



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 18, 2026 – 03:24 PM UTC

PDB ID : 3R1F / pdb_00003r1f
Title : Crystal structure of a key regulator of virulence in Mycobacterium tuberculosis
Authors : Rosenberg, O.S.; Dovey, C.; Finer-Moore, J.; Stroud, R.M.; Cox, J.S.
Deposited on : 2011-03-10
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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

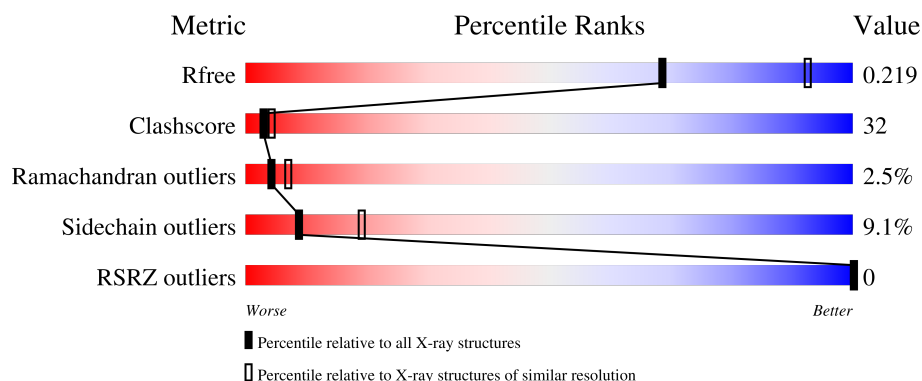
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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.



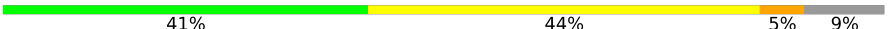
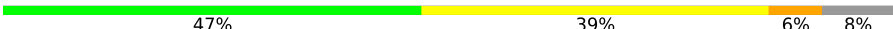
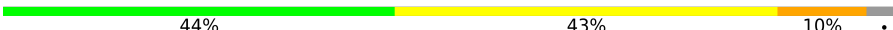
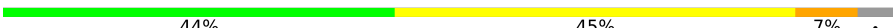
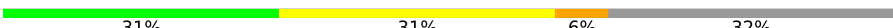
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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 $\leq 5\%$. 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	135	
1	B	135	
1	C	135	
1	D	135	
1	E	135	

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Mol	Chain	Length	Quality of chain
1	F	135	 45% 42% 9% .
1	G	135	 41% 44% 5% 9%
1	H	135	 51% 36% 10% .
1	I	135	 47% 39% 6% 8%
1	J	135	 44% 43% 10% .
1	K	135	 58% 29% . . 8%
1	L	135	 46% 42% 7% .
1	M	135	 49% 35% . 12%
1	N	135	 44% 45% 7% .
1	O	135	 22% 39% 5% 33%
1	P	135	 31% 31% 6% 32%
1	Q	135	 28% 52% 6% 14%
1	R	135	 38% 41% 12% . 9%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 17208 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 ESX-1 secretion-associated regulator EspR.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	123	Total	C	N	O	S	Se	0	0	0
			967	606	178	179	1	3			
1	B	130	Total	C	N	O	S	Se	0	0	0
			1019	636	188	191	1	3			
1	C	123	Total	C	N	O	S	Se	0	0	0
			960	603	175	178	1	3			
1	D	130	Total	C	N	O	S	Se	0	0	0
			1019	636	188	191	1	3			
1	E	125	Total	C	N	O	S	Se	0	0	0
			986	617	183	182	1	3			
1	F	130	Total	C	N	O	S	Se	0	0	0
			1019	636	188	191	1	3			
1	G	123	Total	C	N	O	S	Se	0	0	0
			966	606	178	178	1	3			
1	H	130	Total	C	N	O	S	Se	0	0	0
			1016	633	188	191	1	3			
1	I	124	Total	C	N	O	S	Se	0	0	0
			974	610	179	181	1	3			
1	J	130	Total	C	N	O	S	Se	0	0	0
			1019	636	188	191	1	3			
1	K	124	Total	C	N	O	S	Se	0	0	0
			973	609	179	181	1	3			
1	L	129	Total	C	N	O	S	Se	0	0	0
			1013	633	187	189	1	3			
1	M	119	Total	C	N	O	S	Se	0	0	0
			932	587	170	171	1	3			
1	N	130	Total	C	N	O	S	Se	0	0	0
			1019	636	188	191	1	3			
1	O	90	Total	C	N	O	S	Se	0	0	0
			706	450	121	132	1	2			
1	P	92	Total	C	N	O	S	Se	0	0	0
			721	459	123	135	1	3			

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	Q	116	Total	C	N	O	S	Se	0	0	0
			906	570	165	167	1	3			
1	R	123	Total	C	N	O	S	Se	0	0	0
			974	608	179	183	1	3			

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP P96228
A	-1	ASN	-	expression tag	UNP P96228
A	0	ALA	-	expression tag	UNP P96228
B	-2	SER	-	expression tag	UNP P96228
B	-1	ASN	-	expression tag	UNP P96228
B	0	ALA	-	expression tag	UNP P96228
C	-2	SER	-	expression tag	UNP P96228
C	-1	ASN	-	expression tag	UNP P96228
C	0	ALA	-	expression tag	UNP P96228
D	-2	SER	-	expression tag	UNP P96228
D	-1	ASN	-	expression tag	UNP P96228
D	0	ALA	-	expression tag	UNP P96228
E	-2	SER	-	expression tag	UNP P96228
E	-1	ASN	-	expression tag	UNP P96228
E	0	ALA	-	expression tag	UNP P96228
F	-2	SER	-	expression tag	UNP P96228
F	-1	ASN	-	expression tag	UNP P96228
F	0	ALA	-	expression tag	UNP P96228
G	-2	SER	-	expression tag	UNP P96228
G	-1	ASN	-	expression tag	UNP P96228
G	0	ALA	-	expression tag	UNP P96228
H	-2	SER	-	expression tag	UNP P96228
H	-1	ASN	-	expression tag	UNP P96228
H	0	ALA	-	expression tag	UNP P96228
I	-2	SER	-	expression tag	UNP P96228
I	-1	ASN	-	expression tag	UNP P96228
I	0	ALA	-	expression tag	UNP P96228
J	-2	SER	-	expression tag	UNP P96228
J	-1	ASN	-	expression tag	UNP P96228
J	0	ALA	-	expression tag	UNP P96228
K	-2	SER	-	expression tag	UNP P96228
K	-1	ASN	-	expression tag	UNP P96228
K	0	ALA	-	expression tag	UNP P96228
L	-2	SER	-	expression tag	UNP P96228

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Chain	Residue	Modelled	Actual	Comment	Reference
L	-1	ASN	-	expression tag	UNP P96228
L	0	ALA	-	expression tag	UNP P96228
M	-2	SER	-	expression tag	UNP P96228
M	-1	ASN	-	expression tag	UNP P96228
M	0	ALA	-	expression tag	UNP P96228
N	-2	SER	-	expression tag	UNP P96228
N	-1	ASN	-	expression tag	UNP P96228
N	0	ALA	-	expression tag	UNP P96228
O	-2	SER	-	expression tag	UNP P96228
O	-1	ASN	-	expression tag	UNP P96228
O	0	ALA	-	expression tag	UNP P96228
P	-2	SER	-	expression tag	UNP P96228
P	-1	ASN	-	expression tag	UNP P96228
P	0	ALA	-	expression tag	UNP P96228
Q	-2	SER	-	expression tag	UNP P96228
Q	-1	ASN	-	expression tag	UNP P96228
Q	0	ALA	-	expression tag	UNP P96228
R	-2	SER	-	expression tag	UNP P96228
R	-1	ASN	-	expression tag	UNP P96228
R	0	ALA	-	expression tag	UNP P96228

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	2	Total O 2 2	0	0
2	B	1	Total O 1 1	0	0
2	C	1	Total O 1 1	0	0
2	D	2	Total O 2 2	0	0
2	F	1	Total O 1 1	0	0
2	H	1	Total O 1 1	0	0
2	I	1	Total O 1 1	0	0
2	L	3	Total O 3 3	0	0
2	M	1	Total O 1 1	0	0

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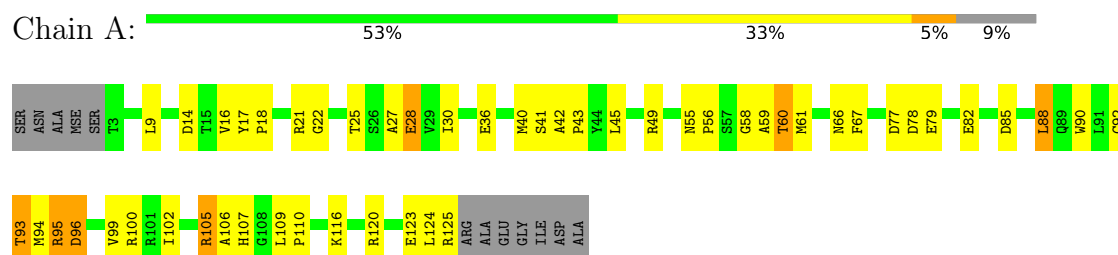
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	N	4	Total	O	0	0
			4	4		
2	P	2	Total	O	0	0
			2	2		

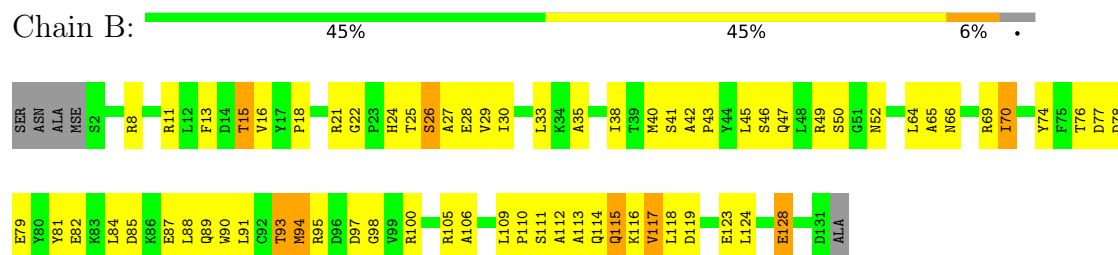
3 Residue-property plots [i](#)

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.

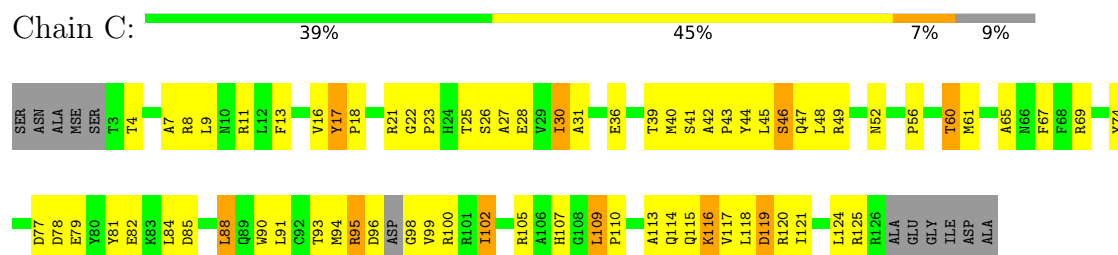
• Molecule 1: ESX-1 secretion-associated regulator EspR



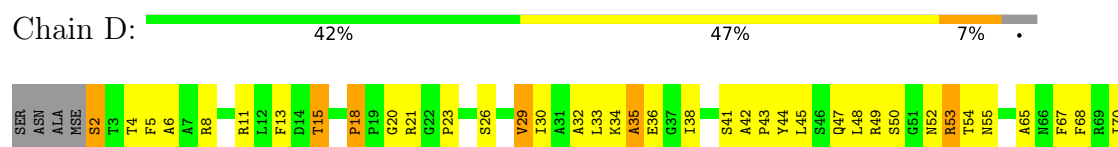
• Molecule 1: ESX-1 secretion-associated regulator EspR

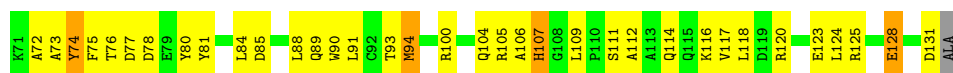


• Molecule 1: ESX-1 secretion-associated regulator EspR



• Molecule 1: ESX-1 secretion-associated regulator EspR





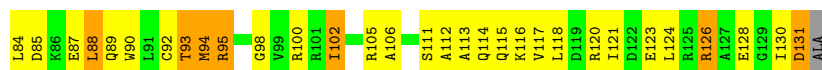
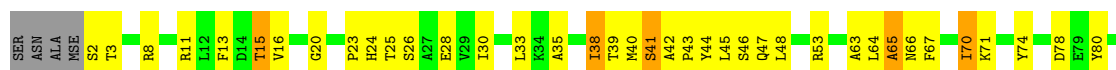
- Molecule 1: ESX-1 secretion-associated regulator EspR

Chain E: 44% 41% 7% 7%



- Molecule 1: ESX-1 secretion-associated regulator EspR

Chain F: 45% 42% 9% .



- Molecule 1: ESX-1 secretion-associated regulator EspR

Chain G: 41% 44% 5% 9%



- Molecule 1: ESX-1 secretion-associated regulator EspR

Chain H: 51% 36% 10% .



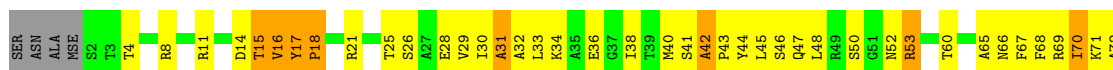
- Molecule 1: ESX-1 secretion-associated regulator EspR

Chain I: 47% 39% 6% 8%

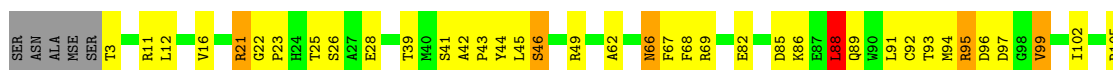




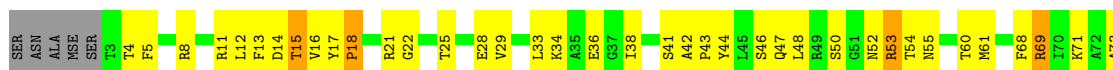
- Molecule 1: ESX-1 secretion-associated regulator EspR



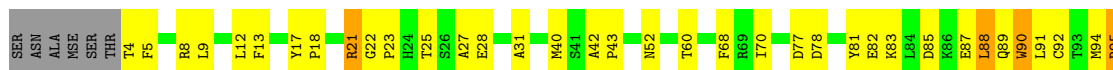
- Molecule 1: ESX-1 secretion-associated regulator EspR



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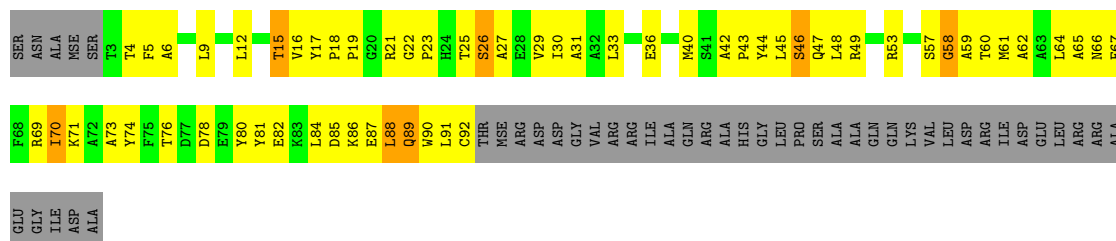
- Molecule 1: ESX-1 secretion-associated regulator EspR





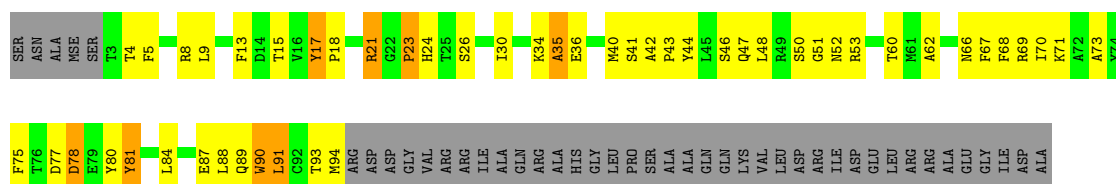
• Molecule 1: ESX-1 secretion-associated regulator EspR

Chain O: 22% 39% 5% 33%



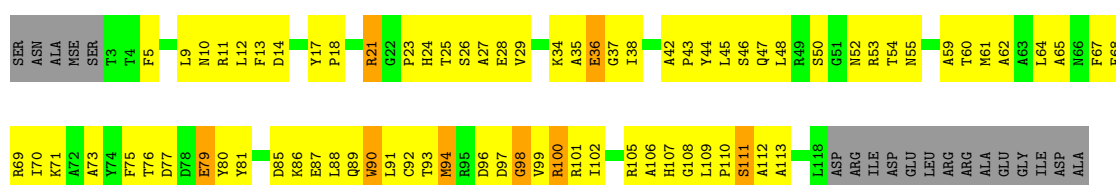
• Molecule 1: ESX-1 secretion-associated regulator EspR

Chain P: 31% 31% 6% 32%



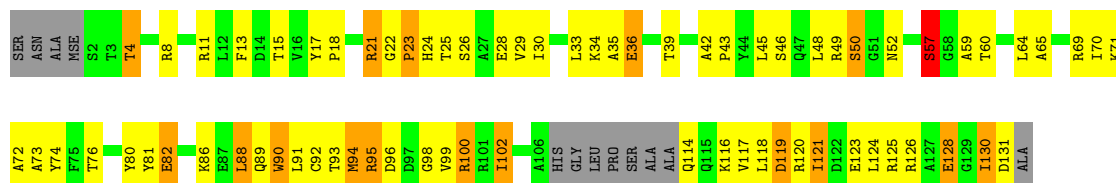
• Molecule 1: ESX-1 secretion-associated regulator EspR

Chain Q: 28% 52% 6% 14%



• Molecule 1: ESX-1 secretion-associated regulator EspR

Chain R: 38% 41% 12% 9%



4 Data and refinement statistics

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α , β , γ	148.49Å 148.49Å 129.67Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.84 – 2.50 48.84 – 2.50	Depositor EDS
% Data completeness (in resolution range)	91.0 (48.84-2.50) 91.0 (48.84-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.44 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.7.1_743	Depositor
R, R_{free}	0.197 , 0.232 0.197 , 0.219	Depositor DCC
R_{free} test set	5688 reflections (4.55%)	wwPDB-VP
Wilson B-factor (Å ²)	32.1	Xtriage
Anisotropy	0.261	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 7.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.045 for -h,-k,l 0.048 for h,-h-k,-l 0.438 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	17208	wwPDB-VP
Average B, all atoms (Å ²)	35.0	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 71.56 % 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 2.5717e-06. 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

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	0.62	0/983	0.96	4/1324 (0.3%)
1	B	0.62	0/1035	1.01	5/1393 (0.4%)
1	C	0.63	0/975	1.00	3/1313 (0.2%)
1	D	0.60	0/1035	1.00	2/1393 (0.1%)
1	E	0.63	0/1001	1.03	3/1346 (0.2%)
1	F	0.60	0/1035	0.95	3/1393 (0.2%)
1	G	0.63	0/981	0.98	4/1320 (0.3%)
1	H	0.60	0/1032	0.98	3/1389 (0.2%)
1	I	0.59	0/990	1.01	3/1334 (0.2%)
1	J	0.63	0/1035	1.09	7/1393 (0.5%)
1	K	0.63	0/989	1.05	4/1332 (0.3%)
1	L	0.61	0/1029	1.04	5/1385 (0.4%)
1	M	0.56	0/947	0.92	0/1276
1	N	0.63	0/1035	1.01	1/1393 (0.1%)
1	O	0.57	0/721	1.04	1/975 (0.1%)
1	P	0.59	0/735	1.02	2/992 (0.2%)
1	Q	0.54	0/922	0.97	1/1243 (0.1%)
1	R	0.56	0/987	0.92	2/1325 (0.2%)
All	All	0.60	0/17467	1.00	53/23519 (0.2%)

There are no bond length outliers.

The worst 5 of 53 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	R	86	LYS	N-CA-C	-8.31	103.74	114.04
1	L	94	MSE	N-CA-C	-7.79	99.75	110.35
1	C	109	LEU	N-CA-C	7.61	119.23	109.65
1	O	73	ALA	N-CA-C	-7.16	104.58	113.38
1	H	18	PRO	CA-C-N	7.04	127.01	119.76

There are no chirality outliers.

There are no planarity outliers.

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	967	0	957	57	0
1	B	1019	0	1009	63	0
1	C	960	0	948	70	0
1	D	1019	0	1009	75	0
1	E	986	0	981	72	0
1	F	1019	0	1009	83	1
1	G	966	0	959	69	2
1	H	1016	0	1000	74	0
1	I	974	0	964	57	0
1	J	1019	0	1009	75	1
1	K	973	0	960	51	0
1	L	1013	0	1004	66	0
1	M	932	0	921	69	1
1	N	1019	0	1009	75	2
1	O	706	0	691	65	0
1	P	721	0	707	60	0
1	Q	906	0	900	96	0
1	R	974	0	965	94	0
2	A	2	0	0	0	0
2	B	1	0	0	1	0
2	C	1	0	0	0	0
2	D	2	0	0	0	0
2	F	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	L	3	0	0	0	0
2	M	1	0	0	0	1
2	N	4	0	0	0	0
2	P	2	0	0	0	0
All	All	17208	0	17002	1099	4

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 32.

The worst 5 of 1099 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:G:94:MSE:HE2	1:H:94:MSE:CG	1.54	1.36
1:G:94:MSE:HE1	1:H:94:MSE:HA	1.28	1.13
1:O:15:THR:HG21	1:O:88:LEU:HG	1.25	1.12
1:G:94:MSE:HE2	1:H:94:MSE:HG3	1.17	1.10
1:M:94:MSE:HB2	1:N:94:MSE:HE2	1.33	1.09

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:126:ARG:NH2	1:G:126:ARG:O[3_654]	2.05	0.15
1:M:52:ASN:ND2	1:N:50:SER:O[2_544]	2.13	0.07
1:G:53:ARG:NH2	1:J:14:ASP:OD1[2_544]	2.16	0.04
1:N:4:THR:OG1	2:M:133:HOH:O[3_655]	2.17	0.03

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	121/135 (90%)	106 (88%)	11 (9%)	4 (3%)	3	4
1	B	128/135 (95%)	116 (91%)	10 (8%)	2 (2%)	7	14
1	C	119/135 (88%)	106 (89%)	12 (10%)	1 (1%)	16	31
1	D	128/135 (95%)	115 (90%)	9 (7%)	4 (3%)	3	5
1	E	121/135 (90%)	104 (86%)	14 (12%)	3 (2%)	4	7
1	F	128/135 (95%)	116 (91%)	11 (9%)	1 (1%)	16	31
1	G	119/135 (88%)	106 (89%)	9 (8%)	4 (3%)	3	4
1	H	128/135 (95%)	114 (89%)	11 (9%)	3 (2%)	5	8
1	I	122/135 (90%)	99 (81%)	21 (17%)	2 (2%)	7	14
1	J	128/135 (95%)	116 (91%)	10 (8%)	2 (2%)	7	14

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	K	122/135 (90%)	112 (92%)	9 (7%)	1 (1%)	16	31
1	L	127/135 (94%)	112 (88%)	12 (9%)	3 (2%)	4	8
1	M	115/135 (85%)	103 (90%)	11 (10%)	1 (1%)	14	27
1	N	128/135 (95%)	111 (87%)	13 (10%)	4 (3%)	3	5
1	O	88/135 (65%)	64 (73%)	21 (24%)	3 (3%)	3	4
1	P	90/135 (67%)	79 (88%)	8 (9%)	3 (3%)	3	4
1	Q	114/135 (84%)	85 (75%)	24 (21%)	5 (4%)	2	2
1	R	119/135 (88%)	99 (83%)	12 (10%)	8 (7%)	1	1
All	All	2145/2430 (88%)	1863 (87%)	228 (11%)	54 (2%)	4	7

5 of 54 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	93	THR
1	B	26	SER
1	H	95	ARG
1	P	35	ALA
1	Q	35	ALA

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	98/103 (95%)	93 (95%)	5 (5%)	21	43
1	B	104/103 (101%)	94 (90%)	10 (10%)	8	17
1	C	97/103 (94%)	90 (93%)	7 (7%)	13	28
1	D	104/103 (101%)	97 (93%)	7 (7%)	15	31
1	E	100/103 (97%)	92 (92%)	8 (8%)	11	24
1	F	104/103 (101%)	91 (88%)	13 (12%)	4	9
1	G	98/103 (95%)	87 (89%)	11 (11%)	6	12
1	H	103/103 (100%)	94 (91%)	9 (9%)	9	21

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	I	99/103 (96%)	89 (90%)	10 (10%)	7	15
1	J	104/103 (101%)	95 (91%)	9 (9%)	9	21
1	K	99/103 (96%)	90 (91%)	9 (9%)	9	19
1	L	103/103 (100%)	94 (91%)	9 (9%)	9	21
1	M	94/103 (91%)	87 (93%)	7 (7%)	13	27
1	N	104/103 (101%)	95 (91%)	9 (9%)	9	21
1	O	72/103 (70%)	63 (88%)	9 (12%)	4	9
1	P	74/103 (72%)	70 (95%)	4 (5%)	20	41
1	Q	92/103 (89%)	83 (90%)	9 (10%)	7	16
1	R	100/103 (97%)	85 (85%)	15 (15%)	3	6
All	All	1749/1854 (94%)	1589 (91%)	160 (9%)	9	19

5 of 160 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	N	15	THR
1	Q	94	MSE
1	N	76	THR
1	O	89	GLN
1	R	50	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 34 such sidechains are listed below:

Mol	Chain	Res	Type
1	P	52	ASN
1	Q	52	ASN
1	R	52	ASN
1	E	89	GLN
1	D	115	GLN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	120/135 (88%)	-1.64	0 100 100	21, 31, 61, 77	0
1	B	127/135 (94%)	-1.65	0 100 100	21, 31, 47, 57	0
1	C	120/135 (88%)	-1.59	0 100 100	19, 32, 62, 71	0
1	D	127/135 (94%)	-1.64	0 100 100	21, 30, 50, 59	0
1	E	122/135 (90%)	-1.62	0 100 100	20, 33, 57, 67	0
1	F	127/135 (94%)	-1.66	0 100 100	18, 29, 44, 54	0
1	G	120/135 (88%)	-1.60	0 100 100	21, 31, 56, 70	0
1	H	127/135 (94%)	-1.66	0 100 100	19, 28, 48, 63	0
1	I	121/135 (89%)	-1.63	0 100 100	21, 30, 60, 74	0
1	J	127/135 (94%)	-1.67	0 100 100	19, 28, 48, 62	0
1	K	121/135 (89%)	-1.65	0 100 100	17, 29, 55, 74	0
1	L	126/135 (93%)	-1.65	0 100 100	22, 30, 47, 61	0
1	M	116/135 (85%)	-1.50	0 100 100	26, 37, 55, 64	0
1	N	127/135 (94%)	-1.58	0 100 100	23, 33, 45, 61	0
1	O	88/135 (65%)	-1.61	0 100 100	30, 36, 51, 60	0
1	P	89/135 (65%)	-1.65	0 100 100	23, 33, 42, 53	0
1	Q	113/135 (83%)	-1.60	0 100 100	27, 36, 57, 69	0
1	R	120/135 (88%)	-1.60	0 100 100	26, 35, 62, 75	0
All	All	2138/2430 (87%)	-1.62	0 100 100	17, 33, 55, 77	0

There are no RSRZ outliers to report.

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 oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.