



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 02:22 PM UTC

PDB ID : 4Q0C / pdb_00004q0c
Title : 3.1 Å resolution crystal structure of the B. pertussis BvgS periplasmic domain
Authors : Dupre, E.; Herrou, J.; Lensink, M.F.; Wintjens, R.; Lebedev, A.; Crosson, S.;
Villeret, V.; Loch, C.; Antoine, R.; Jacob-Dubuisson, F.
Deposited on : 2014-04-01
Resolution : 3.10 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

<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
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

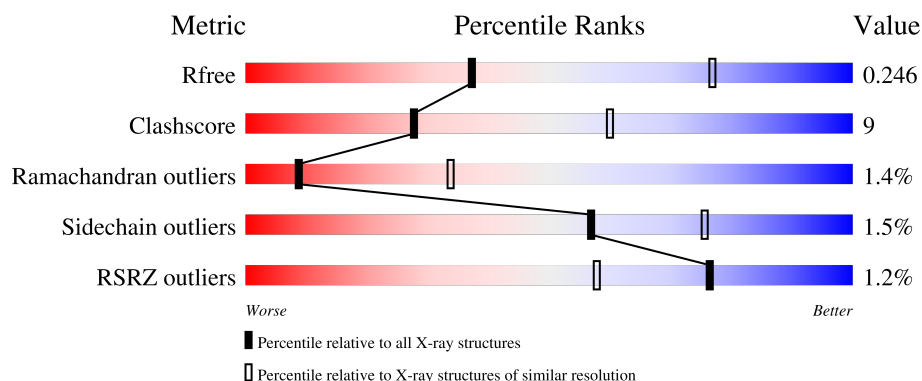
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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	584	% 69% 18% • 12%
1	B	584	% 68% 18% • 12%
1	C	584	% 68% 18% • 12%
1	D	584	% 67% 18% •• 12%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 15649 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 Virulence sensor protein BvgS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	513	Total	C	N	O	S	0	0	0
			3895	2469	683	734	9			
1	B	513	Total	C	N	O	S	0	0	0
			3913	2485	683	736	9			
1	C	513	Total	C	N	O	S	0	0	0
			3919	2488	684	738	9			
1	D	513	Total	C	N	O	S	0	0	0
			3922	2493	682	738	9			

There are 276 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-32	MET	-	initiating methionine	UNP P16575
A	-31	GLN	-	expression tag	UNP P16575
A	-30	TYR	-	expression tag	UNP P16575
A	-29	LYS	-	expression tag	UNP P16575
A	-28	LEU	-	expression tag	UNP P16575
A	-27	ALA	-	expression tag	UNP P16575
A	-26	LEU	-	expression tag	UNP P16575
A	-25	ASN	-	expression tag	UNP P16575
A	-24	GLY	-	expression tag	UNP P16575
A	-23	LYS	-	expression tag	UNP P16575
A	-22	THR	-	expression tag	UNP P16575
A	-21	LEU	-	expression tag	UNP P16575
A	-20	LYS	-	expression tag	UNP P16575
A	-19	GLY	-	expression tag	UNP P16575
A	-18	GLU	-	expression tag	UNP P16575
A	-17	THR	-	expression tag	UNP P16575
A	-16	THR	-	expression tag	UNP P16575
A	-15	THR	-	expression tag	UNP P16575
A	-14	GLU	-	expression tag	UNP P16575
A	-13	ALA	-	expression tag	UNP P16575
A	-12	VAL	-	expression tag	UNP P16575

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	ASP	-	expression tag	UNP P16575
A	-10	ALA	-	expression tag	UNP P16575
A	-9	ALA	-	expression tag	UNP P16575
A	-8	THR	-	expression tag	UNP P16575
A	-7	ALA	-	expression tag	UNP P16575
A	-6	GLU	-	expression tag	UNP P16575
A	-5	LYS	-	expression tag	UNP P16575
A	-4	VAL	-	expression tag	UNP P16575
A	-3	PHE	-	expression tag	UNP P16575
A	-2	LYS	-	expression tag	UNP P16575
A	-1	GLN	-	expression tag	UNP P16575
A	0	TYR	-	expression tag	UNP P16575
A	1	ALA	-	expression tag	UNP P16575
A	2	ASN	-	expression tag	UNP P16575
A	3	ASP	-	expression tag	UNP P16575
A	4	ASN	-	expression tag	UNP P16575
A	5	GLY	-	expression tag	UNP P16575
A	6	VAL	-	expression tag	UNP P16575
A	7	ASP	-	expression tag	UNP P16575
A	8	GLY	-	expression tag	UNP P16575
A	9	GLU	-	expression tag	UNP P16575
A	10	TRP	-	expression tag	UNP P16575
A	11	THR	-	expression tag	UNP P16575
A	12	TYR	-	expression tag	UNP P16575
A	13	ASP	-	expression tag	UNP P16575
A	14	ASP	-	expression tag	UNP P16575
A	15	ALA	-	expression tag	UNP P16575
A	16	THR	-	expression tag	UNP P16575
A	17	LYS	-	expression tag	UNP P16575
A	18	THR	-	expression tag	UNP P16575
A	19	PHE	-	expression tag	UNP P16575
A	20	THR	-	expression tag	UNP P16575
A	21	VAL	-	expression tag	UNP P16575
A	22	THR	-	expression tag	UNP P16575
A	23	GLU	-	expression tag	UNP P16575
A	24	LEU	-	expression tag	UNP P16575
A	25	VAL	-	expression tag	UNP P16575
A	26	PRO	-	expression tag	UNP P16575
A	27	ARG	-	expression tag	UNP P16575
A	28	GLY	-	expression tag	UNP P16575
A	29	SER	-	expression tag	UNP P16575
A	545	GLU	-	expression tag	UNP P16575

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Chain	Residue	Modelled	Actual	Comment	Reference
A	546	HIS	-	expression tag	UNP P16575
A	547	HIS	-	expression tag	UNP P16575
A	548	HIS	-	expression tag	UNP P16575
A	549	HIS	-	expression tag	UNP P16575
A	550	HIS	-	expression tag	UNP P16575
A	551	HIS	-	expression tag	UNP P16575
B	-32	MET	-	initiating methionine	UNP P16575
B	-31	GLN	-	expression tag	UNP P16575
B	-30	TYR	-	expression tag	UNP P16575
B	-29	LYS	-	expression tag	UNP P16575
B	-28	LEU	-	expression tag	UNP P16575
B	-27	ALA	-	expression tag	UNP P16575
B	-26	LEU	-	expression tag	UNP P16575
B	-25	ASN	-	expression tag	UNP P16575
B	-24	GLY	-	expression tag	UNP P16575
B	-23	LYS	-	expression tag	UNP P16575
B	-22	THR	-	expression tag	UNP P16575
B	-21	LEU	-	expression tag	UNP P16575
B	-20	LYS	-	expression tag	UNP P16575
B	-19	GLY	-	expression tag	UNP P16575
B	-18	GLU	-	expression tag	UNP P16575
B	-17	THR	-	expression tag	UNP P16575
B	-16	THR	-	expression tag	UNP P16575
B	-15	THR	-	expression tag	UNP P16575
B	-14	GLU	-	expression tag	UNP P16575
B	-13	ALA	-	expression tag	UNP P16575
B	-12	VAL	-	expression tag	UNP P16575
B	-11	ASP	-	expression tag	UNP P16575
B	-10	ALA	-	expression tag	UNP P16575
B	-9	ALA	-	expression tag	UNP P16575
B	-8	THR	-	expression tag	UNP P16575
B	-7	ALA	-	expression tag	UNP P16575
B	-6	GLU	-	expression tag	UNP P16575
B	-5	LYS	-	expression tag	UNP P16575
B	-4	VAL	-	expression tag	UNP P16575
B	-3	PHE	-	expression tag	UNP P16575
B	-2	LYS	-	expression tag	UNP P16575
B	-1	GLN	-	expression tag	UNP P16575
B	0	TYR	-	expression tag	UNP P16575
B	1	ALA	-	expression tag	UNP P16575
B	2	ASN	-	expression tag	UNP P16575
B	3	ASP	-	expression tag	UNP P16575

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Chain	Residue	Modelled	Actual	Comment	Reference
B	4	ASN	-	expression tag	UNP P16575
B	5	GLY	-	expression tag	UNP P16575
B	6	VAL	-	expression tag	UNP P16575
B	7	ASP	-	expression tag	UNP P16575
B	8	GLY	-	expression tag	UNP P16575
B	9	GLU	-	expression tag	UNP P16575
B	10	TRP	-	expression tag	UNP P16575
B	11	THR	-	expression tag	UNP P16575
B	12	TYR	-	expression tag	UNP P16575
B	13	ASP	-	expression tag	UNP P16575
B	14	ASP	-	expression tag	UNP P16575
B	15	ALA	-	expression tag	UNP P16575
B	16	THR	-	expression tag	UNP P16575
B	17	LYS	-	expression tag	UNP P16575
B	18	THR	-	expression tag	UNP P16575
B	19	PHE	-	expression tag	UNP P16575
B	20	THR	-	expression tag	UNP P16575
B	21	VAL	-	expression tag	UNP P16575
B	22	THR	-	expression tag	UNP P16575
B	23	GLU	-	expression tag	UNP P16575
B	24	LEU	-	expression tag	UNP P16575
B	25	VAL	-	expression tag	UNP P16575
B	26	PRO	-	expression tag	UNP P16575
B	27	ARG	-	expression tag	UNP P16575
B	28	GLY	-	expression tag	UNP P16575
B	29	SER	-	expression tag	UNP P16575
B	545	GLU	-	expression tag	UNP P16575
B	546	HIS	-	expression tag	UNP P16575
B	547	HIS	-	expression tag	UNP P16575
B	548	HIS	-	expression tag	UNP P16575
B	549	HIS	-	expression tag	UNP P16575
B	550	HIS	-	expression tag	UNP P16575
B	551	HIS	-	expression tag	UNP P16575
C	-32	MET	-	initiating methionine	UNP P16575
C	-31	GLN	-	expression tag	UNP P16575
C	-30	TYR	-	expression tag	UNP P16575
C	-29	LYS	-	expression tag	UNP P16575
C	-28	LEU	-	expression tag	UNP P16575
C	-27	ALA	-	expression tag	UNP P16575
C	-26	LEU	-	expression tag	UNP P16575
C	-25	ASN	-	expression tag	UNP P16575
C	-24	GLY	-	expression tag	UNP P16575

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-23	LYS	-	expression tag	UNP P16575
C	-22	THR	-	expression tag	UNP P16575
C	-21	LEU	-	expression tag	UNP P16575
C	-20	LYS	-	expression tag	UNP P16575
C	-19	GLY	-	expression tag	UNP P16575
C	-18	GLU	-	expression tag	UNP P16575
C	-17	THR	-	expression tag	UNP P16575
C	-16	THR	-	expression tag	UNP P16575
C	-15	THR	-	expression tag	UNP P16575
C	-14	GLU	-	expression tag	UNP P16575
C	-13	ALA	-	expression tag	UNP P16575
C	-12	VAL	-	expression tag	UNP P16575
C	-11	ASP	-	expression tag	UNP P16575
C	-10	ALA	-	expression tag	UNP P16575
C	-9	ALA	-	expression tag	UNP P16575
C	-8	THR	-	expression tag	UNP P16575
C	-7	ALA	-	expression tag	UNP P16575
C	-6	GLU	-	expression tag	UNP P16575
C	-5	LYS	-	expression tag	UNP P16575
C	-4	VAL	-	expression tag	UNP P16575
C	-3	PHE	-	expression tag	UNP P16575
C	-2	LYS	-	expression tag	UNP P16575
C	-1	GLN	-	expression tag	UNP P16575
C	0	TYR	-	expression tag	UNP P16575
C	1	ALA	-	expression tag	UNP P16575
C	2	ASN	-	expression tag	UNP P16575
C	3	ASP	-	expression tag	UNP P16575
C	4	ASN	-	expression tag	UNP P16575
C	5	GLY	-	expression tag	UNP P16575
C	6	VAL	-	expression tag	UNP P16575
C	7	ASP	-	expression tag	UNP P16575
C	8	GLY	-	expression tag	UNP P16575
C	9	GLU	-	expression tag	UNP P16575
C	10	TRP	-	expression tag	UNP P16575
C	11	THR	-	expression tag	UNP P16575
C	12	TYR	-	expression tag	UNP P16575
C	13	ASP	-	expression tag	UNP P16575
C	14	ASP	-	expression tag	UNP P16575
C	15	ALA	-	expression tag	UNP P16575
C	16	THR	-	expression tag	UNP P16575
C	17	LYS	-	expression tag	UNP P16575
C	18	THR	-	expression tag	UNP P16575

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Chain	Residue	Modelled	Actual	Comment	Reference
C	19	PHE	-	expression tag	UNP P16575
C	20	THR	-	expression tag	UNP P16575
C	21	VAL	-	expression tag	UNP P16575
C	22	THR	-	expression tag	UNP P16575
C	23	GLU	-	expression tag	UNP P16575
C	24	LEU	-	expression tag	UNP P16575
C	25	VAL	-	expression tag	UNP P16575
C	26	PRO	-	expression tag	UNP P16575
C	27	ARG	-	expression tag	UNP P16575
C	28	GLY	-	expression tag	UNP P16575
C	29	SER	-	expression tag	UNP P16575
C	545	GLU	-	expression tag	UNP P16575
C	546	HIS	-	expression tag	UNP P16575
C	547	HIS	-	expression tag	UNP P16575
C	548	HIS	-	expression tag	UNP P16575
C	549	HIS	-	expression tag	UNP P16575
C	550	HIS	-	expression tag	UNP P16575
C	551	HIS	-	expression tag	UNP P16575
D	-32	MET	-	initiating methionine	UNP P16575
D	-31	GLN	-	expression tag	UNP P16575
D	-30	TYR	-	expression tag	UNP P16575
D	-29	LYS	-	expression tag	UNP P16575
D	-28	LEU	-	expression tag	UNP P16575
D	-27	ALA	-	expression tag	UNP P16575
D	-26	LEU	-	expression tag	UNP P16575
D	-25	ASN	-	expression tag	UNP P16575
D	-24	GLY	-	expression tag	UNP P16575
D	-23	LYS	-	expression tag	UNP P16575
D	-22	THR	-	expression tag	UNP P16575
D	-21	LEU	-	expression tag	UNP P16575
D	-20	LYS	-	expression tag	UNP P16575
D	-19	GLY	-	expression tag	UNP P16575
D	-18	GLU	-	expression tag	UNP P16575
D	-17	THR	-	expression tag	UNP P16575
D	-16	THR	-	expression tag	UNP P16575
D	-15	THR	-	expression tag	UNP P16575
D	-14	GLU	-	expression tag	UNP P16575
D	-13	ALA	-	expression tag	UNP P16575
D	-12	VAL	-	expression tag	UNP P16575
D	-11	ASP	-	expression tag	UNP P16575
D	-10	ALA	-	expression tag	UNP P16575
D	-9	ALA	-	expression tag	UNP P16575

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-8	THR	-	expression tag	UNP P16575
D	-7	ALA	-	expression tag	UNP P16575
D	-6	GLU	-	expression tag	UNP P16575
D	-5	LYS	-	expression tag	UNP P16575
D	-4	VAL	-	expression tag	UNP P16575
D	-3	PHE	-	expression tag	UNP P16575
D	-2	LYS	-	expression tag	UNP P16575
D	-1	GLN	-	expression tag	UNP P16575
D	0	TYR	-	expression tag	UNP P16575
D	1	ALA	-	expression tag	UNP P16575
D	2	ASN	-	expression tag	UNP P16575
D	3	ASP	-	expression tag	UNP P16575
D	4	ASN	-	expression tag	UNP P16575
D	5	GLY	-	expression tag	UNP P16575
D	6	VAL	-	expression tag	UNP P16575
D	7	ASP	-	expression tag	UNP P16575
D	8	GLY	-	expression tag	UNP P16575
D	9	GLU	-	expression tag	UNP P16575
D	10	TRP	-	expression tag	UNP P16575
D	11	THR	-	expression tag	UNP P16575
D	12	TYR	-	expression tag	UNP P16575
D	13	ASP	-	expression tag	UNP P16575
D	14	ASP	-	expression tag	UNP P16575
D	15	ALA	-	expression tag	UNP P16575
D	16	THR	-	expression tag	UNP P16575
D	17	LYS	-	expression tag	UNP P16575
D	18	THR	-	expression tag	UNP P16575
D	19	PHE	-	expression tag	UNP P16575
D	20	THR	-	expression tag	UNP P16575
D	21	VAL	-	expression tag	UNP P16575
D	22	THR	-	expression tag	UNP P16575
D	23	GLU	-	expression tag	UNP P16575
D	24	LEU	-	expression tag	UNP P16575
D	25	VAL	-	expression tag	UNP P16575
D	26	PRO	-	expression tag	UNP P16575
D	27	ARG	-	expression tag	UNP P16575
D	28	GLY	-	expression tag	UNP P16575
D	29	SER	-	expression tag	UNP P16575
D	545	GLU	-	expression tag	UNP P16575
D	546	HIS	-	expression tag	UNP P16575
D	547	HIS	-	expression tag	UNP P16575
D	548	HIS	-	expression tag	UNP P16575

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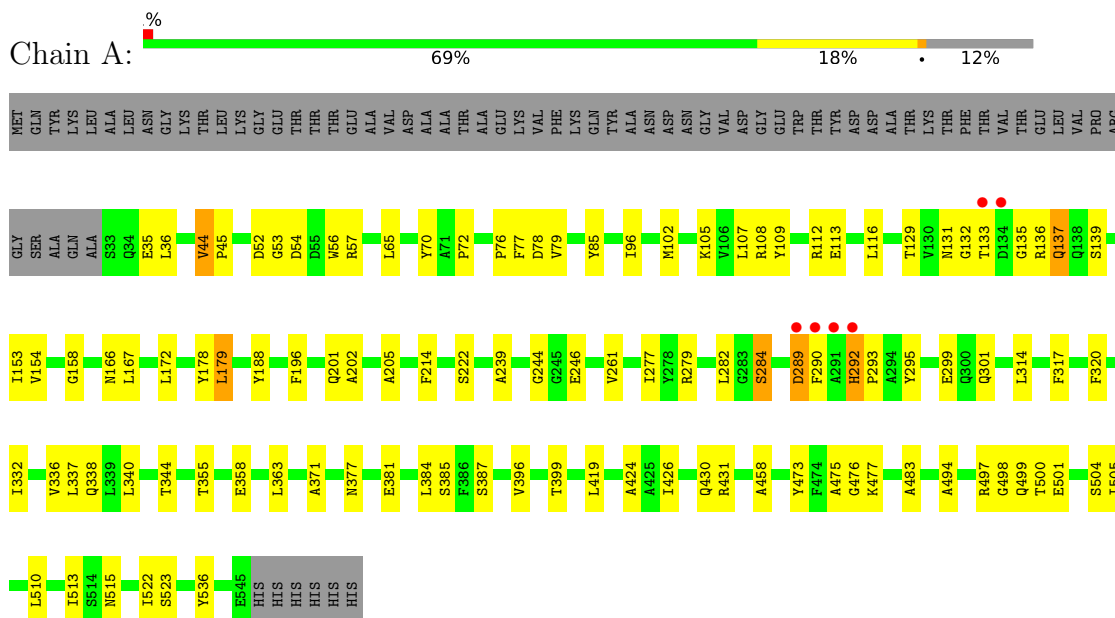
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Chain	Residue	Modelled	Actual	Comment	Reference
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D	550	HIS	-	expression tag	UNP P16575
D	551	HIS	-	expression tag	UNP P16575

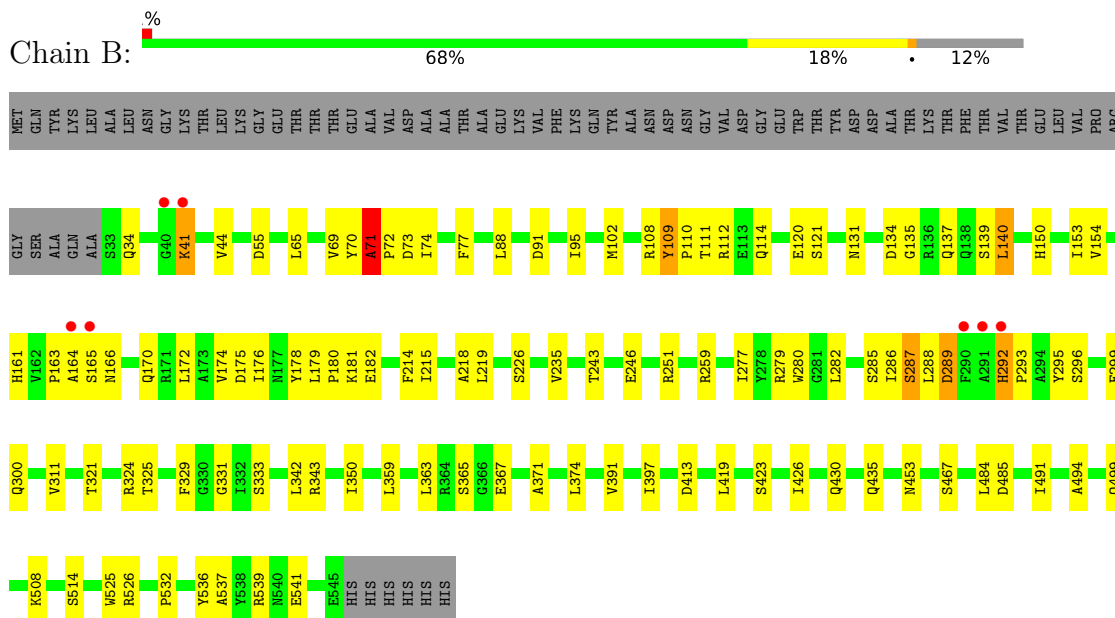
3 Residue-property plots [i](#)

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.

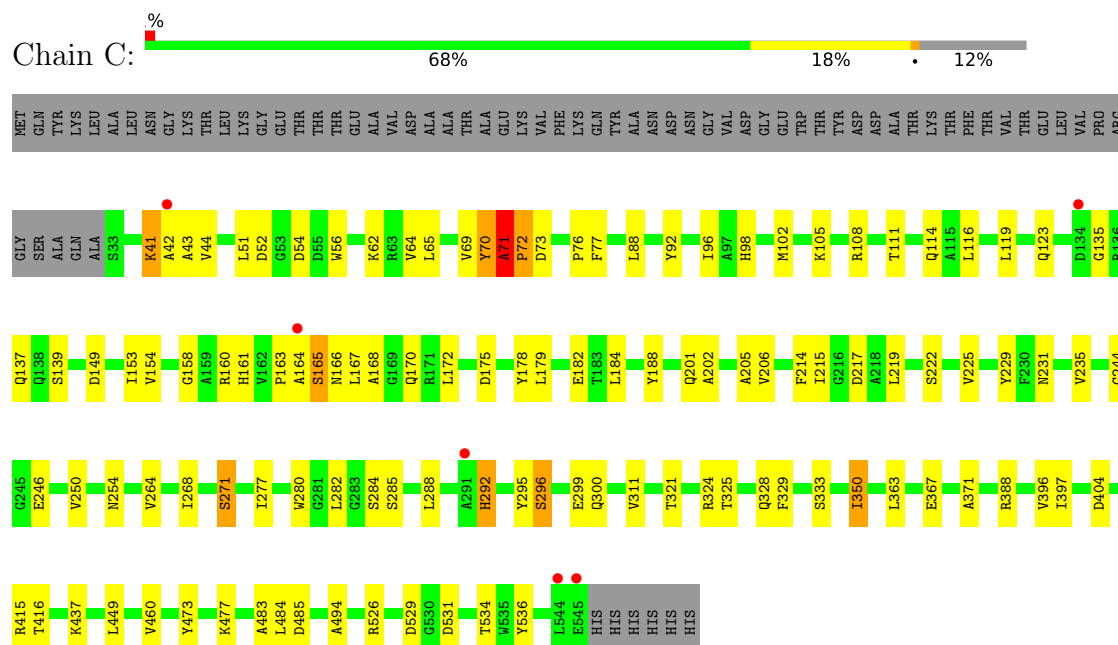
• Molecule 1: Virulence sensor protein BvgS



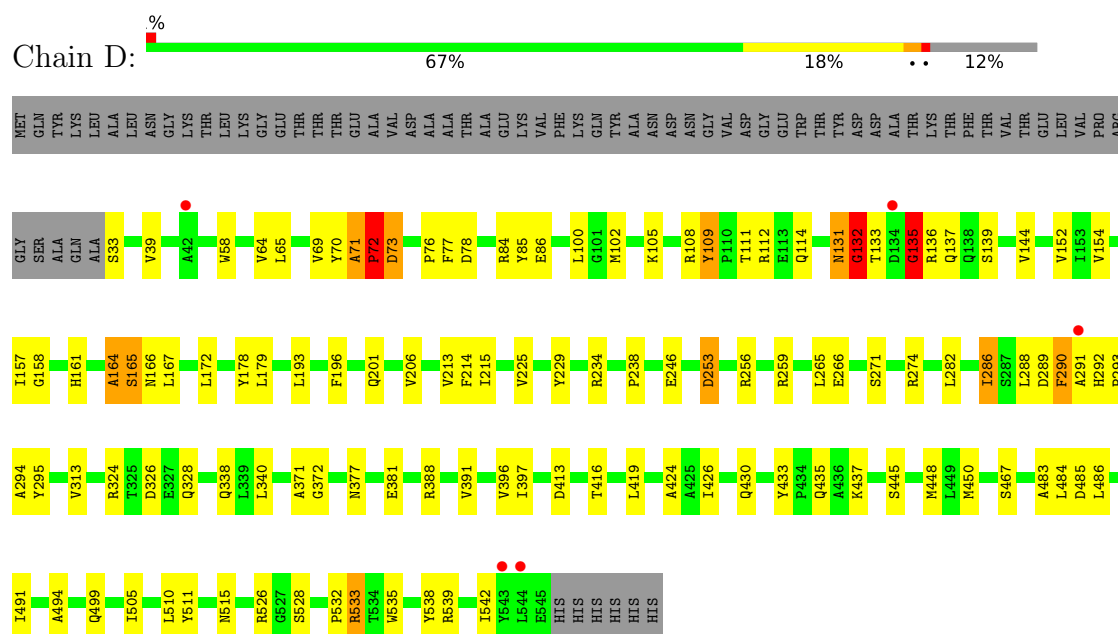
• Molecule 1: Virulence sensor protein BvgS



• Molecule 1: Virulence sensor protein BvgS



• Molecule 1: Virulence sensor protein BvgS



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	72.45Å 285.82Å 128.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.99 – 3.10 19.99 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.4 (19.99-3.10) 98.9 (19.99-3.10)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.25 (at 3.09Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.181 , 0.245 0.185 , 0.246	Depositor DCC
R_{free} test set	2000 reflections (4.10%)	wwPDB-VP
Wilson B-factor (Å ²)	44.6	Xtriage
Anisotropy	0.242	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 28.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	15649	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.38% of the height of the origin peak. No significant pseudotranslation is detected.*

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 [i](#)

5.1 Standard geometry [i](#)

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	0.67	0/3978	1.08	18/5433 (0.3%)
1	B	0.68	0/3995	1.06	13/5455 (0.2%)
1	C	0.67	0/4002	1.05	11/5463 (0.2%)
1	D	0.66	0/4006	1.05	14/5469 (0.3%)
All	All	0.67	0/15981	1.06	56/21820 (0.3%)

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	B	0	1
1	C	0	2
1	D	0	1
All	All	0	4

There are no bond length outliers.

All (56) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	44	VAL	CA-C-N	9.14	129.19	119.78
1	A	44	VAL	C-N-CA	9.14	129.19	119.78
1	A	136	ARG	N-CA-C	-8.30	100.59	111.71
1	B	121	SER	N-CA-C	8.21	121.15	111.71
1	A	52	ASP	N-CA-C	8.13	122.30	112.38
1	D	164	ALA	N-CA-C	-8.06	102.49	111.28
1	A	188	TYR	CA-C-N	7.29	126.93	119.56
1	A	188	TYR	C-N-CA	7.29	126.93	119.56
1	A	54	ASP	N-CA-C	-7.00	103.70	111.82
1	D	433	TYR	CA-C-N	6.84	126.44	119.19
1	D	433	TYR	C-N-CA	6.84	126.44	119.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	137	GLN	N-CA-C	-6.70	104.99	113.43
1	D	196	PHE	CA-C-N	6.63	127.16	119.47
1	D	196	PHE	C-N-CA	6.63	127.16	119.47
1	D	133	THR	N-CA-C	-6.58	105.13	113.02
1	B	536	TYR	N-CA-C	-6.49	104.28	111.36
1	C	71	ALA	CA-C-N	-6.41	113.03	119.56
1	C	71	ALA	C-N-CA	-6.41	113.03	119.56
1	D	72	PRO	N-CA-C	6.36	121.90	113.57
1	B	70	TYR	N-CA-C	6.35	117.81	108.86
1	C	244	GLY	N-CA-C	-6.35	102.63	112.85
1	A	289	ASP	N-CA-C	6.34	118.27	111.36
1	C	165	SER	N-CA-C	6.21	119.32	111.69
1	C	526	ARG	N-CA-C	-6.07	104.67	111.28
1	B	71	ALA	CA-C-N	-6.05	112.62	119.28
1	B	71	ALA	C-N-CA	-6.05	112.62	119.28
1	A	536	TYR	N-CA-C	-5.99	104.83	111.36
1	C	54	ASP	N-CA-C	-5.98	104.89	111.82
1	C	72	PRO	N-CA-C	5.96	121.58	113.84
1	A	109	TYR	CA-C-N	5.90	125.77	119.28
1	A	109	TYR	C-N-CA	5.90	125.77	119.28
1	A	179	LEU	CA-C-N	5.59	125.87	119.83
1	A	179	LEU	C-N-CA	5.59	125.87	119.83
1	C	350	ILE	N-CA-C	5.57	116.33	108.36
1	D	132	GLY	N-CA-C	-5.53	100.07	113.18
1	B	109	TYR	CA-C-N	5.47	125.82	119.47
1	B	109	TYR	C-N-CA	5.47	125.82	119.47
1	A	79	VAL	N-CA-C	5.40	115.90	108.12
1	B	289	ASP	N-CA-C	-5.39	99.32	110.80
1	B	135	GLY	CA-C-N	5.25	131.15	121.70
1	B	135	GLY	C-N-CA	5.25	131.15	121.70
1	C	123	GLN	N-CA-C	-5.13	105.76	111.36
1	D	290	PHE	N-CA-C	5.12	117.51	110.35
1	A	196	PHE	CA-C-N	5.10	125.39	119.47
1	A	196	PHE	C-N-CA	5.10	125.39	119.47
1	D	64	VAL	N-CA-C	5.08	115.22	108.11
1	A	135	GLY	N-CA-C	-5.05	101.21	113.18
1	B	453	ASN	N-CA-C	5.05	117.90	111.69
1	C	268	ILE	CA-C-N	5.05	125.58	120.38
1	C	268	ILE	C-N-CA	5.05	125.58	120.38
1	D	109	TYR	CA-C-N	5.04	125.31	119.47
1	D	109	TYR	C-N-CA	5.04	125.31	119.47
1	B	44	VAL	CA-C-N	5.03	124.93	119.85

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	44	VAL	C-N-CA	5.03	124.93	119.85
1	D	135	GLY	CA-C-N	5.03	130.76	121.70
1	D	135	GLY	C-N-CA	5.03	130.76	121.70

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	289	ASP	Peptide
1	C	292	HIS	Peptide
1	C	70	TYR	Peptide
1	D	135	GLY	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	3895	0	3818	64	0
1	B	3913	0	3867	71	0
1	C	3919	0	3861	81	0
1	D	3922	0	3878	86	0
All	All	15649	0	15424	278	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 (278) 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:D:158:GLY:HA2	1:D:328:GLN:HE22	1.42	0.84
1:D:76:PRO:HG3	1:D:282:LEU:HD11	1.60	0.84
1:B:172:LEU:HD11	1:B:215:ILE:HG12	1.61	0.83
1:C:165:SER:N	1:C:166:ASN:HA	2.01	0.76
1:B:296:SER:O	1:B:300:GLN:HG2	1.87	0.75
1:C:172:LEU:HD11	1:C:215:ILE:HG12	1.69	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:120:GLU:HA	1:B:251:ARG:HD2	1.70	0.72
1:B:71:ALA:HB3	1:B:72:PRO:HD3	1.72	0.71
1:C:296:SER:HB3	1:C:299:GLU:H	1.54	0.71
1:D:388:ARG:HD3	1:D:511:TYR:CE1	2.25	0.71
1:C:325:THR:HG23	1:D:533:ARG:HD3	1.75	0.69
1:B:69:VAL:HG23	1:B:108:ARG:HG3	1.74	0.69
1:D:58:TRP:CD2	1:D:256:ARG:HD3	2.29	0.67
1:C:154:VAL:HB	1:C:214:PHE:HB3	1.77	0.67
1:D:164:ALA:O	1:D:166:ASN:N	2.21	0.66
1:A:317:PHE:CD2	1:A:320:PHE:HB2	2.31	0.65
1:D:69:VAL:HG23	1:D:108:ARG:HG3	1.78	0.65
1:A:515:ASN:HD22	1:B:280:TRP:HE3	1.43	0.65
1:C:72:PRO:O	1:C:73:ASP:HB2	1.96	0.65
1:D:135:GLY:HA2	1:D:137:GLN:H	1.62	0.64
1:C:396:VAL:HG12	1:C:483:ALA:HA	1.79	0.64
1:A:317:PHE:HD2	1:A:320:PHE:HB2	1.62	0.63
1:C:76:PRO:HG3	1:C:282:LEU:HD11	1.81	0.63
1:C:416:THR:HG22	1:C:437:LYS:HD3	1.80	0.63
1:A:53:GLY:O	1:A:57:ARG:HG3	1.99	0.63
1:D:72:PRO:O	1:D:73:ASP:HB2	1.98	0.62
1:B:293:PRO:HB2	1:B:295:TYR:CZ	2.35	0.62
1:C:363:LEU:HD11	1:C:371:ALA:HB2	1.81	0.62
1:A:53:GLY:HA2	1:A:56:TRP:HB2	1.81	0.62
1:C:71:ALA:HB1	1:C:72:PRO:HD3	1.80	0.62
1:C:222:SER:HB2	1:C:284:SER:OG	2.00	0.62
1:C:71:ALA:HB1	1:C:72:PRO:CD	2.29	0.62
1:D:371:ALA:HB3	1:D:494:ALA:HB3	1.83	0.61
1:C:70:TYR:HD1	1:C:71:ALA:HB3	1.66	0.61
1:C:531:ASP:OD2	1:C:534:THR:OG1	2.17	0.61
1:D:65:LEU:HB2	1:D:102:MET:HE3	1.83	0.60
1:D:396:VAL:HG12	1:D:483:ALA:HA	1.82	0.60
1:A:510:LEU:HD23	1:A:513:ILE:HD12	1.83	0.60
1:B:285:SER:HA	1:B:288:LEU:HD13	1.84	0.60
1:A:289:ASP:N	1:A:290:PHE:HA	2.17	0.59
1:C:111:THR:H	1:C:114:GLN:HG3	1.67	0.59
1:B:296:SER:HB3	1:B:299:GLU:H	1.67	0.58
1:C:311:VAL:HB	1:C:350:ILE:HD13	1.85	0.58
1:B:137:GLN:C	1:B:139:SER:H	2.12	0.58
1:C:477:LYS:HG3	1:D:539:ARG:NH2	2.19	0.58
1:A:158:GLY:C	1:C:367:GLU:HG2	2.29	0.58
1:C:449:LEU:HD22	1:D:538:TYR:CZ	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:167:LEU:HD23	1:A:172:LEU:HD22	1.87	0.57
1:C:201:GLN:OE1	1:D:485:ASP:HA	2.05	0.57
1:D:172:LEU:HD11	1:D:215:ILE:HG13	1.85	0.57
1:C:324:ARG:HD2	1:C:328:GLN:HB3	1.87	0.57
1:B:329:PHE:CD2	1:B:350:ILE:HG13	2.40	0.57
1:C:285:SER:HA	1:C:288:LEU:HD12	1.86	0.56
1:B:71:ALA:HB2	1:B:110:PRO:O	2.05	0.56
1:D:484:LEU:HD13	1:D:486:LEU:HD12	1.86	0.56
1:A:475:ALA:O	1:B:539:ARG:NH2	2.38	0.56
1:D:419:LEU:HD22	1:D:426:ILE:HG12	1.88	0.56
1:D:164:ALA:C	1:D:166:ASN:H	2.13	0.56
1:B:164:ALA:C	1:B:166:ASN:H	2.14	0.56
1:B:154:VAL:HG22	1:B:235:VAL:HG22	1.88	0.56
1:D:165:SER:O	1:D:165:SER:OG	2.16	0.56
1:A:317:PHE:HE2	1:A:320:PHE:CD2	2.24	0.56
1:B:299:GLU:OE2	1:B:508:LYS:NZ	2.39	0.56
1:C:96:ILE:HA	1:C:264:VAL:HG11	1.87	0.55
1:C:158:GLY:HA2	1:C:328:GLN:NE2	2.21	0.55
1:B:537:ALA:O	1:B:541:GLU:HG2	2.06	0.55
1:D:137:GLN:HG2	1:D:139:SER:HB3	1.89	0.55
1:A:131:ASN:OD1	1:A:133:THR:HG22	2.05	0.55
1:B:77:PHE:CE1	1:B:246:GLU:HG3	2.42	0.55
1:B:371:ALA:HB3	1:B:494:ALA:HB3	1.89	0.55
1:A:154:VAL:HB	1:A:214:PHE:HB3	1.88	0.54
1:C:163:PRO:HG2	1:C:170:GLN:HE21	1.72	0.54
1:D:111:THR:OG1	1:D:114:GLN:HG3	2.07	0.54
1:B:34:GLN:O	1:B:108:ARG:N	2.31	0.54
1:C:69:VAL:HG13	1:C:108:ARG:HG3	1.90	0.54
1:C:165:SER:HB2	1:C:168:ALA:H	1.72	0.54
1:D:234:ARG:HD2	1:D:338:GLN:OE1	2.08	0.54
1:B:71:ALA:HB2	1:B:111:THR:HA	1.88	0.54
1:C:231:ASN:HD21	1:D:528:SER:HA	1.73	0.54
1:C:51:LEU:HB2	1:C:56:TRP:CE2	2.43	0.53
1:D:158:GLY:CA	1:D:328:GLN:HE22	2.17	0.53
1:A:132:GLY:HA3	1:A:244:GLY:H	1.73	0.53
1:B:55:ASP:OD1	1:B:259:ARG:NH1	2.41	0.53
1:D:71:ALA:HB3	1:D:72:PRO:HD3	1.90	0.53
1:A:337:LEU:HD23	1:A:340:LEU:HD12	1.89	0.53
1:D:157:ILE:HG23	1:D:328:GLN:HE21	1.72	0.53
1:D:416:THR:HA	1:D:437:LYS:O	2.09	0.53
1:B:311:VAL:HB	1:B:350:ILE:HD13	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:64:VAL:HG11	1:C:105:LYS:HD3	1.90	0.53
1:A:419:LEU:HD22	1:A:426:ILE:HG12	1.90	0.53
1:B:287:SER:HB3	1:B:343:ARG:NH1	2.24	0.52
1:C:219:LEU:HD22	1:C:282:LEU:HD13	1.91	0.52
1:C:473:TYR:O	1:D:539:ARG:HD2	2.09	0.52
1:A:295:TYR:CE1	1:A:505:ILE:HG23	2.45	0.52
1:C:137:GLN:C	1:C:139:SER:H	2.16	0.52
1:C:280:TRP:HE3	1:D:515:ASN:HD22	1.58	0.52
1:C:329:PHE:CD2	1:C:350:ILE:HG13	2.45	0.52
1:A:153:ILE:HG13	1:A:239:ALA:HB2	1.92	0.52
1:A:292:HIS:H	1:A:293:PRO:CD	2.23	0.52
1:D:77:PHE:CE1	1:D:246:GLU:HG3	2.44	0.52
1:A:76:PRO:HG3	1:A:282:LEU:HD11	1.91	0.51
1:B:41:LYS:HE3	1:B:279:ARG:HD2	1.92	0.51
1:B:277:ILE:HG23	1:B:282:LEU:HB2	1.92	0.51
1:B:154:VAL:HB	1:B:214:PHE:HB3	1.93	0.51
1:D:238:PRO:HD3	1:D:290:PHE:CD2	2.46	0.51
1:A:396:VAL:HG12	1:A:483:ALA:HA	1.92	0.50
1:D:426:ILE:O	1:D:430:GLN:HG2	2.12	0.50
1:B:88:LEU:HD13	1:B:280:TRP:CD1	2.47	0.50
1:D:111:THR:HG1	1:D:114:GLN:HG3	1.77	0.50
1:A:201:GLN:NE2	1:B:485:ASP:HA	2.27	0.49
1:A:476:GLY:O	1:A:477:LYS:HD3	2.12	0.49
1:B:77:PHE:CZ	1:B:246:GLU:HG3	2.47	0.49
1:B:426:ILE:O	1:B:430:GLN:HG2	2.13	0.49
1:A:201:GLN:HE22	1:B:485:ASP:HA	1.78	0.49
1:C:460:VAL:HG22	1:C:484:LEU:HD11	1.94	0.49
1:C:206:VAL:HG21	1:C:214:PHE:HB2	1.93	0.49
1:A:137:GLN:C	1:A:139:SER:H	2.21	0.48
1:D:33:SER:HB3	1:D:109:TYR:CE1	2.49	0.48
1:D:377:ASN:CG	1:D:424:ALA:HB2	2.38	0.48
1:B:91:ASP:O	1:B:95:ILE:HG13	2.14	0.48
1:C:111:THR:N	1:C:114:GLN:HG3	2.28	0.48
1:B:131:ASN:HD22	1:B:243:THR:HB	1.78	0.48
1:C:285:SER:O	1:C:288:LEU:HB2	2.12	0.48
1:D:172:LEU:HB3	1:D:193:LEU:HD23	1.95	0.48
1:B:419:LEU:HD22	1:B:426:ILE:HG12	1.95	0.47
1:B:467:SER:HB3	1:B:526:ARG:HE	1.78	0.47
1:C:149:ASP:OD1	1:C:217:ASP:HB2	2.14	0.47
1:C:154:VAL:HG22	1:C:235:VAL:HG22	1.96	0.47
1:C:473:TYR:CE1	1:D:532:PRO:HA	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:279:ARG:HG3	1:B:514:SER:HB2	1.96	0.47
1:A:70:TYR:HD1	1:A:72:PRO:HD2	1.79	0.47
1:A:317:PHE:CE2	1:A:320:PHE:CD2	3.02	0.47
1:D:105:LYS:HE2	1:D:105:LYS:HB3	1.72	0.47
1:A:96:ILE:HD13	1:A:261:VAL:HG13	1.97	0.47
1:A:179:LEU:HD23	1:A:179:LEU:HA	1.78	0.47
1:A:377:ASN:CG	1:A:424:ALA:HB2	2.40	0.47
1:B:423:SER:HB3	1:B:426:ILE:HG13	1.97	0.47
1:C:250:VAL:HG12	1:C:254:ASN:HB3	1.97	0.47
1:D:178:TYR:CD1	1:D:179:LEU:HG	2.50	0.47
1:B:91:ASP:OD2	1:B:279:ARG:NH2	2.46	0.47
1:B:331:GLY:HA2	1:B:525:TRP:CE2	2.50	0.47
1:D:397:ILE:HG23	1:D:484:LEU:HD21	1.96	0.47
1:A:65:LEU:HB2	1:A:102:MET:HE3	1.98	0.46
1:B:109:TYR:HA	1:B:110:PRO:HD3	1.80	0.46
1:D:100:LEU:O	1:D:102:MET:HG2	2.15	0.46
1:D:391:VAL:HB	1:D:491:ILE:HB	1.96	0.46
1:A:295:TYR:OH	1:A:344:THR:HG22	2.15	0.46
1:A:371:ALA:HB3	1:A:494:ALA:HB3	1.97	0.46
1:D:58:TRP:CE2	1:D:256:ARG:HD3	2.51	0.46
1:D:167:LEU:HD21	1:D:213:VAL:HG11	1.97	0.46
1:A:377:ASN:O	1:A:381:GLU:HG3	2.16	0.46
1:B:391:VAL:HB	1:B:491:ILE:HB	1.97	0.46
1:A:78:ASP:OD1	1:A:85:TYR:OH	2.27	0.46
1:A:477:LYS:HG2	1:B:539:ARG:HH21	1.81	0.46
1:D:206:VAL:HG21	1:D:214:PHE:HB2	1.96	0.46
1:B:287:SER:HB3	1:B:343:ARG:HH12	1.81	0.46
1:C:41:LYS:HG3	1:C:43:ALA:H	1.81	0.46
1:A:35:GLU:HA	1:A:107:LEU:HA	1.98	0.46
1:A:112:ARG:HB3	1:A:113:GLU:OE2	2.15	0.45
1:B:174:VAL:HG12	1:B:175:ASP:O	2.16	0.45
1:C:77:PHE:CE1	1:C:246:GLU:HG3	2.51	0.45
1:C:201:GLN:HE21	1:C:201:GLN:HB3	1.59	0.45
1:C:404:ASP:O	1:C:415:ARG:NH2	2.40	0.45
1:D:253:ASP:OD1	1:D:253:ASP:N	2.49	0.45
1:C:225:VAL:HA	1:C:229:TYR:HB2	1.97	0.45
1:A:77:PHE:CE1	1:A:246:GLU:HG3	2.51	0.45
1:C:271:SER:HB2	1:D:271:SER:OG	2.17	0.45
1:B:359:LEU:HD22	1:B:374:LEU:HD21	1.98	0.45
1:B:467:SER:HB3	1:B:526:ARG:NE	2.31	0.45
1:B:65:LEU:HB2	1:B:102:MET:HE3	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:88:LEU:HD22	1:C:92:TYR:HE2	1.81	0.44
1:A:222:SER:HB2	1:A:284:SER:HB2	1.99	0.44
1:A:363:LEU:HD23	1:A:384:LEU:HD21	2.00	0.44
1:A:385:SER:HB2	1:A:497:ARG:HA	1.97	0.44
1:D:39:VAL:CG2	1:D:84:ARG:HB3	2.47	0.44
1:D:340:LEU:HD21	1:D:510:LEU:HD23	1.98	0.44
1:A:431:ARG:HB3	1:A:431:ARG:HH11	1.82	0.44
1:D:70:TYR:CE1	1:D:112:ARG:HG3	2.51	0.44
1:C:477:LYS:CD	1:D:542:ILE:HG21	2.47	0.44
1:A:202:ALA:O	1:A:205:ALA:HB3	2.17	0.44
1:B:178:TYR:CD1	1:B:179:LEU:HG	2.53	0.44
1:B:153:ILE:HG12	1:B:215:ILE:CD1	2.47	0.44
1:C:485:ASP:HA	1:D:201:GLN:NE2	2.32	0.44
1:B:277:ILE:HD13	1:B:277:ILE:HA	1.82	0.44
1:C:41:LYS:HD2	1:C:42:ALA:H	1.83	0.44
1:D:484:LEU:HB3	1:D:486:LEU:HG	1.99	0.44
1:A:314:LEU:HD12	1:A:317:PHE:CD1	2.53	0.43
1:A:332:ILE:HD13	1:A:522:ILE:HG12	2.00	0.43
1:C:449:LEU:HD21	1:D:535:TRP:HZ3	1.82	0.43
1:D:265:LEU:HD23	1:D:265:LEU:HA	1.73	0.43
1:B:363:LEU:HD12	1:B:363:LEU:HA	1.70	0.43
1:C:388:ARG:NH1	1:D:86:GLU:OE2	2.50	0.43
1:D:137:GLN:HG2	1:D:139:SER:H	1.84	0.43
1:D:256:ARG:O	1:D:259:ARG:HB3	2.19	0.43
1:B:163:PRO:HG2	1:B:170:GLN:HE21	1.84	0.43
1:C:116:LEU:O	1:C:119:LEU:HB3	2.18	0.43
1:C:325:THR:CG2	1:D:533:ARG:HD3	2.44	0.43
1:D:78:ASP:OD1	1:D:85:TYR:OH	2.34	0.43
1:C:175:ASP:HB3	1:C:178:TYR:HB2	2.00	0.43
1:A:399:THR:HG22	1:A:458:ALA:HB2	2.01	0.43
1:B:292:HIS:H	1:B:293:PRO:CD	2.31	0.43
1:D:324:ARG:HD2	1:D:328:GLN:HB3	1.99	0.43
1:C:167:LEU:HD23	1:C:172:LEU:HD22	2.00	0.43
1:D:58:TRP:CE3	1:D:256:ARG:HD3	2.53	0.43
1:B:73:ASP:HB2	1:B:108:ARG:NH2	2.34	0.43
1:A:430:GLN:H	1:A:430:GLN:HG2	1.69	0.43
1:D:467:SER:HB3	1:D:526:ARG:NE	2.34	0.43
1:D:467:SER:HB3	1:D:526:ARG:NH2	2.33	0.43
1:A:44:VAL:HA	1:A:45:PRO:HD3	1.72	0.42
1:C:321:THR:HG22	1:C:333:SER:HB2	2.00	0.42
1:C:397:ILE:HG23	1:C:484:LEU:HD21	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:274:ARG:HG2	1:D:286:ILE:HD12	2.00	0.42
1:A:426:ILE:O	1:A:430:GLN:HG2	2.19	0.42
1:C:135:GLY:HA2	1:C:137:GLN:HB2	2.00	0.42
1:C:166:ASN:HB3	1:C:188:TYR:HE1	1.84	0.42
1:C:311:VAL:HB	1:C:350:ILE:CD1	2.49	0.42
1:C:371:ALA:HB3	1:C:494:ALA:HB3	2.01	0.42
1:D:154:VAL:HB	1:D:214:PHE:HB3	2.01	0.42
1:D:238:PRO:HD3	1:D:290:PHE:CG	2.54	0.42
1:B:172:LEU:HD11	1:B:215:ILE:CG1	2.42	0.42
1:D:137:GLN:C	1:D:139:SER:H	2.26	0.42
1:D:448:MET:HE2	1:D:448:MET:HB3	1.87	0.42
1:B:365:SER:OG	1:B:367:GLU:HG3	2.19	0.42
1:C:62:LYS:O	1:C:64:VAL:N	2.43	0.42
1:C:295:TYR:HB2	1:C:300:GLN:HG3	2.01	0.42
1:D:131:ASN:HB3	1:D:132:GLY:H	1.59	0.42
1:A:355:THR:OG1	1:A:358:GLU:HB2	2.18	0.42
1:A:473:TYR:CE1	1:B:532:PRO:HA	2.55	0.42
1:C:167:LEU:HD22	1:C:188:TYR:CE1	2.55	0.42
1:D:158:GLY:HA2	1:D:328:GLN:NE2	2.22	0.42
1:D:292:HIS:N	1:D:293:PRO:CD	2.82	0.42
1:D:450:MET:HE2	1:D:450:MET:HB3	1.95	0.42
1:C:485:ASP:HA	1:D:201:GLN:HE22	1.85	0.42
1:D:413:ASP:HA	1:D:435:GLN:HB3	2.01	0.42
1:C:69:VAL:O	1:C:108:ARG:HA	2.20	0.42
1:C:178:TYR:CD1	1:C:179:LEU:HG	2.55	0.42
1:D:225:VAL:HA	1:D:229:TYR:HB2	2.02	0.42
1:A:332:ILE:O	1:A:336:VAL:HG23	2.20	0.41
1:B:111:THR:HB	1:B:114:GLN:HG3	2.02	0.41
1:C:51:LEU:HB2	1:C:56:TRP:NE1	2.35	0.41
1:C:70:TYR:CD1	1:C:71:ALA:HB3	2.50	0.41
1:D:292:HIS:N	1:D:293:PRO:HD3	2.35	0.41
1:A:431:ARG:HB3	1:A:431:ARG:NH1	2.35	0.41
1:B:176:ILE:HD11	1:B:181:LYS:HE2	2.03	0.41
1:B:219:LEU:HD23	1:B:219:LEU:HA	1.83	0.41
1:A:36:LEU:HD11	1:A:108:ARG:HD2	2.02	0.41
1:B:179:LEU:HA	1:B:180:PRO:HD3	1.86	0.41
1:B:397:ILE:HG23	1:B:484:LEU:HD21	2.01	0.41
1:A:299:GLU:OE2	1:A:504:SER:OG	2.23	0.41
1:B:134:ASP:O	1:B:140:LEU:HD22	2.20	0.41
1:D:326:ASP:HB2	1:D:328:GLN:CB	2.51	0.41
1:D:377:ASN:O	1:D:381:GLU:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:336:VAL:O	1:A:340:LEU:HG	2.20	0.41
1:A:498:GLY:O	1:A:500:THR:HG23	2.21	0.41
1:D:484:LEU:HD13	1:D:486:LEU:CD1	2.50	0.41
1:A:113:GLU:HA	1:A:116:LEU:HB2	2.02	0.41
1:A:277:ILE:HA	1:A:277:ILE:HD13	1.80	0.41
1:C:65:LEU:HB2	1:C:102:MET:HE3	2.02	0.41
1:C:202:ALA:O	1:C:205:ALA:HB3	2.21	0.41
1:B:112:ARG:HH21	1:B:134:ASP:HB3	1.86	0.41
1:C:536:TYR:CE1	1:D:539:ARG:HD3	2.56	0.41
1:D:152:VAL:HG11	1:D:288:LEU:HD23	2.03	0.41
1:D:313:VAL:HG12	1:D:372:GLY:HA3	2.01	0.41
1:A:137:GLN:O	1:A:139:SER:N	2.53	0.40
1:A:178:TYR:CD1	1:A:179:LEU:HG	2.56	0.40
1:A:501:GLU:O	1:A:505:ILE:HG13	2.21	0.40
1:B:71:ALA:O	1:B:72:PRO:C	2.64	0.40
1:D:144:VAL:HG21	1:D:266:GLU:HG3	2.02	0.40
1:B:150:HIS:O	1:B:218:ALA:HB2	2.22	0.40
1:B:413:ASP:HA	1:B:435:GLN:HB2	2.02	0.40
1:C:44:VAL:HG11	1:C:98:HIS:HB3	2.03	0.40
1:C:153:ILE:HG12	1:C:215:ILE:CD1	2.50	0.40
1:B:435:GLN:H	1:B:435:GLN:HG2	1.61	0.40
1:C:179:LEU:HD12	1:C:184:LEU:HD21	2.03	0.40
1:D:295:TYR:CE1	1:D:505:ILE:HG23	2.57	0.40
1:B:321:THR:HG22	1:B:333:SER:HB2	2.02	0.40
1:B:342:LEU:HA	1:B:342:LEU:HD12	1.91	0.40
1:C:71:ALA:CB	1:C:72:PRO:CD	2.98	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	511/584 (88%)	486 (95%)	22 (4%)	3 (1%)	21	52
1	B	511/584 (88%)	483 (94%)	22 (4%)	6 (1%)	10	37
1	C	511/584 (88%)	477 (93%)	26 (5%)	8 (2%)	7	30
1	D	511/584 (88%)	484 (95%)	16 (3%)	11 (2%)	5	24
All	All	2044/2336 (88%)	1930 (94%)	86 (4%)	28 (1%)	9	34

All (28) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	41	LYS
1	B	71	ALA
1	B	161	HIS
1	C	41	LYS
1	C	71	ALA
1	C	161	HIS
1	C	292	HIS
1	D	71	ALA
1	D	165	SER
1	D	291	ALA
1	D	294	ALA
1	A	166	ASN
1	B	165	SER
1	C	296	SER
1	C	164	ALA
1	D	136	ARG
1	D	161	HIS
1	A	292	HIS
1	B	292	HIS
1	B	499	GLN
1	D	131	ASN
1	D	132	GLY
1	A	499	GLN
1	C	52	ASP
1	C	529	ASP
1	D	289	ASP
1	D	499	GLN
1	D	73	ASP

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	397/472 (84%)	390 (98%)	7 (2%)	51	73
1	B	402/472 (85%)	394 (98%)	8 (2%)	48	72
1	C	403/472 (85%)	399 (99%)	4 (1%)	68	79
1	D	405/472 (86%)	400 (99%)	5 (1%)	63	78
All	All	1607/1888 (85%)	1583 (98%)	24 (2%)	57	75

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

Mol	Chain	Res	Type
1	A	105	LYS
1	A	129	THR
1	A	284	SER
1	A	301	GLN
1	A	338	GLN
1	A	387	SER
1	A	523	SER
1	B	74	ILE
1	B	140	LEU
1	B	182	GLU
1	B	226	SER
1	B	286	ILE
1	B	287	SER
1	B	324	ARG
1	B	325	THR
1	C	160	ARG
1	C	182	GLU
1	C	271	SER
1	C	277	ILE
1	D	72	PRO
1	D	253	ASP
1	D	286	ILE
1	D	445	SER
1	D	533	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	300	GLN
1	A	435	GLN
1	A	515	ASN
1	B	114	GLN
1	B	227	GLN
1	B	306	HIS
1	B	461	GLN
1	C	170	GLN
1	C	227	GLN
1	C	231	ASN
1	C	306	HIS
1	C	430	GLN
1	D	137	GLN
1	D	201	GLN
1	D	223	HIS
1	D	227	GLN
1	D	328	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 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 ⓘ

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, 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	513/584 (87%)	-0.63	6 (1%) 76 58	10, 29, 70, 241	0
1	B	513/584 (87%)	-0.57	7 (1%) 73 53	11, 34, 74, 202	0
1	C	513/584 (87%)	-0.52	6 (1%) 76 58	8, 32, 79, 156	0
1	D	513/584 (87%)	-0.50	5 (0%) 79 61	15, 36, 81, 168	0
All	All	2052/2336 (87%)	-0.55	24 (1%) 76 58	8, 33, 78, 241	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	290	PHE	4.6
1	C	134	ASP	4.3
1	B	164	ALA	3.9
1	B	40	GLY	3.9
1	D	134	ASP	3.9
1	C	545	GLU	3.6
1	A	134	ASP	3.4
1	B	290	PHE	3.4
1	A	292	HIS	3.2
1	D	544	LEU	3.1
1	B	41	LYS	3.1
1	A	291	ALA	2.8
1	B	292	HIS	2.8
1	C	164	ALA	2.7
1	D	291	ALA	2.6
1	C	544	LEU	2.4
1	A	289	ASP	2.3
1	B	291	ALA	2.3
1	D	42	ALA	2.2
1	A	133	THR	2.1
1	B	165	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	543	TYR	2.1
1	C	291	ALA	2.1
1	C	42	ALA	2.0

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.