89%)	1130 (98%)	24 (2%)	61 64

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	50	VAL
2	C	49	LEU
2	D	49	LEU
3	E	47	GLN
3	E	79	SER
3	F	26	VAL
3	F	74	SER
2	G	18	LEU
2	G	49	LEU
2	G	76	VAL
2	H	18	LEU
2	H	49	LEU
2	K	41	SER
2	K	49	LEU
2	K	75	GLU
2	L	45	LYS
2	L	49	LEU
2	L	68	VAL
1	M	47	GLN

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Mol	Chain	Res	Type
2	O	49	LEU
2	O	54	SER
2	P	41	SER
2	P	68	VAL
2	P	79	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
2	H	65	HIS
2	K	50	GLN
2	K	65	HIS
2	L	50	GLN
2	L	65	HIS
2	O	5	ASN
2	O	36	GLN
2	P	65	HIS
2	P	84	HIS

5.3.3 RNA

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	MLZ	E	70	3	8,9,10	0.91	1 (12%)	7,9,11	1.23	0
3	MLZ	F	70	3	8,9,10	0.76	0	7,9,11	1.33	1 (14%)

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	MLZ	E	70	3	-	0/6/8/10	0/0/0/0
3	MLZ	F	70	3	-	0/6/8/10	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	70	MLZ	CB-CA	-2.03	1.51	1.53

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	F	70	MLZ	O-C-CA	-2.16	119.85	125.49

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

1 ligand is 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	FLC	C	86	-	3,12,12	2.92	3 (100%)	3,17,17	0.59	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
4	FLC	C	86	-	-	0/6/16/16	0/0/0/0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	86	FLC	CA-CB	-3.27	1.49	1.54
4	C	86	FLC	CG-CB	-3.10	1.50	1.54
4	C	86	FLC	OHB-CB	-2.29	1.39	1.43

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	86	FLC	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	87/98 (88%)	0.24	0 100 100	19, 30, 52, 59	0
1	B	91/98 (92%)	0.11	1 (1%) 82 86	17, 29, 51, 84	0
1	I	83/98 (84%)	0.09	2 (2%) 62 69	22, 35, 55, 81	0
1	J	86/98 (87%)	0.36	1 (1%) 81 85	21, 37, 59, 78	0
1	M	85/98 (86%)	0.33	6 (7%) 19 25	32, 42, 79, 97	0
1	N	83/98 (84%)	0.32	4 (4%) 34 43	29, 42, 73, 81	1 (1%)
2	C	85/96 (88%)	0.07	1 (1%) 81 85	19, 30, 47, 64	0
2	D	85/96 (88%)	0.22	1 (1%) 81 85	23, 31, 51, 65	0
2	G	83/96 (86%)	0.12	1 (1%) 81 85	25, 39, 60, 77	0
2	H	85/96 (88%)	0.16	2 (2%) 62 69	27, 38, 70, 84	0
2	K	84/96 (87%)	0.05	2 (2%) 62 69	23, 34, 50, 70	0
2	L	84/96 (87%)	0.09	1 (1%) 81 85	26, 36, 53, 71	0
2	O	83/96 (86%)	0.70	8 (9%) 10 15	38, 53, 78, 97	0
2	P	84/96 (87%)	0.52	4 (4%) 34 43	35, 50, 72, 81	0
3	E	81/98 (82%)	0.17	4 (4%) 33 43	21, 30, 61, 72	0
3	F	85/98 (86%)	0.05	0 100 100	20, 33, 58, 64	0
All	All	1354/1552 (87%)	0.22	38 (2%) 56 66	17, 37, 67, 97	1 (0%)

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	1	VAL	5.7
2	H	1	VAL	5.4
2	D	1	VAL	4.6
1	B	73	HIS	4.5
2	O	37	ARG	3.6

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Mol	Chain	Res	Type	RSRZ
2	O	43	ILE	3.6
3	E	81	ASP	3.6
3	E	31	ARG	3.4
1	J	73	HIS	3.3
2	O	72	GLY	3.2
1	M	73	HIS	3.2
2	O	33	GLY	3.0
3	E	76	PHE	3.0
1	N	81	ASP	2.9
2	P	31	LEU	2.8
2	O	38	ASP	2.7
2	H	41	SER	2.7
1	I	76	PHE	2.6
1	N	84	ARG	2.6
1	I	31	ARG	2.6
2	O	73	ASP	2.6
1	N	80	VAL	2.5
1	M	79	SER	2.4
2	G	74	ASP	2.4
3	E	80	VAL	2.4
2	P	73	ASP	2.4
2	K	73	ASP	2.3
1	M	85	GLU	2.3
2	P	37	ARG	2.3
2	P	23	LYS	2.2
2	O	61	ILE	2.2
1	M	84	ARG	2.2
1	N	76	PHE	2.1
1	M	3	ILE	2.1
2	L	72	GLY	2.1
2	K	74	ASP	2.0
2	O	29	THR	2.0
1	M	87	ALA	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (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, 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	LLDF	B-factors(Å^2)	Q<0.9
3	MLZ	F	70	10/11	0.92	0.13	-	41,51,65,66	0
3	MLZ	E	70	10/11	0.95	0.10	-	38,39,50,50	0

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, 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	LLDF	B-factors(Å^2)	Q<0.9
4	FLC	C	86	13/13	0.83	0.14	1.08	32,39,52,53	0

6.5 Other polymers (i)

There are no such residues in this entry.